

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:27 ; Search time 45 Seconds  
(without alignments)  
1592.513 Million cell updates/sec

Title: US-10-039-073-1  
Perfect score: 5052  
Sequence: 1 MFHSSAMVNSHRKPMFNIHR.....NIKWLXNLPRLTWLMVNT 960

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pdp:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pdp:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pdp:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pdp:\*  
5: /cgn2\_6/ptodata/1/1aa/ECTUS\_COMB.pdp:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	100.0	960	US-09-345-650-1	Sequence 1, Appli
2	2507.5	49.6	948	US-09-620-312D-1105	Sequence 1105, Ap
3	2027	40.1	1025	US-08-530-792D-23	Sequence 23, Appl
4	2016.5	39.9	1026	US-08-530-792D-22	Sequence 22, Appl
5	1444	28.6	957	US-09-949-016-6154	Sequence 6154, Ap
6	1440	28.5	964	US-09-949-016-7431	Sequence 7431, Ap
7	1264.5	25.0	967	US-09-139-802-201	Sequence 201, App
8	1264.5	25.0	967	US-09-659-786-201	Sequence 201, App
9	1125	24.2	919	US-09-919-039-222	Sequence 222, App
10	1165	23.1	977	US-08-335-844A-22	Sequence 22, Appl
11	1165	23.1	977	US-09-129-366-22	Sequence 22, Appl
12	1117	22.1	972	US-08-335-844A-24	Sequence 24, Appl
13	1117	22.1	972	US-09-129-366-24	Sequence 24, Appl
14	1100	21.8	972	US-08-335-844A-23	Sequence 23, Appl
15	1100	21.8	972	US-09-129-366-23	Sequence 23, Appl
16	1083	21.4	699	US-08-270-767-45507	Sequence 45507, A
17	986	19.5	593	US-08-637-670-38	Sequence 38, Appl
18	908	18.0	608	US-08-637-670-36	Sequence 36, Appl
19	884	17.5	850	US-09-902-540-10199	Sequence 10199, A
20	868	17.2	990	US-09-657-931A-11	Sequence 11, Appl
21	867	17.2	848	US-09-583-110-2738	Sequence 2738, Ap
22	863	17.1	995	US-09-657-931A-1	Sequence 1, Appli
23	844	16.7	815	US-09-107-433-5059	Sequence 5059, Ap
24	841.5	16.7	946	US-09-657-931A-10	Sequence 10, Appl
25	820	16.2	1009	US-09-657-931A-13	Sequence 13, Appl
26	818.5	16.2	986	US-09-657-931A-12	Sequence 12, Appl
27	785.5	15.5	942	US-09-657-931A-9	Sequence 9, Appli

28	711.5	14.1	616	4	US-08-637-670-26	Sequence 26, Appl
29	709	14.0	620	4	US-08-637-670-40	Sequence 40, Appl
30	693.5	13.7	616	4	US-08-637-670-28	Sequence 28, Appl
31	692.5	13.7	917	4	US-09-902-540-12845	Sequence 12845, A
32	679.5	13.5	923	4	US-09-328-352-4371	Sequence 4371, Ap
33	659	13.0	528	4	US-08-637-670-27	Sequence 27, Appl
34	647	12.8	912	4	US-09-902-540-16181	Sequence 16181, A
35	543	10.7	582	4	US-09-270-767-45532	Sequence 45532, A
36	482	9.5	386	4	US-08-637-670-24	Sequence 24, Appl
37	477.5	9.5	346	4	US-08-637-670-35	Sequence 35, Appl
38	466	9.2	362	4	US-08-637-670-37	Sequence 37, Appl
39	460.5	9.1	359	4	US-08-637-670-39	Sequence 39, Appl
40	459	9.1	350	4	US-08-637-670-39	Sequence 25, Appl
41	458	9.1	350	4	US-08-637-670-25	Sequence 25, Appl
42	440	8.7	680	4	US-09-902-540-11278	Sequence 11278, A
43	391	7.7	867	4	US-09-602-777A-104	Sequence 104, App
44	379.5	7.5	242	4	US-09-248-796A-18160	Sequence 18160, A
45	364.5	7.2	380	4	US-09-270-767-44186	Sequence 44186, A

ALIGNMENTS

RESULT 1

US-09-345-650-1  
; Sequence 1, Application US/09345650  
; Patent No. 6362324  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: 17867, A No. 6362324el Human Aminopeptidase  
; FILE REFERENCE: 5800-36  
; CURRENT APPLICATION NUMBER: US/09/345.650  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-345-650-1

Query Match	100.0%;	Score	5052;	DB	3;	Length	960;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	960;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MFHSSAMVNSHRKPMFNIHRGFCYCLTALPQICSOFSVPSSVYHFTEDPCAFPVATNGE	60				
Qy	61	RFPQQLRLPSVVIPLHYDLFVHPNLTSDFVASEKIEVLVSNATQFTILHKSOLLEITNA	120				
Db	61	RFPQQLRLPSVVIPLHYDLFVHPNLTSDFVASEKIEVLVSNATQFTILHKSOLLEITNA	120				
Qy	121	TLOSEDSRYMKPKGKELVLSYPAHEQIALVPEKLTPLHLYVYVAMDFOAKLGDGEGFY	180				
Db	121	TLOSEDSRYMKPKGKELVLSYPAHEQIALVPEKLTPLHLYVYVAMDFOAKLGDGEGFY	180				
Qy	181	KSTYRTLGGETRIILAVTDPEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPKVK	240				
Db	181	KSTYRTLGGETRIILAVTDPEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPKVK	240				
Qy	241	TIELEGGLEDHFFETTVKMSTYLVAIYVCDPFHSLSGFTSSGCVKSVIYASPKRNQTHVAL	300				
Db	241	TIELEGGLEDHFFETTVKMSTYLVAIYVCDPFHSLSGFTSSGCVKSVIYASPKRNQTHVAL	300				
Qy	301	QASLKLDFFYKYFDIYYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLPDPKTSASD	360				
Db	301	QASLKLDFFYKYFDIYYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLPDPKTSASD	360				
Qy	361	KLWTRVIAHSLAHQWFGNLTVMEMWMDIWLKEGFAKYMELIYVATYPELQFDDYFLNV	420				
Db	361	KLWTRVIAHSLAHQWFGNLTVMEMWMDIWLKEGFAKYMELIYVATYPELQFDDYFLNV	420				

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Qy 421 CFEVITKDSLSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGIQ 480
Db 421 CFEVITKDSLSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGIQ 480
Qy 481 YLKKFSYRNKNDLWSLSNCSLESFTSGVCHSDPKMTSNMLAFIAGENAEVKEWMTT 540
Db 481 YLKKFSYRNKNDLWSLSNCSLESFTSGVCHSDPKMTSNMLAFIAGENAEVKEWMTT 540
Qy 541 WTLOKGIPLLVVKQDGCSLRLOQRFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Db 541 WTLOKGIPLLVVKQDGCSLRLOQRFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Qy 601 HRHLKSKTDPLDPEKTSWVKFNVDNGYIIVHVEGHWDQLITQLNQNHLLRPKDRV 660
Db 601 HRHLKSKTDPLDPEKTSWVKFNVDNGYIIVHVEGHWDQLITQLNQNHLLRPKDRV 660
Qy 661 GLIHDVQLVAGRLTLDKALDMTYYLQHETSSPALLEGSLYLSFYHMDRRNISISE 720
Db 661 GLIHDVQLVAGRLTLDKALDMTYYLQHETSSPALLEGSLYLSFYHMDRRNISISE 720
Qy 721 NLKRYLQYFKPVIDRQSWSDKGSWDRMLRSALLKLACDLNHAPCIQKAAELFSQWMS 780
Db 721 NLKRYLQYFKPVIDRQSWSDKGSWDRMLRSALLKLACDLNHAPCIQKAAELFSQWMS 780
Qy 781 SGKLNIPDVLKIVYSGAQTACGNVYLLEQYELSSSAEQNKILYALSTSKHQELKL 840
Db 781 SGKLNIPDVLKIVYSGAQTACGNVYLLEQYELSSSAEQNKILYALSTSKHQELKL 840
Qy 841 IELGMEGVKIKTONLAALLHAIARRPKQQQLAMDVFRENWTHLLKXFDLGSYDIRMIISG 900
Db 841 IELGMEGVKIKTONLAALLHAIARRPKQQQLAMDVFRENWTHLLKXFDLGSYDIRMIISG 900
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RESULT 2

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US-09-620-312D-1105
; Sequence 1105, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Duxui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 1105
; LENGTH: 948
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-312D-1105

Query Match      49.6%; Score 2507.5; DB 4; Length 948;
Best Local Similarity 50.9%; Pred. No. 1.7e-230;
Matches 476; Conservative 173; Mismatches 268; Indels 19; Gaps 7;

Qy 23 YCLTALLPQICISQSPVSSYHFTDPGAFVATNGERPFPQELRLPSPVILPHYDLFV 82
Db 15 FLSSLLALTLV-----STPSWCQSTE---ASPKRSDGTPEPWNKIRLPEYVIPVHYD 67
Qy 83 HPNLTSLDFVASEKIEVLVSNATQFILHSKDEITNATLQSEDSRYMKPGKELKVL 142
Db 68 HANLTTLTGWTKTKVITASOPTSTIILASHHLQISRATLRKAGERLSE--EPQLVLEH 125
Qy 143 PAHEQIALLVPEKLTJPHLYKYVAMDFOAKLDGDFEGFYKSTYRTLGGETRILAVTD 202
Db 126 PQEQIALLAPEPLLVGLPYTVVIHVAGNLSETFHGFYKSTYRTKEGELRILASTQPE 185
Qy 203 QARMAPCPDEPLFKANFSIKIRRESRHIALSNMPKVKTIEGGLEDHPEFTVKNSTY 262
Db 186 AARMAPCPDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLTIEDHFDVTVK 245
Qy 263 LVAYIVCDPHSLSGFTSSGVKVSIVASPKRNOHYALQASLKLDFEYKVFDIYPLSK 322
Db 246 LVAFIISDFESVSKITKSGVKVSIVAVPKINQADYALDANVTLLLEFYEDYFIP 305
Qy 323 LDLIATIPDFAPGAWENGLITYRETSLLPDPKPTSSADKLWVTVRIAHELAHQWFG 382
Db 306 QDLAALIPDFOGAWENGLITYRETSLLPDPKPTSSADKLWVTVRIAHELAHQWFG 365
Qy 383 MEWMDIWLKEGAKYKWEIYVATYVPELOFDDYFLNVCFEVITKDSLSRSPISKAET 442
Db 366 MEWMDLWLNNEGFAKMEFVSVTHPELVKGVDFGKCFDANMEVDALNSHPVSTVE 425
Qy 443 PTQIQEMFDEVSYNKGACILNMLKDFLGEKFKOGIIQYLKCFSYRNKNDLWSLSNS 502
Db 426 PAQIREMFDVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKKNEDLW 485
Qy 503 CLESDFTSQ--GVCHSDPKMTSNMLAFIAGENAEVKEWMTTWTLOKGIPLLVVKQ 560
Db 486 C-PTDGVKGMGDFC-SRSQHSSSSSHHWQGVGVKTMNTWTTLQRGFPPLITIT 543
Qy 561 LQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVIHRLILKSKTDTLDPKTS 620
Db 544 MKOEHYNKG-----SDGAPDTGTLWHVPLTFTITSKDMVHRFLKTKTDVLILP 597
Qy 621 VKENVDSNGYIIVHVEGHGWDQLITQLNQNHLLRPKDRVGLIHDVQLVAGRLTLD 680
Db 598 IKENVGMNGYIIVHVEDDGDWDSLTGLLKGTHTAVSSNDRASLINNAFQLVSI 657
Qy 681 LDMTYYLQHETSSPALLEGSLYLSFYHMDRRNISIDISENLKRYLQYKPKVIDR 740
Db 658 LDLSLYLKHETEIMPVFOGLNELIPMYKLMKEKDMNEVEVTFQKAFILRLDLID 717
Qy 741 DKGSVMDRLRSALLKLACDLNHAPCIQKAAELFSQWMESSGKNLPTDVLKIVYS 800
Db 718 DEGSVSEQMLRSELLLLACVHNTPQCVQRAEGYFRKWKESNGNSLVPDVTLLAV 777
Qy 801 TTAGMNYLLEQYELSSSAEQNKILYALSTSKHQELKLILGMEGVKIKTONLAALL 860
Db 778 STEGMDFLYSKYQFSLSTESKSIQEFALCHTQNKELQLWLLDSSFKGDKIKT 837
Qy 861 AIARRPKGOOLAWDFVRENWTHLLKXFDLGSYDIRMIISGTTAHPFSKDKLOE 920
Db 838 LIGRNPVGYPLAWQFLRKWNKLVQKPELGSSSIAMHVMGTGNTQFSTRTRLEEV 897
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Db 898 LKENGSQLRCVQQTITETIENIGWMDKNFDKIRWL 933
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[illegible]

	Qy	234	SNMPKVTIELEGGLEDHFEHTVVMSTYLVAYIVCDPHSLSGFTSSGVKVSYASPKR	239
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	Qy	294	NOTHYALQASLKLLDFEYKYFDIYYPLSKLDLIAIPDFAFGAMENWGLITTYRETSLLFPD	353
	Dd	388	DQYVHALDTTVKLLEYQNYFIOYPLKLDLVALPDFAENGAMENWGLITTFREETLYDN	447
	Qy	354	KTSSASDKLWTRVIAHELAHQFNGLVTMEWNNDIWLKEGPAKYMELIANVATPELOF	413
	Dd	448	ATSSVADRKLVTIKIAHELAHQFNGLVTMQWMDNLWLNNEGFAFMESVEKIFKELNS	507
	Qy	414	DYFLNVCPEVITKDSINSRPISKPAPETPTIOEMFDEVSNKGACILANMLKDPLGEER	473
	Dd	508	YEDFLDARFKTKRKDSINSHPISSVSQSSEIQEIEMFDSLSPFKGASLLMLKSYLSEDV	567
	Qy	474	FOKGIIOYLKFSYNRAKNDDLWSLSNCSLESPTSFGVCHSDPKMTSMNLAFLGENAE	533
	Dd	568	FQAIIILYHNHSYAAIQSDDLWDSFNE-----VTGKTJLD	602
	Qy	534	VKEMMTTWTLQKIGIPLLVVVKDCGSLRLQOERFLOGVFOEDPEWRALQERYLWHIPTYS	593
	Dd	603	VKOMKMTWTLOXGFPLVTVQRKGTELLQOERFFPSM---QPEIQSDSTSLHWHPISYV	659
	Qy	594	TSSSNVIHRH---ILKSKTDITDLPEKTSWKFVNDSNGYIIVHYEGHCWDOLITQLNQ	650
	Dd	660	TGRNYSYRSVSLDDKKSDVINLTEQOVQMVNTMTGYIIVHYAHDGWAALINQLKR	719
	Qy	651	HTLRPKDRVLIDHVOLFVGAGRLTLDKALDMTYILOHETSPPALLEGLSYLESFYHM	710
	Dd	720	PVYLSDKDRANLINIFELAGLGKVPLOMAFLDIYLRNETHTAPTITEALFOTDLIYNL	779
	Qy	711	DRNRISDISENLRYLLOYFKPVDIRQSWDSKRGSVMDRLMRSLALKLACLADNHAPCI	770
	Dd	780	EKLGHMDLSRLVTRVHKLLONQIQOQTWDTGSFMRSLRSALLEFACAHSLENTTWA	839
	Qy	771	AELFSQMSSSGKLNIPDVLKIVYSGAQTTAGNNYILLEQVELSMSSAEQNKILYALST	830
	Dd	840	TKLFDCGWASNGTQSLPTDVTTPVKVGARTKGMFLFPMYSMSGSAEKKILEALAS	899
	Qy	831	SKHOEKLKLLIELMGEGKVIKTONLAALLHAIRBPQQOQLAWDFVRNETHLLKKFDLG	890
	Dd	900	SADAHKLWLMKSSLDGDIIRTOKUSLIIRTVGROPPGHLLAWDPVKENWNKLVHKPHLG	959
	Qy	891	SYDIRMIISGTTAHPSSKDKLOEVKLPFESBAQSHLDIFOTVLETITPKNKWLEKNLP	950
	Dd	960	SYTIQSIIVAGSTHLFSTKTHLSEVOEFFENQSEATLQRCVQEAFEVIELNQWARNLK	101
	Qy	951	TURTWL 956	
	Dd	1020	TUTLWL 1025	
			RESULT 4	
			US-08-530-792D-22	
			; Sequence 22, Application US/08530792D	
			; Patent No. 5972680	
			; GENERAL INFORMATION:	
			; APPLICANT: Knowles, W. J.; Guralaki, D.; Haigh, W.; Letsinger, J. T.;	
			; APPLICANT: Clairmont, K.; and Hart, J.	
			; TITLE OF INVENTION: Glucose Transporter Vesicle Aminopeptidase	
			; NUMBER OF SEQUENCES: 23	
			; CORRESPONDENCE ADDRESS:	
			; ADDRESSEE: Bayer Corporation	
			; STREET: 400 Morgan Lane	
			; CITY: West Haven	
			; STATE: Connecticut	
			; COUNTRY: U.S.A.	
			; ZIP: 06516	
			; COMPUTER READABLE FORM:	
			; MEDIUM TYPE: 3.5" diskette, 1.44 Mb Storage	
			; COMPUTER: Dell Windows 95 PC	
			; OPERATING SYSTEM: Windows 95	
			; SOFTWARE: WordPerfect for Windows 6.1	
			; CURRENT APPLICATION DATA:	
			; APPLICATION NUMBER: US/08/530,792D	
			; FILING DATE: 09/19/95	
			; CLASSIFICATION: 435	
			; PRIOR APPLICATION DATA:	
			; APPLICATION NUMBER: 08/309,232	
			; FILING DATE: 09/20/94	
			; ATTORNEY/AGENT INFORMATION:	
			; NAME: Brewer, Alice A.	
			; REGISTRATION NUMBER: 32888	
			; REFERENCE/DOCKET NUMBER: MMH 323P1	
			; TELECOMMUNICATION INFORMATION:	
			; TELEPHONE: (203) 812-2705	
			; TELEFAX: (203) 812-5492	
			; INFORMATION FOR SEQ ID NO: 23:	
			; SEQUENCE CHARACTERISTICS:	
			; LENGTH: 1025 amino acids	
			; TYPE: amino acid	
			; STRANDEDNESS: single	
			; TOPOLOGY: linear	
			; MOLECULE TYPE: protein;	
			; ORIGINAL SOURCE:	
			; ORGANISM: Rattus norvegicus	
			; STRAIN: Sprague-Dawley	
			; DEVELOPMENTAL STAGE: adult	
			; TISSUE TYPE: skeletal muscle	
			; IMMEDIATE SOURCE:	
			; LIBRARY: Clontech rat skeletal muscle cDNA library in lambda	
			; LIBRARY: gt11 and mRNA isolated from rat skeletal muscle	
			; CLONE: 12.1 (from lambda gt11 library), PCR product clones 5,	
			; CLONE: 334, and KC44.	
			; FEATURE:	
			; NAME/KEY: complete amino acid sequence for GTvap, long version	
			; IDENTIFICATION METHOD: translation from cDNA	
			US-08-530-792D-23	
			Query Match 40.1%; Score 2027; DB 2; Length 1025;	
			Best Local Similarity 44.4%; Pred. No. 2.2e-184;	
			Matches 402; Conservative 158; Mismatches 310; Indels 36; Gaps 5;	
	Qy	54	PVATNGERPWOBLRPSVVIPLDYHFLVHPNLTSLDVFASEKIEVLVSNAQTQIILHSK	113
	Dd	153	PLATNGKVPFMAQIRLPTAILIQRVELSHPNLTSMTRGVSITSLQALQDTRIILLST	212
	Qy	114	LLEITNATLOSSEDSRYMKPGKELKVLSPYAHEQIALLVPEKLPKLYKYVAMPQAKLG	173
	Dd	213	GHNISVTPMSAVSQ----EQKVEILEYPYHEQIAVAVPESLLTGHNLTKEISANIS	26





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Db 560 TLSQEHFLL-----DPDSNVTRPSEFNYYWVWPITTSIRDRGQQQDYWLIDVRAQNDFLST 614
Qy 595 SSSNVHRLKSKTDTLDLPEKTSWVKFVDSNGYIYVHYEGHGWDLITOLNQHLL 654
Db 615 SGN-----EWLLNLNVGTGYRVNYDEENWRKIOTQLQRDSAI 653
Qy 655 RPKDRVGLIHDVOLFVAGRLTLDKALDMTYIYLQHETSSPALLEGLSYLSFYHMDRRN 714
Db 654 PVINRAQIINDANFLASAHKVPVTLALNNTLFLIEERQYMPWEAALSLSLKFMLPDR-- 711
Qy 715 ISDISENKRYLLOQYFKPVI-----DRQSWSD-KGSVMDRLMSALLKJACDLNHPAICQ 768
Db 712 -SEVYGPKNYLLKKQVTPLEFIHFRNNTNNRREIPENLMDQYSEVNAISTACSNVPCEB 770
Qy 769 KAAELFSQWMESSKLNIPDVLKIVY--SVGAQTAGNYYLLEOYELSMSSAFONKILY 826
Db 771 MVSGLFKQWENNNNNPIHNLRSVTVYCNIAOGBEEBDFAWGQFNATLVNEADKLRA 830
Qy 827 ALSTSKHQEKLKLLIELGMEGVKIKTONLAALHAIARRPKGQOLAWDFVRENWTHLLKK 886
Db 831 ALACSKELWILNRYLSYTLNPDILRKQDATSTIISITNNVIGQGLVWDFVQSNWKKLPND 890
Qy 887 FDLGSYDIRMIIISGTTAHFSKDKQLQVKLPFFSLEAQ--GSHLDIPQTVLETTIKNIKW 944
Db 891 YGGGFSFSLNLIQAVTRRFSTEYELQLEQFKDNEETGFGSGTRALEQALEKTKANIKW 950
Qy 945 LEKNLPTLRTLMVNT 960
Db 951 VKENKEVVLQWFTENS 966

RESULT 8
US-09-659-786-201
; Sequence 201, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-659-786-201

Query Match 25.0%; Score 1264.5; DB 4; Length 967;
Best Local Similarity 31.4%; Pred. No. 2.2e-111;
Matches 325; Conservative 158; Mismatches 386; Indels 167; Gaps 26;

Qy 20 RGFYCLTAI-----LPOICICQSFSPSSYHFTEDPGAPFA----- 56
Db 3 KGFYISKSLGILGLGVAACVCTIIALSVVYSQEKKNANSSPVASTTPSASATTNPASA 62
Qy 57 -TNGERFPWQELRLPSVVPIPLHYDLFVHPNLTSLD-----FVASEKIEVLVSNATQFIIL 110
Db 63 TTLQSKAWNRNRYLPLNTLKPDSYQVTLRPYLTPNDRGLYVPKGSSTVRFCKEATDVIII 122
Qy 111 HSKOLETNTATLQSEEDSRMYKPKGKELKVLSY-----PAHEQIALLVP-EKLTPHLK--- 161
Db 123 HSKKLVNT-----LSQHRVVLRGVSGSQPPDIDKTELVBFTYLVVHLKGS 170
Qy 162 -----YVAMDFQALGDFGFGYKSTVTLGGSTRILAVTDFTPTQARMAFFCFDEPLF 216
Db 171 VKDSQYEMDSFEGELADDLAGFYRSEYME-GNVRKVAVTQQAADARKSFPCFDEPAM 229
Qy 217 KANFSIKIRRESRHIALSNM-PKVKTIELEGGLLED-----HPETTVKMSYLVAVIVC 269
Db 230 KAEFNITLIHPKDLTALSMLPKGPSTPLP-----EDPNWNVTEPHTTPKMSYLLAFIVS 285
Qy 270 DFHLSLGSFTSSGVKVSIVASPKDNQTH--YALQASLKLLDFYEKYEDIYVPLSKDLIA 327
Db 286 EFDYVEKQASNGVLIRIWARPSAIAAGHDYALMNTGPILNFFAGHYDTPYLPKSOIG 345
Qy 328 IPDPFAPGAMENGLITYRETSLLPDKPTSSASDKLWTRVIAHSLAHQWFGNLTVMSEWN 387
Db 346 LPDFNAGAMENGLVITYRENSLLDFPLSSSSNKERVVTVIAHSLAHQWFGNLTVMSEWN 405
Qy 388 DIWLKKEGAKWELIANNVATYPELOFDYF-LNVCFEVITKDSLNSRSPISKPA---ETP 443
Db 406 DLWLNEGPASVVEYLGAADYAEPTWNLDMLVNDVYRMAVDALASSHPLSTPASEINTP 465
Qy 444 TOIQEMFDEVSYNGACILANMLKDFLGEKFKGIIOLYLLKFSYRNAKNDDLASSL----- 499
Db 466 AQISELFDALSYSKGASVLRMLSLFSEDVPKQGLASLYHTFAYONTIYLNLDHLOEAV 525
Qy 500 SNSCLESDFTSGGVCHSDPKMTSNMLAFNGENASVKEMTWTTLQKGIPLLVKQDCSL 559
Db 526 NRSIQLPTT-----VRDIMNRWTLQMGFPVITV--DFSTG 559
Qy 560 RLQOERFLOGVQEDPE-----WRAQERYLWHIPLT-----YST 594
Db 594
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Db 171 VKDSQYEMDSEPEGLADDLAGFYRSEYME-GNVRKVATTQMQAADARKFPCCDEPAM 229
Qy 217 KANFIFIKIRRESRHIALSNM-PKVTIIELEGGLD-----HFETTVMSTYLVAYIVC 269
Db 230 KAEFNITLIHPKDLTALSNMLPKGSTLP-----EDPNWNTFHTTTPKMTYLLAFIVS 285
Qy 270 DPHLSUGFTSSGVKSVIIVASDPKRNQTH--YALQASLKLDFYKYFYIYVPLSKLDLIA 327
Db 286 EFDYVEKQASNGVLIIRIWARPSAIAAGHGDYALNVTGPIILNFFAGHYDTPYLPKSDQIG 345
Qy 328 IPDFAPGAMENWGLTYRETSLLDPKTSASDKLWTRVIAHELAWHGFNLVMTMKN 387
Db 346 LPDFNAGAMENWGLTYRENSLLFPKSSSSNKERVVTVIAHELAWHGFNLVMTMKN 405
Qy 388 DIWLKEGFAKYMELTAVNATPELODDYF-LNVCFEVTIKDLSNRRPISKPA---ETP 443
Db 406 DLWLNNEGFAVVEYLGADYAEFTWNLKDLWLVNDVYRVWAVDALASSHPLSTPASEINTP 465
Qy 444 TQIQEMFDEVSNKGACILNMLKDFLBEKFKQGIQYIKKFSYRNKNDLWSSL----- 499
Db 466 AQISLFLDAISYKSGASVLRMLSSFLSDVFKGLASYLHTPAYQNTIYLNLDHLEAV 525
Qy 500 SNSCLESFTSGVCHSDPKMTSNMLAFLGENAEVKNMTWTLOKGIPLLVKODGCSL 559
Db 526 NNRSTQLPTT-----VRDIMNRWTLQMGPFVITV--DTSTG 559
Qy 560 RLQQRERFLQGVQEDPE---WRALQERYLWHIPLT-----YST 594
Db 560 TLSQEHFLL-----DPDSNVTRPSEFNVMVPIITSIRGROQOQDYMLDVRAQNDFST 614
Qy 595 SSSNVHHRHILKSDTDLDPKTSWVKFNVDNGYIYVHVEGHGWDLITQLNQNHTLL 654
Db 615 SGN-----EWLLNLNVTYGYRVNVDENNRKIQTLQQRDHSAI 653
Qy 655 RPKDRVGLIHDVQLVGAGRLTLDKALDMTYYLQHETSSPALLEGSLYLSFYHMMDRN 714
Db 654 PVINRAQIINDAFNLASAKHVPVTLANTLFLIEERQYMPWEAALSSLYFKLMFDR-- 711
Qy 715 LDISENLKYLLQYFKPVI-----DROSVD-KGSVDRMLRSALLKLACDLNHAPCIQ 768
Db 712 -SEVYGPKNVYLKKQVTLFLHFRNTNNWREIPENLMDQYSEVNAISTAANGVPECEE 770
Qy 769 KAAELFSQWMESSGKLNITPDLVKIY--SVGAQTAGNYYLLEQYELSMSSAEQNKILY 826
Db 771 MVSGFLFKQWENPNPNPIHPNLRSTVYCNATAGGEEEDFAWEQFRNATLVNEADKLRA 830
Qy 827 ALSTSKHQEKLKLIELGHEGKVIKTONLAALLHAIARRPKQOQLAWDFVRENWTHLKK 886
Db 831 ALACSKELWILNRYLSYTLNPLIRKODATSTIISITNNVIGQGLVWDFVQSNKKLPND 890
Qy 887 FDLGSDIRMIISGTTAHFSSKDLQEVKLPFESLEAQ--GSHLDIFOTVLETTIKNIKW 944
Db 891 YGGGSFSSNLQIQTAFRPFSTFYEYELQLEQFKQKNEETGFGSGTTRALEQALEKTKANIKW 950
Qy 945 LEKNLPTLRTWLMVNT 960
Db 951 VKENKEVVQLWFTENS 966
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## RESULT 9

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US-09-919-039-222
; Sequence 222, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
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; SOFTWARE: PERL Program
; SEQ ID NO 222
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 2278688CD1
US-09-919-039-222
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## Query Match 24.2%; Score 1225; DB 4; Length 919;

Best Local Similarity 32.6%; Pred. No. 1.2e-107; Indels 126; Gaps 26;  
Matches 309; Conservative 163; Mismatches 351;

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Qy 55 VATNGERFPQBELRPSVVIPLHYDLFVHPNLTSLDFVASEKIEVL--VSNATOFILHLS 112
Db 42 LAAMPEKRPPE--RLPADVSPINCSLCKPDL--LDFTFECKLEAAQVRQATNQIVMNC 97
Qy 113 KDLBITNATLOSSEDSRYMKPG-----KELKVLSYPAHEQIALLVPEKLTPLHLYYYAM 166
Db 98 ADIDIITASYAPEGBDEBIHATGFYQNEDEKVTLSFPSTLQTG-----TGTLK----I 146
Qy 167 DFOAKLGDGPEGFYKSTVRLTGGETRILAVTDFPTOARMAPPDCEPLFKANFSIKIRR 226
Db 147 DFCVELNDKMGFVRSKYTTSPSGEVRYAANTQFATDARRAFPCWDEPAIKATPDISLVV 206
Qy 227 ESRHIALSNMPKV--KTIELEGGLEDHFETTVKMYSTYLVAYIVCDFHSLSGFTSSGVKV 284
Db 207 PKDRVALSNMVIDRKVPDDENLVEVKFARTVMYSTYLVAVVGEYDFVETRSKDGVCV 266
Qy 285 SIYASPKRKNOTHYALQASLKLDFYKYFYIYVPLSKLDLIAIPDFAPGAMENWGLTY 344
Db 267 RVYTPVGKAEQGFALVAAKTLFPYKDYFNVPYPLPKIDILIAIADFAAGAMENWGLVTV 326
Qy 345 RETSLLLDPKTSASDKLWTRVIAHELAWHGFNLVMTMKNWDLWLKEGFAKYMELIAY 404
Db 327 RETALLDIPKNSCSSRQWVALVGHLELAWHGFNLVMTMKNWTHLWLNNEGFAWIEYLVCV 386
Qy 405 NATYPELQFDDYFLNVCFEVTIK--DSLNSRRPISKPAETPTQIQEMFDEVSNKGACILN 463
Db 387 DHCPEYDIWTFVYSADYVTRAQELDALDNSHPIEVSVGHPSEVDIEIFDAISYKSGASVIR 446
Qy 464 MLKDFLEBEKFKGIIQYIKKFSYRNKNDLWLSNLSNLSLESFTSGVCHSDPKMTSN 523
Db 447 MLHDYIGDKDFKGMNMYLTKFOOKNAATEDLWESLENA----- 485
Qy 524 MLAFLGENAEVKNMTWTLOKGIPLLVK--QDGCRLRLOQBERFLOQ---VFQEDPE 576
Db 486 -----SGKPIAAVNTWTQMGFFLIYVEAEQVEDDLRLSLQKFCAGSYVGEDCPQ 539
Qy 577 WRALQERYLWHIPLTYSTSSS-NVIHRHILKSDT---TLDLPEKTSWVKFNVDNGYII 632
Db 540 WM-----VPITISTSEDPNQAKLILMDKPEMNVVLKNVCPDQWVKLNLGTGVFYR 590
Qy 633 VHYEGHGDQILITQLNQNHTLLRPKDRVGLIHDVQLVGAGRLTLDKALDMTYYLQHETS 692
Db 591 TQYSSAMLESLLPGIRD--LSLPEVDRLGLQNDLFLSARAGII----- 631
Qy 693 SPALLEGSLYLSFYHMMDRNIDIS------ENLKRYLLQYFKPVIDR 736
Db 632 --STVEYKWNFAFVNEPNYTVWSDLSNLSLSTLSHTDFYBEIQFVKDVFSPIGER 689
Qy 737 QSWSDK--GSVMDRLRSALLKLACDLNHAPCIQKAAELFSQWMESSGKLNITPDLVKI 793
Db 690 LGWDPKPEGHL--DALLRGLVLGKLGAGHAKATLEEARRRPKDHVE--GKQILSADLRSP 746
Qy 794 VYSV----GAQTAGNYYLLEQYELSMSSAEQNKILYALSTSKHQEKLKLIELGMEKV 849
Db 747 VYLTVLKHGDOGTTL--DIMLKLHKQADMQEBEKNRIERVGLGATLPLDLTKQLVLTALSSEV 804
Qy 850 IKTONLAALLHAIARRPK-GOQLAWDFVRENWTHLKKFGLDGSYDIRMIISGTTAHFSSK 908
Db 805 -RPQDTVSVIGGVAGGSKHGRKAANKFIKDNWEELYNRYQ--GGFLISRLIKLSVEGFAVD 862
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Db      831 KDFRLALGCHKDVTKALLGLLRALDRNSSFVFMQDIPSAFNVDVAANPIGEEEIFNLE 890
QY      879 NWTLLKCFDLGSDYIRMIISGTTAHHFSSKDKLQEVKLFESLEAQSH---LDIFQTVL 935
Db      891 RWPDIIESIGTKHTYEVKIPACTSGIRSQQIDQLK---NLQKNGMNAQFGAFDKAI 946
QY      936 ETTIKNIKWLKKNLPTL 952
Db      947 ERAQNRVDWIKKHFKL 963

RESULT 13
US-09-129-366-24
; Sequence 24, Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATI
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/129,366
; FILING DATE: 05-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,844
; FILING DATE: 09-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-241A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-129-366-24

Query Match 22.1%; Score 1117; DB 4; Length 972;
Best Local Similarity 28.6%; Pred. No. 3e-97;
Matches 279; Conservative 199; Mismatches 391; Indels 108; Gaps 25;

QY      39 SVPSSTVHFT-----EDPGA-----FVATNGERFPQQLPSVITPLHYDLF 81
Db      32 SIGLYFTFRKAFTDEKPGDKDTGGKKDKNSPSAA-----ELLPPNKRPLSYDLT 83

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Db 583 VPLWYQEGNSKEVKTWLRKDEPLVNLVNNRDTSLVNNADRHGFRQNYDANGWKKI1KQ 642

QY 647 LNQNTLRLPKDORVGLIHDVOLFVAGRLTLDKALDMTYYLQHE----- 690

Db 643 LKKDHKVFGRTRNAIISDAFAAATIDAIDYETVFELLEYAKNEBEFLPWKEALSGMFAV 702

QY 691 -----TSSPALLEGSLYESFYHMDRRNISDISENKRYLLQYFKPVIDRQSWSDK 742

Db 703 LKEFGNEPETKPARAYMMSILEPMY-----NKSSIDYIVKYNLDDTLFTKINTQ----- 751

QY 743 GSWDRMLRSALLKLACDLNHAFCIQKAAELF-SQWMESSGKLNIPDVLKI-----V 794

Db 752 -----KDIDAYCSLGSKDCIKQYKDI FYDEVMPKCKAGEAATKCVKVSAPLRANV 802

QY 795 YSVGAQTAGWN-----YLLEQVELSMSSAEQNKILYALSTSKHQEKLKLI--ELG 844

Db 803 YCYGVQ-EGGEAEFEKVMGLYLAEDVQL-----EKGILFKALACHKDVTKALKELLRALD 856

QY 845 MEGKVIKTONLAALLHAIARRPKGOQLAWDPVRENWTHLLKKFDLGSYDIRMIIISGTTAH 904

Db 857 RKSSFVRLQDVPTAFRAVSENVPVGEFNFILMERWEEITASLETEHRAVDKVGACCTG 916

QY 905 FSSKDKLOEVKLFESLEAQGSHLDIFQTVLETITKNIKWLEKNLPTL 952

Db 917 IRSQQIIDQLK-NLQNNNAQAKKFGSPTQEIKEGHEKIAWIKKHFRHL 963

Search completed: September 26, 2005, 06:11:24  
Job time : 49 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:27 ; Search time 1880 Seconds  
(without alignments)  
207.843 Million cell updates/sec

Title: US-10-039-073-1  
Perfect score: 5052  
Sequence: 1 MFHSSAMVNSHRKPMFNHR.....NIKMLEKNLPTLTWLMVNT 960

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	100.0	960	13 US-10-039-073-1	Sequence 1, Appli
2	5052	100.0	960	14 US-10-168-475-6	Sequence 6, Appli
3	4141	82.0	785	15 US-10-363-616-459	Sequence 459, App
4	3799	75.2	728	9 US-09-764-853-646	Sequence 646, App
5	3770	74.6	722	9 US-09-764-853-819	Sequence 819, App
6	2516.5	49.8	941	15 US-10-220-443-2	Sequence 2, Appli
7	2515.5	49.8	941	15 US-10-264-237-2723	Sequence 2723, Ap
8	2515.5	49.8	941	18 US-10-472-533-329	Sequence 329, App
9	2515.5	49.8	944	14 US-10-106-698-6381	Sequence 6381, Ap
10	2512.5	49.7	941	9 US-09-989-722-353	Sequence 353, App
11	2512.5	49.7	941	9 US-09-989-723-353	Sequence 353, App

12	2512.5	49.7	941	9	US-09-989-279-353	Sequence 353, App
13	2512.5	49.7	941	9	US-09-989-721-353	Sequence 353, App
14	2512.5	49.7	941	9	US-09-989-731-353	Sequence 353, App
15	2512.5	49.7	941	9	US-09-989-732-353	Sequence 353, App
16	2512.5	49.7	941	9	US-09-991-073-353	Sequence 353, App
17	2512.5	49.7	941	9	US-09-990-442-353	Sequence 353, App
18	2512.5	49.7	941	9	US-09-991-163-353	Sequence 353, App
19	2512.5	49.7	941	9	US-09-993-604-353	Sequence 353, App
20	2512.5	49.7	941	9	US-09-990-456-353	Sequence 353, App
21	2512.5	49.7	941	9	US-09-989-721-353	Sequence 353, App
22	2512.5	49.7	941	9	US-09-992-598-353	Sequence 353, App
23	2512.5	49.7	941	9	US-09-989-293A-353	Sequence 353, App
24	2512.5	49.7	941	9	US-09-989-735-353	Sequence 353, App
25	2512.5	49.7	941	9	US-09-990-444-353	Sequence 353, App
26	2512.5	49.7	941	9	US-09-991-181-353	Sequence 353, App
27	2512.5	49.7	941	9	US-09-989-730-353	Sequence 353, App
28	2512.5	49.7	941	9	US-09-990-436-353	Sequence 353, App
29	2512.5	49.7	941	9	US-09-993-687-353	Sequence 353, App
30	2512.5	49.7	941	10	US-09-989-724-353	Sequence 353, App
31	2512.5	49.7	941	10	US-09-997-666-353	Sequence 353, App
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33	2512.5	49.7	941	10	US-09-989-728-353	Sequence 353, App
34	2512.5	49.7	941	10	US-09-990-441-353	Sequence 353, App
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36	2512.5	49.7	941	10	US-09-997-428-353	Sequence 353, App
37	2512.5	49.7	941	10	US-09-997-666-353	Sequence 353, App
38	2512.5	49.7	941	10	US-09-990-438-353	Sequence 353, App
39	2512.5	49.7	941	10	US-09-990-562-353	Sequence 353, App
40	2512.5	49.7	941	10	US-09-990-711-353	Sequence 353, App
41	2512.5	49.7	941	10	US-09-989-726-353	Sequence 353, App
42	2512.5	49.7	941	10	US-09-998-156-353	Sequence 353, App
43	2512.5	49.7	941	10	US-09-990-437-353	Sequence 353, App
44	2512.5	49.7	941	10	US-09-991-157-353	Sequence 353, App
45	2512.5	49.7	941	10	US-09-997-514-353	Sequence 353, App

ALIGNMENTS

RESULT 1  
US-10-039-073-1  
; Sequence 1, Application US/10039073  
; Publication No. US20020098177A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; TITLE OF INVENTION: 17867, A No. US20020098177A1el Human Aminopeptidase  
; FILE REFERENCE: 35800/240749(5800-36  
; CURRENT APPLICATION NUMBER: US/10/039,073  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 09/345,650  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-039-073-1

Query Match	100.0%	Score	5052;	DB	13;	Length	960;
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Matches	960;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	61	RFPQQLRLPSVWIPHYDLFVHPNLSLDFVASEKIEVLVSNATQFIILHSKDLITNA	120				
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Db 121 TLQSEEDSRYPKPGKELKVLSPYAHEQIALLVPEKLTPLHKYVYVAMDFQAKLGDGFGFY 180
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Db 181 KSTVRTLGGETRIILAVTDPEFTQARMAPPCDEPLFKANFISIKIRRESRHIALSNMPKVK 240
Qy 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASPDKNQTHYAL 300
Db 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASPDKNQTHYAL 300
Qy 301 QASLKLDLFYKFDIYIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLFPDKPTSSASD 360
Db 301 QASLKLDLFYKFDIYIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLFPDKPTSSASD 360
Qy 361 KLWVTRVIAHSLAHQWFGNLTVMEMWNDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 420
Db 361 KLWVTRVIAHSLAHQWFGNLTVMEMWNDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 420
Qy 421 CFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIIQ 480
Db 421 CFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIIQ 480
Qy 481 YLKKFSYRNAKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMLAFIGENAEVKEWMTT 540
Db 481 YLKKFSYRNAKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMLAFIGENAEVKEWMTT 540
Qy 541 WTLOKGIPLLVVKQDGCRLRLOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Db 541 WTLOKGIPLLVVKQDGCRLRLOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Qy 601 HRHLKSKTDTLDLPEKTSWVKFNVDNSGYIYVHVEGHWQDLITQLNQHTLLRPKDRV 660
Db 601 HRHLKSKTDTLDLPEKTSWVKFNVDNSGYIYVHVEGHWQDLITQLNQHTLLRPKDRV 660
Qy 661 GLIHDVQLVAGRLTLDKALDMTYIYLQHETSSPALLEGSLYESFYHMDRRNISDI 720
Db 661 GLIHDVQLVAGRLTLDKALDMTYIYLQHETSSPALLEGSLYESFYHMDRRNISDI 720
Qy 721 NLKRYLLOQFKPVTDROSWSKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Db 721 NLKRYLLOQFKPVTDROSWSKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS 780
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RESULT 2

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US-10-168-425-6
; Sequence 6, Application US/10168425
; Publication No. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junning
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Darniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
```

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; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
; PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124706A1 60116897CD1
US-10-168-425-6
```

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Query Match 100.0%; Score 5052; DB 14; Length 960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFHSSAMVNSHRKPMENIHRGFYCLTAILPOICICSOFSVPSSVYHFTEDPGAPVATNGE 60
Db 1 MFHSSAMVNSHRKPMENIHRGFYCLTAILPOICICSOFSVPSSVYHFTEDPGAPVATNGE 60
Qy 61 RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQPIILHSHKDLITNA 120
Db 61 RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQPIILHSHKDLITNA 120
Qy 121 TLQSEEDSRYPKPGKELKVLSPYAHEQIALLVPEKLTPLHKYVYVAMDFQAKLGDGFGFY 180
Db 121 TLQSEEDSRYPKPGKELKVLSPYAHEQIALLVPEKLTPLHKYVYVAMDFQAKLGDGFGFY 180
Qy 181 KSTVRTLGGETRIILAVTDPEFTQARMAPPCDEPLFKANFISIKIRRESRHIALSNMPKVK 240
Db 181 KSTVRTLGGETRIILAVTDPEFTQARMAPPCDEPLFKANFISIKIRRESRHIALSNMPKVK 240
Qy 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASPDKNQTHYAL 300
Db 241 TIELEGGLEDHFFETTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVASPDKNQTHYAL 300
Qy 301 QASLKLDLFYKFDIYIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLFPDKPTSSASD 360
Db 301 QASLKLDLFYKFDIYIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLFPDKPTSSASD 360
Qy 361 KLWVTRVIAHSLAHQWFGNLTVMEMWNDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 420
Db 361 KLWVTRVIAHSLAHQWFGNLTVMEMWNDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 420
Qy 421 CFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIIQ 480
Db 421 CFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIIQ 480
Qy 481 YLKKFSYRNAKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMLAFIGENAEVKEWMTT 540
Db 481 YLKKFSYRNAKNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMLAFIGENAEVKEWMTT 540
Qy 541 WTLOKGIPLLVVKQDGCRLRLOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Db 541 WTLOKGIPLLVVKQDGCRLRLOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSNVI 600
Qy 601 HRHLKSKTDTLDLPEKTSWVKFNVDNSGYIYVHVEGHWQDLITQLNQHTLLRPKDRV 660
Db 601 HRHLKSKTDTLDLPEKTSWVKFNVDNSGYIYVHVEGHWQDLITQLNQHTLLRPKDRV 660
Qy 661 GLIHDVQLVAGRLTLDKALDMTYIYLQHETSSPALLEGSLYESFYHMDRRNISDI 720
Db 661 GLIHDVQLVAGRLTLDKALDMTYIYLQHETSSPALLEGSLYESFYHMDRRNISDI 720
Qy 721 NLKRYLLOQFKPVTDROSWSKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS 780
Db 721 NLKRYLLOQFKPVTDROSWSKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS 780
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QY 781 SGKLNPTDVLKIVSVGAQTAGWNYYLLEQVELSMSSABQNKILYALYSTSHQKBLKL 840
DB 781 SGKLNPTDVLKIVSVGAQTAGWNYYLLEQVELSMSSAEQNKILYALYSTSHQKBLKL 840
QY 841 IELHMEGKVIKTONLAALHAJARPKGOOLAWDFVRENWTHLLKKFDLGSYDIRMIISG 900
DB 841 IELHMEGKVIKTONLAALHAJARPKGOOLAWDFVRENWTHLLKKFDLGSYDIRMIISG 900
QY 901 TTAHFSSKDKLQEVKLFPFESLAQGSGLDIFQTVLETTIKNIKLEKNLPTLRWLWNT 960
DB 901 TTAHFSSKDKLQEVKLFPFESLAQGSGLDIFQTVLETTIKNIKLEKNLPTLRWLWNT 960

RESULT 3
US-10-363-616-459
; Sequence 459, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 459
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-459

Query Match 82.0%; Score 4141; DB 15; Length 785;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 782; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFHSSAMVNSHRKPMFNIHRGFCYCTAILPQICISQFSVPSSYHFTDPGAPPVATNGE 60
DB 1 MFHSSAMVNSHRKPMFNIHRGFCYCTAILPQICISQFSVPSSYHFTDPGAPPVATNGE 60
QY 61 RPPMOELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSKOLEITNA 120
DB 61 RPPMOELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSKOLEITNA 120
QY 121 TIQSEEDSRKMPGKELKLSYPAHEQIALLVPEKLTPLHKLYVAMDFOAKLGDGFEFGY 180
DB 121 TIQSEEDSRKMPGKELKLSYPAHEQIALLVPEKLTPLHKLYVAMDFOAKLGDGFEFGY 180
QY 181 KSTYRTLGGETRILAVTDPEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK 240
DB 181 KSTYRTLGGETRILAVTDPEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK 240
QY 241 TIEEGGLLEDFHFTTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVYASPKRKNQTHYAL 300
DB 241 TIEEGGLLEDFHFTTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVYASPKRKNQTHYAL 300
QY 301 QASLKLLDPYEKYFDIYYPPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSASD 360
DB 301 QASLKLLDPYEKYFDIYYPPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSASD 360
QY 361 KLWTVTRVIAHELAHQWFGNLTVMWNNDIWLKEGPAKYMELIAVNATYPELQFDDYFLNV 420
DB 361 KLWTVTRVIAHELAHQWFGNLTVMWNNDIWLKEGPAKYMELIAVNATYPELQFDDYFLNV 420
QY 421 CFEVITKDSLSNRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 480
DB 421 CFEVITKDSLSNRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 480
QY 481 YLKKEFSYRNAKNDLLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMTT 540
DB 481 YLKKEFSYRNAKNDLLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMTT 540
QY 541 WTQKGIPLLVVKQDGCSSLRQOERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSSNVI 600
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DB 541 WTQKGIPLLVVKQDGCSSLRQOERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSSNVI 600
QY 601 HRHILKSKTDTLDLPEKTSWVKFNVDNNGYIIVHYEGHWDQLITQLNQNHHTLLRPKDRV 660
DB 601 HRHILKSKTDTLDLPEKTSWVKFNVDNNGYIIVHYEGHWDQLITQLNQNHHTLLRPKDRV 660
QY 661 GLIHDVFLQVAGRLTLDKALDMTYLLOHETSSPALLEGLSYLESFYHMDRRNISDISE 720
DB 661 GLIHDVFLQVAGRLTLDKALDMTYLLOHETSSPALLEGLSYLESFYHMDRRNISDISE 720
QY 721 NLKRYLLOQYKPVTDROSWSKGVMDRMLRSALLKLACDLNHAAPCIQKAAELFQMMES 780
DB 721 NLKRYLLOQYKPVTDROSWSKGVMDRMLRSALLKLACDLNHAAPCIQKAAELFQMMES 780
QY 781 SGKL 784
DB 781 SGKL 784

RESULT 4
US-09-764-853-646
; Sequence 646, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE REFERENCE: P0206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 646
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-646

Query Match 75.2%; Score 3799; DB 9; Length 728;
Best Local Similarity 100.0%; Pred. No. 2,1e-295;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 VKTIEEGGLLEDFHFTTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVYASPKRKNQTHY 298
DB 7 VKTIEEGGLLEDFHFTTVKMSYLVAYIVCDPHSLSGFTSSGVKVSIVYASPKRKNQTHY 66
QY 299 ALQASLKLLDPYEKYFDIYYPPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSA 358
DB 67 ALQASLKLLDPYEKYFDIYYPPLSKLDLIAIPDFAPGAMENWGLITYRETSLLFPDKTSSA 126
QY 359 SDKLWTVTRVIAHELAHQWFGNLTVMWNNDIWLKEGPAKYMELIAVNATYPELQFDDYFL 418
DB 127 SDKLWTVTRVIAHELAHQWFGNLTVMWNNDIWLKEGPAKYMELIAVNATYPELQFDDYFL 186
QY 419 NVCFEVTIKDSLSNRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 478
DB 187 NVCFEVTIKDSLSNRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKQGI 246
QY 479 IQYLKKEFSYRNAKNDLLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMM 538
DB 247 IQYLKKEFSYRNAKNDLLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEKMM 306
QY 539 TTWTLQKGIPLLVVKQDGCSSLRQOERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSSN 598
DB 307 TTWTLQKGIPLLVVKQDGCSSLRQOERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSSN 366
QY 599 VIHRLKSKTDTLDLPEKTSWVKFNVDNNGYIIVHYEGHWDQLITQLNQNHHTLLRPK 658
DB 367 VIHRLKSKTDTLDLPEKTSWVKFNVDNNGYIIVHYEGHWDQLITQLNQNHHTLLRPK 426
QY 659 RVGLIHDVFLQVAGRLTLDKALDMTYLLOHETSSPALLEGLSYLESFYHMDRRNISDI 718
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Db 427 RVGLIHDVFLVGVAGRLTLDKALDWTYYLQHTSSPALLGLSYLESFYHMMDRRNISDI 486
Qy 719 SENLKRYLLQYFKPVIDRQSDSGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 778
Db 487 SENLKRYLLQYFKPVIDRQSDSGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 546
Qy 779 ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQBKLL 838
Db 547 ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQBKLL 606
Qy 839 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 898
Db 607 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 666
Qy 899 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDI FQTVLETTITKNIKWLEKNLPTLRTWLMV 958
Db 667 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDI FQTVLETTITKNIKWLEKNLPTLRTWLMV 726
Qy 959 NT 960
Db 727 NT 728

RESULT 5
US-09-764-853-819
; Sequence 819, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 819
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (237)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (719)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (720)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (721)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-819

Query Match 74.6%; Score 3770; DB 9; Length 722;
Best Local Similarity 99.3%; Pred. No. 4.3e-293;
Matches 717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 239 VKTIELEGGLEDHFETTVKMSYLVIVAYICDFHSLGFTSSGGVKVSIYASPKDRNOTHY 298
Db 1 VKTIELEGGLEDHFETTVKMSYLVIVAYICDFHSLGFTSSGGVKVSIYASPKDRNOTHY 60
Qy 299 ALQASLKLLDFEYKFDIYYPLSKLDLIAIPDPFAPGAMENWGLITYRETSLLFPDKTSSA 358
Db 61 ALQASLKLLDFEYKFDIYYPLSKLDLIAIPDPFAPGAMENWGLITYRETSLLFPDKTSSA 120
Qy 359 SDKLVWTRVIAHELAHQWFGNLVTMEWWDNIWLKEGFAKYMELIAVNAATPELOFDDYFL 418
Db 121 SDKLVWTRVIAHELAHQWFGNLVTMEWWDNIWLKEGFAKYMELIAVNAATPELOFDDYFL 180
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Qy 419 NVCFEVITKDSLNSRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGBKEFKOGI 478
Db 181 NVCFEVITKDSLNSRPIKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGBKEFKYXGI 240
Qy 479 IQYLKXFSYRNAKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFI GENAEVKEMM 538
Db 241 IQYLKXFSYRNAKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFI GENAEVKEMM 300
Qy 539 TTWTLOKGIPLLVKQDGCISLRLOQERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN 598
Db 301 TTWTLOKGIPLLVKQDGCISLRLOQERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN 360
Qy 599 VIHRHILKSKTDTLDLPEKTSWVKFNVDNSGYIVHYEGHGWDLITQLNQNHITLLRPKD 658
Db 361 VIHRHILKSKTDTLDLPEKTSWVKFNVDNSGYIVHYEGHGWDLITQLNQNHITLLRPKD 420
Qy 659 RVGLIHDVFLVGVAGRLTLDKALDWTYYLQHTSSPALLGLSYLESFYHMMDRRNISDI 718
Db 421 RVGLIHDVFLVGVAGRLTLDKALDWTYYLQHTSSPALLGLSYLESFYHMMDRRNISDI 480
Qy 719 SENLKRYLLQYFKPVIDRQSDSGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 778
Db 481 SENLKRYLLQYFKPVIDRQSDSGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM 540
Qy 779 ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQBKLL 838
Db 541 ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQYELSMSSAEQNKILYALSTSKHQBKLL 600
Qy 839 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 898
Db 601 KLIELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMII 660
Qy 899 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDI FQTVLETTITKNIKWLEKNLPTLRTWLMV 958
Db 661 SGTTAHFSSKDKLOEVKLPFESLEAQGSHLDI FQTVLETTITKNIKWLEKNLPTLRTWLMV 720
Qy 959 NT 960
Db 721 XT 722

RESULT 6
US-10-220-443-2
; Sequence 2, Application US/10220443
; Publication No. US20030215820A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Stewart
; TITLE OF INVENTION: REGULATORS OF TYPE-1 TUMOR NECROSIS FACTOR RECEPTOR AND OTHER CYTOKINES
; TITLE OF INVENTION: RECEPTOR SHEDDING
; FILE REFERENCE: 218732
; CURRENT APPLICATION NUMBER: US/10/220,443
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06464
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,586
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-443-2

Query Match 49.8%; Score 2516.5; DB 15; Length 941;
Best Local Similarity 51.1%; Pred. No. 2.4e-192;
Matches 478; Conservative 171; Mismatches 268; Indels 19; Gaps 7;

Qy 23 YCLTAILPQICICQSFVSSVHYFTDPGAFPPVATNGEREPPWQELRLPSVVIPLHYDLFV 82
Db 15 FLSSLLALLTV----STPSWCQSTE---ASPKRSQGTGTPPPMKNKIRLUPFVIVPHYDLLI 67
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Qy	323	LDLIAIPDPAPGAMENWGIIITYBETSIILFDPKTSASDKLWTRVIAIHELAHQFGLVTT	382
Db	309	QDLAAIPDFQSGAMENWGIIITYRESALLFDEKSSASSKGIITMTVAHELAHQFGLVTT	368
Qy	383	MEWNNDILWKEGFACYMELIAYNATYPELOQDFPLVNCPEVITKDSLNSRISKPAET	442
Db	369	MEWNNDLWLNIEGFACFMBEVSUVTPELKVGDYFFGKCFDAMEVDALNSHPVSTPEVN	428
Qy	443	PTQIQBWPDEVSYNKGACILNMLKDFLEBKEFKGIIQYLKKFSYRNAXNDLWSSLSNS	502
Db	429	PAQIREMFPDDVSVDKGACILNMLRELYLSADAFKGGIYOYLQKHSYKNTKNEIDLWDSSAI	488
Qy	503	CLESDDPTSG--GYCHSDPKWTTSNMLAFJLGCENAEVKEWMTTWTLOKGIPLLVWQDGCSLR	560
Db	489	C-PTDGKVGMDGFC-SRSQHSSSSSHMHQEGVDVKTWMTWTWLQRGFPLITIIVGRNVH	546
Qy	561	LQOERFLOGVFOEDPEWRALQERYLWHIPLYSTSSSNVHRHLKSKTDTLDPKTSW	620
Db	547	MKEOEHYMKG-----SDGAPDGTGLYLMHWPLFITTSKSDMVRFLFKTKTDLVTLPLPEVEM	600
Qy	621	VKENVDSNGYIYVHVHEGHWQDOLIQLNQNHHTLLRPKDRVGLIHDVFPQVAGRLTLDKA	680
Db	601	IKFNVCMGNYIYVHVIEDDGDMSDLTGLLKGTHTAVSSNDRASLINNAQVLSIGKLSIEKA	660
Qy	681	LDMTYYLQHETSSPALLEGSLVLESFYFHYMDORRNISDIENMLKRYLLOYKFPKVIDQOSW	740
Db	661	LDLSLXLKHETIEMPVQFQGNELIPMYKLNEKRDKNVEVETQFAFLTLRLRLDILDKQTWT	720
Qy	741	DKGSVMDRLRSALLKACLADLNHAPCIQKAAELFSOWMSSGKLNIPTDLVKLVYWSVGAQ	800
Db	721	DEGSVSERMLRELLLLACVHNYQFCVQVABGYFRKWKESNGNLSLPVDVTLAVFVGAQ	780
Qy	801	TTAGWNYLLEQVELSSNAEQNKILIYALSTSQHOGKLLKLIELGMEGKVKTQNLQALHLH	860
Db	781	STEGWDFLYSKYQFSLSSSTEPSQIEFALCRTQNKEKLQWLLEDSEFKDGDKIKTOFFQIILT	840
Qy	861	AIARRPKGOOLAWDFVRENWTHLLKKFDFLGSYDRIWIIISGTTTAFHSSKDKLQEVKLPFFES	920
Db	841	LIGENPVGYPLANQVFLRKXWVKLVQKFPGLSGSSIAHWVMGTNTQFSTRTELEVEKGFSS	900
Qy	921	LEAQGSHLDIFQTVLETTIKNIKULEKNLPLTRTWL	956
Db	901	LKENGSQLRCVOQTTEIETEEENIGWMDKNFDIRVWL	936

;	APPLICANT:	Wood, William I.
;	APPLICANT:	Zhang, Zemin
;	TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
;	TITLE OF INVENTION:	Acids Encoding the Same
;	FILE REFERENCE:	P2730PIC63
;	CURRENT APPLICATION NUMBER:	US/09/989,722
;	CURRENT FILING DATE:	2001-11-19
;	PRIOR APPLICATION NUMBER:	60/049787
;	PRIOR FILING DATE:	1997-06-16
;	PRIOR APPLICATION NUMBER:	60/062250
;	PRIOR FILING DATE:	1997-10-17
;	PRIOR APPLICATION NUMBER:	60/065186
;	PRIOR FILING DATE:	1997-11-12
;	PRIOR APPLICATION NUMBER:	60/065311
;	PRIOR FILING DATE:	1997-11-13
;	PRIOR APPLICATION NUMBER:	60/066770
;	PRIOR FILING DATE:	1997-11-24
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;	PRIOR APPLICATION NUMBER:	60/078910
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;	PRIOR FILING DATE:	1998-06-10

RESULT 10  
US-09-989-722-353

; Patient No: 052002007/2067/AL  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Denosoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickev

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, PRIOR APPLICATION NUMBER: 60/092182
, PRIOR FILING DATE: 1998-07-09

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Qy	23	YCLTAIIPQICQSFQSPSYSHFTDPGAPPVATNGERPQWBLRPLSPVVPIPHYDLFV	82
Db	15	FLSSLLALLTV-----STPSCOSTE---ASPKRSDGTPPWNKIRLPEYVIPHYDLLI	67
Qy	83	HPNLTSLDFVASEKIEVLVSNATQFIILHKSOLIEITNATLQSEEDSYMKPGKELVLSY	142
Db	68	HANUTLITFWGTTKVEITASQPTSTIILHSHHQLQISRATURKGAGERLSE--EPLQVLHE	125
Qy	143	PAHEQIALLVPEKLTPLHLKTVYVDMFOAKLGDGPEGFYKSYTYRTLGGETRILAVTDEPT	202
Db	126	PPQEQIALLAPEPLLVGLPVTVIVHYAGNLSETHGFYKSYTYRTKEGELRILASTQPEPT	185
Qy	203	QARMAFPCEPPLPKANFSIKIRRESHIALSNMPKVKTILEGGLLEDPHETTVKMSY	262
Db	186	AARMAFPCEPAPAFKASFIKIRREPRLAISNNPLVKSVTVAEGLIEDHFDVTVKMSY	245
Qy	263	LVAVIVCDPHSLGFTSSGVKVSIVYASPDKRNOTHYALQASLKLDFVEKYFDIYVPLSK	322
Db	246	LVAFIISDFESVKITSGVKVSIVYVPDKINQADYALDAAVTLLFEYEDYFSIYPPLPK	305
Qy	323	LDLIAIPDFAPGAMENGLITYRETSLLFPDKTSSASDKLWTVTRVIAHELAHQWFGNLVT	382
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Qy	383	MEWNNDIWLKEGPAKYMELIAVNATYPELQFDYDFLVNVCPEVITKOSLNSRPISKPAET	442
Db	366	MEWNNDLWLNEGFAKPFMEFVSUVTHPELVKGVGYFFGKCFDAMEVDALNSSHVPSTPVEN	425
Qy	443	PTQIQEMFDEVSYNKGACILNMLKDFLGEBEKFQKGIIOYLKKFSYRNAKNDLWSSLNS	502
Db	426	PAQIREMFDDVSVDKGCACILNMLREYLSADAFKSGIVOYLQKISYKNTONEDLWDSWASI	485
Qy	503	CLESDFTSG--GVCHSDPKMTNNMLAPLGSNAEYKEMMTWTLOKGIPLLWKVDGGSGLR	560
Db	486	C-PTDGKVGMDGFC-SRSQHSSSSSHHWQGVQVDVKTMMNTWTLORGEPLITITVGRNVH	543
Qy	561	LQOERFLQGVQEDPEWRAQLQERYLWHIPITYSTSSSNVIRHRLKSKTDTLDLPEKTSW	620
Db	544	MKEOHYMKG-----SDGAPOTGLYHWPVITFTSKSNMYHRFLAKTKDVLIVLPEEVEW	597









APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-24



[illegible]



[illegible]



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:26 ; Search time 182 Seconds  
(without alignments)  
2701.077 Million cell updates/sec

Title: US-10-039-073-1

Perfect score: 5052

Sequence: 1 MFHSSAMVNSHRKPMFNTHR.....NIKWLKXNPLTIRTWLMVNT 960

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	5052	100.0	Q9HBX2	Q9hb22 homo sapien
2	5047	99.9	Q725K1	Q725k1 homo sapien
3	4789.5	94.8	Q6P179	Q6p179 homo sapien
4	2768	54.8	Q8TD32	Q8td32 homo sapien
5	2516.5	49.8	ART1_HUMAN	Q9hz08 h adipocyte
6	2512.5	49.7	Q6UWY6	Q6uw66 homo sapien
7	2480	49.1	ART1_MOUSE	Q9eqh2 mus musculus
8	2430	48.1	ART1_RAT	Q9j122 rattus norv
9	2034	40.3	Q6PE23	Q6pe23 brachydanio
10	2027	40.1	LCAP_RAT	P97629 r leucyl-cy
11	2022	40.0	Q8C129	Q8cl29 mus musculus
12	1999	39.6	Q8C9W5	Q8c9w5 mus musculus
13	1883	37.3	Q6PCG5	Q6pcg5 xenopus lae
14	1847	36.6	Q8RVJ3	Q8rvj4 homo sapien
15	1690	33.5	Q8C4S7	Q8c4s7 mus musculus
16	1564	31.0	Q8C4S7	Q8c4s7 mus musculus
17	1455.5	28.8	Q8C4S7	Q8c4s7 mus musculus
18	1444	28.6	Q8C4S7	Q8c4s7 mus musculus
19	1391.5	27.5	Q9VFW7	Q9vfw7 drosophila
20	1391	27.5	Q9VFW7	Q9vfw7 drosophila
21	1390.5	27.5	Q9VFW7	Q9vfw7 drosophila
22	1389.5	27.5	Q9VFW7	Q9vfw7 drosophila
23	1373.5	27.2	Q8GN05	Q8gn05 drosophila
24	1371.5	27.1	Q8GN05	Q8gn05 drosophila
25	1367	27.1	Q8GN05	Q8gn05 drosophila
26	1367	27.1	Q8GN05	Q8gn05 drosophila
27	1361.5	26.9	Q8VFX0	Q8vfx0 drosophila
28	1343	26.6	Q8VFX0	Q8vfx0 drosophila
29	1340	26.5	Q9VFW9	Q9vfw9 drosophila
30	1339	26.5	Q9VFW9	Q9vfw9 drosophila
31	1329.5	26.3	Q8BZ14	Q8bz14 mus musculus

32	1329.5	26.3	862	2	Q8IGR1	Q8igr1 drosophila
33	1327	26.3	1025	1	THDE_RAT	Q10836 rattus norv
34	1322	26.2	1024	2	Q6UWJ4	Q6uwj4 homo sapien
35	1320	26.1	1024	1	THDE_HUMAN	Q9UKU6 homo sapien
36	1312	26.0	964	1	AMPN_RAT	P15684 rattus norv
37	1310	25.9	1025	1	THDE_MOUSE	Q8K093 mus musculus
38	1298	25.7	966	1	AMPN_FELCA	P79171 felis silve
39	1290.5	25.5	1007	2	Q9U0D1	Q9u0d1 aplysia cal
40	1280.5	25.3	866	2	Q9W0S4	Q9w0e4 drosophila
41	1280.5	25.3	1053	2	Q8IRH0	Q8irh0 drosophila
42	1280.5	25.3	1075	2	Q8IRH1	Q8irh1 drosophila
43	1275	25.2	997	2	Q7QAH5	Q7qah5 anopheles g
44	1274	25.2	965	1	AMPN_RABIT	P15541 oryctolagus
45	1272.5	25.2	866	2	Q9GPG3	Q9gpg3 drosophila

#### ALIGNMENTS

#### RESULT 1

Q9HBX2 PRELIMINARY; PRT; 960 AA.  
AC Q9HBX2;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE AminoPeptidase.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schomburg L.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191545; AAG38383.1; --  
DR MEROPS; M01.024; --  
DR GO; GO:0004177; F:aminopeptidase activity; IEA.  
DR GO; GO:0004179; P:membrane alanyl aminopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001930; Peptidase M1.  
DR InterPro; IPR006025; Pept M Zn\_BS.  
DR Pfam; PF01433; Peptidase M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Aminopeptidase.  
SQ SEQUENCE 960 AA; 110461 MW; 261EFC06870D644E CRC64;

Query Match	100.0%;	Score 5052;	DB 2;	Length 960;
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Db	1	MFHSSAMVNSHRKPMFNTHRGFYCLTALPQICICSQFSPSSVSYHFTDPCAPPVATNGE	60	
Qy	61	RFPQELRLPSVWIPLHYDLFVHPNLSLTSDFVASEKIEVLVSNATQFIILHSHKOLEITNA	120	
Db	61	RFPQELRLPSVWIPLHYDLFVHPNLSLTSDFVASEKIEVLVSNATQFIILHSHKOLEITNA	120	
Qy	121	TQSEEDSRNYPKPKELVSLYPAHQEQIALLVPEKLTPLHKYVYVAMDQAKLGDFEGFY	180	
Db	121	TQSEEDSRNYPKPKELVSLYPAHQEQIALLVPEKLTPLHKYVYVAMDQAKLGDFEGFY	180	
Qy	181	KSTVTLGGETRIILAVTDFEPTQARMAPCFDEPLKAFNFSIKIRRESRHIALSNMPKVK	240	
Db	181	KSTVTLGGETRIILAVTDFEPTQARMAPCFDEPLKAFNFSIKIRRESRHIALSNMPKVK	240	
Qy	241	TIELEGGLEDHFTTVKMSYLVAVIVCDPHSLSGFTSSGVKVSIVYASPDKNQTHYAL	300	
Db	241	TIELEGGLEDHFTTVKMSYLVAVIVCDPHSLSGFTSSGVKVSIVYASPDKNQTHYAL	300	
Qy	301	QASIKLLDIFYEKYFDIYVPLSKLDLIAIPDPAPGNMWNGLITYRETSLLDPDKTSSASD	360	

Db 301 QASLKLLDFYKFDIYYPLSKJLDLIAIPDFAPGAMENWGLIITYRETSLLFDPKTSASD 360  
Qy 361 KLWTRVIAHIAHQAOWFNLVTMEWWDIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420  
Db 361 KLWTRVIAHIAHQAOWFNLVTMEWWDIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420  
Qy 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGLIQ 480  
Db 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGLIQ 480  
Qy 481 YLKKFSYRNAKNDLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540  
Db 481 YLKKFSYRNAKNDLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540  
Qy 541 WTLQKGIPLLVVKQDGCRLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNVI 600  
Db 541 WTLQKGIPLLVVKQDGCRLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNVI 600  
Qy 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIIVHVEGHGWDQLITQLNQNHTLLRPKDRV 660  
Db 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIIVHVEGHGWDQLITQLNQNHTLLRPKDRV 660  
Qy 661 GLIHDVFLVAGRLTLDKALDMTYIYLQHETSSPALLGLESLYLESFYHMDRRNISISE 720  
Db 661 GLIHDVFLVAGRLTLDKALDMTYIYLQHETSSPALLGLESLYLESFYHMDRRNISISE 720  
Qy 721 NLKRYLLOYFPKVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCTQKAELFQSMWES 780  
Db 721 NLKRYLLOYFPKVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCTQKAELFQSMWES 780  
Qy 781 SGKLNIPDVLKIVYVGAQTAGNWLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840  
Db 781 SGKLNIPDVLKIVYVGAQTAGNWLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840  
Qy 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900  
Db 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900  
Qy 901 TTAHFSSKDKLQEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPTLRTWLWMVT 960  
Db 901 TTAHFSSKDKLQEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPTLRTWLWMVT 960

RESULT 2  
Q725K1 ID Q725K1 PRELIMINARY; PRT; 960 AA.  
AC Q725K1;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Leukocyte-derived arginine aminopeptidase long form variant.  
GN Name=1-rap;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12799365; DOI=10.1074/jbc.M305076200;  
RA Tanioka T., Hattori A., Masuda S., Nomura Y., Nakayama H.,  
RA Mizutani S., Tsujimoto M.;  
RT "Human leukocyte-derived arginine aminopeptidase:The third member of  
RT the oxytocinase subfamily of aminopeptidases.";  
RL J. Biol. Chem. 278:32275-32283 (2003).  
DR EMBL; AB109031; BAC78818.1; -;  
DR MEROPS; M01.024; -;  
DR GO; GO:0004177; F:aminopeptidase activity; IEA.  
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001930; Peptidase\_M1.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR Pfam; PF01433; Peptidase\_M1; 1.

DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Aminopeptidase.  
SQ SEQUENCE 960 AA; 110447 MW; 27898FE2107E814E CRC64;  
Query Match 99.9%; Score 5047; DB 2; Length 960;  
Best Local Similarity 99.9%; Pred. No. 9.4e-291;  
Matches 959; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MFHSSAMVNSHRKPMFNIHRGFYCLTALPQICICSQFSSVPSSHYFTEDPGAFVATNGE 60  
Db 1 MFHSSAMVNSHRKPMFNIHRGFYCLTALPQICICSQFSSVPSSHYFTEDPGAFVATNGE 60  
Qy 61 RFPWQELRLPSVPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQIILHSDKLEITNA 120  
Db 61 RFPWQELRLPSVPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQIILHSDKLEITNA 120  
Qy 121 TLQSEEDSRYPKPEKELKVLSPAEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGPEGFY 180  
Db 121 TLQSEEDSRYPKPEKELKVLSPAEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGPEGFY 180  
Qy 181 KSTYRTLGGETRIILAVTDFPTQARMAPCFDEPLKPAFNSIKIRRESRIHALSNMPKV 240  
Db 181 KSTYRTLGGETRIILAVTDFPTQARMAPCFDEPLKPAFNSIKIRRESRIHALSNMPKV 240  
Qy 241 TIELEGLLLEDHPETTVMSTYLVAYIVCDPHSLSGFTSGGVKSVIYASDPKRNQTHYAL 300  
Db 241 TIELEGLLLEDHPETTVMSTYLVAYIVCDPHSLSGFTSGGVKSVIYASDPKRNQTHYAL 300  
Qy 301 QASLKLLDFYKFDIYYPLSKJLDLIAIPDFAPGAMENWGLIITYRETSLLFDPKTSASD 360  
Db 301 QASLKLLDFYKFDIYYPLSKJLDLIAIPDFAPGAMENWGLIITYRETSLLFDPKTSASD 360  
Qy 361 KLWTRVIAHIAHQAOWFNLVTMEWWDIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420  
Db 361 KLWTRVIAHIAHQAOWFNLVTMEWWDIWLKEGFAKYMELIAVNATYPELQFDYFLNV 420  
Qy 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGLIQ 480  
Db 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSNKGACILNMLKDFLGEKEFKGLIQ 480  
Qy 481 YLKKFSYRNAKNDLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540  
Db 481 YLKKFSYRNAKNDLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEYKEMWTT 540  
Qy 541 WTLQKGIPLLVVKQDGCRLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNVI 600  
Db 541 WTLQKGIPLLVVKQDGCRLRLOQERFLQGVFQEDPEWRALQERYLWHIPLTYSTSSNVI 600  
Qy 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIIVHVEGHGWDQLITQLNQNHTLLRPKDRV 660  
Db 601 HRHILKSKTDTLDLPEKTSWVKFNVDNSNGYIIVHVEGHGWDQLITQLNQNHTLLRPKDRV 660  
Qy 661 GLIHDVFLVAGRLTLDKALDMTYIYLQHETSSPALLGLESLYLESFYHMDRRNISISE 720  
Db 661 GLIHDVFLVAGRLTLDKALDMTYIYLQHETSSPALLGLESLYLESFYHMDRRNISISE 720  
Qy 721 NLKRYLLOYFPKVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCTQKAELFQSMWES 780  
Db 721 NLKRYLLOYFPKVIDRQSWSDKGSVWDRMLRSALLKLACDLNHAPCTQKAELFQSMWES 780  
Qy 781 SGKLNIPDVLKIVYVGAQTAGNWLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840  
Db 781 SGKLNIPDVLKIVYVGAQTAGNWLLEQYELSMSSAEONKILYALSTSKHQEKLLKL 840  
Qy 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900  
Db 841 IELGMEGVKIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKXFDLGSYDIRMIISG 900  
Qy 901 TTAHFSSKDKLQEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPTLRTWLWMVT 960  
Db 901 TTAHFSSKDKLQEVKLPFESLEAGSHLDIFQTVLETITKNIKWLEKNLPTLRTWLWMVT 960

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RESULT 3
Q6P179 PRELIMINARY; PRT; 915 AA.
AC Q6P179;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LRAP protein.
GN Name=LRAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC065240; AAH65240.1; -
DR GO; GO:0004179; P:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 915 AA; 105525 MW; 10075BE1C076377F CRC64;

Query Match 94.8%; Score 4789.5; DB 2; Length 915;
Best Local Similarity 95.3%; Pred. No. 1.7e-275;
Matches 915; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 MFHSAMVNSHRKPNFNIHRGFCYCLTALPQICICQSFVSSSYFTEDPGAFPVATNGE 60
DB 1 MFHSAMVNSHRKPNFNIHRGFCYCLTALPQICICQSFVSSSYFTEDPGAFPVATNGE 60
QY 61 RFPWELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFILHKSLEITNA 120
DB 61 RFPWELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFILHKSLEITNA 120
QY 121 TLQSEEDSRYPKPKELVSLYPAEHQIALLVPEKLTPLHLYKYVAMDFQAKLGDGFEFY 180
DB 121 TLQSEEDSRYPKPKELVSLYPAEHQIALLVPEKLTPLHLYKYVAMDFQAKLGDGFEFY 180
QY 181 KSTYTLGGETRILAVTDPEPTQARMAPCFDEPLFKANFSIKIRRSRHIALSNMPKV 240
DB 181 KSTYTLGGETRILAVTDPEPTQARMAPCFDEPLFKANFSIKIRRSRHIALSNMPKV 240
QY 241 TIEGLGLEDHEDFETTVKMSYLVAVIVCDFHSLSGFTSSGVKVIYASPKRNTQHYAL 300
DB 238 -----KSVIYASPKRNTQHYAL 255
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QY 301 QASLKLLDFYKDYFDIYYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLEDPKTSASD 360
DB 256 QASLKLLDFYKDYFDIYYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLEDPKTSASD 315
QY 361 KLWTRVIAHSLAHQWFGNLTVMWMDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 420
DB 316 KLWTRVIAHSLAHQWFGNLTVMWMDIWLKEGFAKYMELIAVNATYPELQFDDYFLNV 375
QY 421 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGSEKFKQGIQ 480
DB 376 CFEVITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGSEKFKQGIQ 435
QY 481 YLKKFSYRNAKNDLWSSLSNCSLESPTSISGCHSDPKMTSNMLAFGLGNAEVKEMTT 540
DB 436 YLKKFSYRNAKNDLWSSLSNCSLESPTSISGCHSDPKMTSNMLAFGLGNAEVKEMTT 495
QY 541 WTLQKGIPLLVKQDGSRLQQRERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSNNVI 600
DB 496 WTLQKGIPLLVKQDGSRLQQRERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSNNVI 555
QY 601 HRHILKSKTDTLDLPEKTSWYKFNVDNSNGYIVHYEGHGWDLITQLNQNHTLLRPKDRV 660
DB 556 HRHILKSKTDTLDLPEKTSWYKFNVDNSNGYIVHYEGHGWDLITQLNQNHTLLRPKDRV 615
QY 661 GLIHDVQLVAGRLTLDKALDWTYYLQHETSSPALLEGSLYSFYHMDRRNITSDISE 720
DB 616 GLIHDVQLVAGRLTLDKALDWTYYLQHETSSPALLEGSLYSFYHMDRRNITSDISE 675
QY 721 NLKRYLLQYKPKVIDRQSWSDKGSWDMRLSALLKLACDINHAPCIQKAAELFSQMMES 780
DB 676 NLKRYLLQYKPKVIDRQSWSDKGSWDMRLSALLKLACDINHAPCIQKAAELFSQMMES 735
QY 781 SGKLNIPDVLKIVYSGAQTAGNVLLEQYELSSSAEQNKILYALSTSKHQEKLLKL 840
DB 736 SGKLNIPDVLKIVYSGAQTAGNVLLEQYELSSSAEQNKILYALSTSKHQEKLLKL 795
QY 841 IELQMEGKVIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFGLGSDIRMIISG 900
DB 796 IELQMEGKVIKTONLAALLHAIARRPKGQQLAWDFVRENWTHLLKKFGLGSDIRMIISG 855
QY 901 TTAHFSSKDKLQEVKLPFESLEAOGSHLDIFQTVLETITKIKWLEKNLPLRTLWLVNT 960
DB 856 TTAHFSSKDKLQEVKLPFESLEAOGSHLDIFQTVLETITKIKWLEKNLPLRTLWLVNT 915

RESULT 4
Q8TD32 PRELIMINARY; PRT; 532 AA.
AC Q8TD32;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase short form.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21374137; PubMed=11481040;
RA Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;
RT "Genomic organization of the human adipocyte-derived leucine
RT aminopeptidase gene and its relationship to the placental leucine
RT aminopeptidase/oxycotinase gene.";
RL J. Biochem. 130:235-241 (2001).
[2]
RP SEQUENCE FROM N.A.
RA Tanioka T., Hattori A., Masuda S., Nomura Y., Nakayama H.,
RT "Human leukocyte-derived arginine aminopeptidase: The third member of
RT the oxycotinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 274:1000-1003 (1999).
EMBL; AY028805; AAK37776.1; -
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DR MEROPS; M01.024; --
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase M1.
DR Pfam; PF01433; Peptidase M1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 532 AA; 60937 MW; DA0F4F00AD980D71 CRC64;

Query Match          54.8%; Score 2768; DB 2; Length 532;
Best Local Similarity 99.6%; Pred. No. 6.6e-156;
Matches 523; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFHSSAMVNSHRKPMFNHHRGFYCLTALPQICSCQSPSPSSVHYFTEDPGAPVATNGE 60
Db 1 MFHSSAMVNSHRKPMFNHHRGFYCLTALPQICSCQSPSPSSVHYFTEDPGAPVATNGE 60

Qy 61 RFPQQLRLPSVVIPLHYDLFVHNLTSLSDFVASEKIEVLVSNATQRTILHSHKDLITNA 120
Db 61 RFPQQLRLPSVVIPLHYDLFVHNLTSLSDFVASEKIEVLVSNATQRTILHSHKDLITNA 120

Qy 121 TLQSEEDSRVYKMGKELKVLSPAHQIALLVPEKLTPLHLKYVYVAMDFQAKLGDGFGFY 180
Db 121 TLQSEEDSRVYKMGKELKVLSPAHQIALLVPEKLTPLHLKYVYVAMDFQAKLGDGFGFY 180

Qy 181 KSTYRTLGGETRIILAVTDFTQARMAPPCCDEPLFKANFSIKIRRSRHIALSNMPKVK 240
Db 181 KSTYRTLGGETRIILAVTDFTQARMAPPCCDEPLFKANFSIKIRRSRHIALSNMPKVK 240

Qy 241 TIELEGGLEDHFFETVMKSYLVAYIVCDPHSLSGFTSGVKYVIYASPDKNQTHYAL 300
Db 241 TIELEGGLEDHFFETVMKSYLVAYIVCDPHSLSGFTSGVKYVIYASPDKNQTHYAL 300

Qy 301 QASLKLLDFYKDYFYIYPLSKLLDIAIPDPAPGAMENWGLITYRETSLFLDPKTSASD 360
Db 301 QASLKLLDFYKDYFYIYPLSKLLDIAIPDPAPGAMENWGLITYRETSLFLDPKTSASD 360

Qy 361 KLWTRVIAHLAHQWFGNLTVMWINDIWLKEGFAKYMELIANNATYPELQFDYFLNV 420
Db 361 KLWTRVIAHLAHQWFGNLTVMWINDIWLKEGFAKYMELIANNATYPELQFDYFLNV 420

Qy 421 CFVITKDLNSRRPISKPAFTPTQIQEMFDEVSNKGCACILNMLKDFLGEKEFKGLIQ 480
Db 421 CFVITKDLNSRRPISKPAFTPTQIQEMFDEVSNKGCACILNMLKDFLGEKEFKGLIQ 480

Qy 481 YLKFSYRNAXNDLWSSLNSCLESDFTSGGVCHSDPKMTSNML 525
Db 481 YLKFSYRNAXNDLWSSLNSCLESDFTSGGVCHSDPKMTSNMV 525

RESULT 5
ART1 HUMAN STANDARD; PRT; 929 AA.
AC Q9NZ08; O60278; Q8NEL4; Q8TAD0; Q9UHF8; Q9UKY2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipocyte-derived leucine aminopeptidase precursor (BC 3.4.11.-) (A-
DE LAP) (ARTS-1) (Aminopeptidase PILS) (Puromycin-insensitive leucyl-
DE specific aminopeptidase) (PILS-AP) (Type 1 tumor necrosis factor
DE receptor shedding aminopeptidase regulator).
GN Name=ARTS1; Synonyms=APPILS, KIAA0525;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=White adipose tissue;
RX MEDLINE=99238715; PubMed=10220586;

RA Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;
RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly
RL J. Biochem. 125:931-938 (1999).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RX MEDLINE=21374137; PubMed=11481040;
RA Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;
RT "Genomic organization of the human adipocyte-derived leucine
RL aminopeptidase gene and its relationship to the placental leucine
RL J. Biochem. 130:235-241 (2001).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC Schomburg L.;
RT "Molecular characterization of human aminopeptidase PILS.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC Cui X., Alsaaty S., Lawrence M., Combs C.A., Rouhani F.N.,
RL Levine S.J.;
RT "Identification of an aminopeptidase regulator of type I tumor
RL necrosis factor receptor shedding.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND REVISION TO 718.
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RL Nomura N., Ohara O.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE OF 62-929 FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RL Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RL code for large proteins in vitro.";
RL DNA Res. 5:31-39 (1998).
[7]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[8]
RN SEQUENCE OF 25-37, AND CHARACTERIZATION.
RX MEDLINE=20512052; PubMed=11056387;
RA Hattori A., Kitatani K., Matsumoto H., Miyazawa S., Rogi T.,
RA Tsuruoka N., Mizutani S., Natori Y., Tsujimoto M.;
RT "Characterization of recombinant human adipocyte-derived leucine
RL aminopeptidase expressed in Chinese hamster ovary cells.";
RL J. Biochem. 128:755-762 (2000).
CC -1- FUNCTION: May play a role in the inactivation of peptide hormones.
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```
Db 706 DEGSVSRMLRSQALLLACVHNYQPCVQRAEGYFRFKWKESNGNLSLPVDVTLAVFAVGAQ 765
Qy 801 TTAGNNYLLQYELSMSSAEONKILYALSTKSHOEKLLKLIELGMEGVKIKTONLAALLH 860
Db 766 STEGWDFLYSKYQSLSTESKQLEFALCRQNKKEKQWLDESFKGDKIKTQFPQLT 825
Qy 861 AIARRPKGOQLAWDFVRENWTHLLKFDGLGSYDIRMIISGTTAHHFSSKDKLQEVKLPFES 920
Db 826 LIGRNPVGYLAWQFLRKNWKLQKPELGSSIAHVMVGTGTFSTRTRLEEVKGFSS 885
Qy 921 LEAQSGLHDIFQTVLETTITKNIKLEKNLPLRTWL 956
Db 886 LKENGSQLRCVQQTETIEENIGWMDKNFKIRVWL 921

RESULT 6
Q6UWY6 PRELIMINARY; PRT; 941 AA.
AC Q6UWY6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ARTS-1.
GN ORFNames=UNQ584;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yaneura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358590; AAQ88953.1; -.
DR GO; GO:0004179; F-membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR Pfam; PF01433; Peptidase_M1.
DR PRINTS; PR00756; ALADIPTASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 941 AA; 107143 MW; C3DC8ACFCF5B8CC CRC64;

Query Match 49.7%; Score 2512.5; DB 2; Length 941;
Best Local Similarity 51.0%; Pred. No. 2.1e-140;
Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;

Qy 23 YCLTAILPQICQSFVSPSSHYHTEDPGAPVATNGERFPWQBLRPLPSVVIPLHYDLFV 82
Db 15 FLSSLLALLTV-----STPSWCQSTE---ASPKESDGTTPFPWKNIRLPEYVIPHYDILI 67
Qy 83 HPNLTSLDFVASEKIEVLVSNATQFIILHSKDLBITNATLQSEDSRYMKPGKELKVLVS 142
Db 68 HANLTLTFWGTTKVEITASQPTSTIILHSHLQISRATLKGAGERLSE--EPLQVLEH 125
Qy 143 PAHEQIALLVEKLTPHLKYYVAMDFOAKLGDGEGFYKSTYRTLGGETRILAVTDPEPT 202
Db 126 PPQEQIALLAPELLVGLPYTVVIHYAGNLSETPHGFYKSTYRTKEGELRILASTQPEPT 185
Qy 203 QARNAFCDFDEPLKAFKNSIKIRRESHIALSNPKVKTTLEGGLEDHPEFTVVKYSTY 262
Db 186 AARMAFFCFDEPAPKAGFSIKIRREPHRLATISNNPLVKSVTVAEGLIEDHFDVTVKYSTY 245
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Qy 263 LVAVIVCDHFHLSGFTSSGVKVSIIYASPDKRNOTHYALQASLKLLDFEYKVDIYYPLSK 322
Db 246 LVAFISDFESVKITSGVKVSVYAVPDKINQADYALDAVTLLEFYEDYFSYPDPK 305
Qy 323 LDJIAIPDFAPGAVENGLITYRETSLLFPDKTSSASDKLWTRVIAHELAHQWFGNLVT 382
Db 306 QDLAAIPDFQSGAMENGLTTRYRESALLFDAKSSASSKLGITVVAHELAHQWFGNLVT 365
Qy 383 MEWNNDILWKEGFAKYNELIAYNATYPELOFDDYFLNVCFEYITKDSINSRPSKPAET 442
Db 366 MEWNNDLWLNKGFAPKMEFVSVTHPELVKGYDFGKCFDAMEVDALNSHPSTVEN 425
Qy 443 PTOIQEMFDEVYNGKACILNMLKDFLGEEKFKOGIIQYLKFSYRNAKNDLWSSLSNS 502
Db 426 PAQIREMFDDVSYDKGACILNMLREYLSADAFKSGIVQYLQKSYKNTKNEDLWDSWASI 485
Qy 503 CLESDFTS--GVCHSDPKMTSNMLAFGLGNAEVEKEMTTTWTLOKGIPLLVVKDGCGLR 560
Db 486 C-PTDGVKGMDFC-SRSQHSSSSSHHWQEGVDVKTMMNTWTLLQGFPLITITVRGNVH 543
Qy 561 LQGERFLOGVFOEDPEWRALQERYLWHIPLTYSTSSNVIRHLKSKTDTLDLPEKTSW 620
Db 544 MKQEHYMKG-----SDGAPDTGYLWHVPLTFTITSKSNMVHRLKTKTDVLILPEVEW 597
Qy 621 VKFNVDNSGYIIVHYEGHGWDLITOLNQNHLLRPKDRVGLIHDVFLQVAGAGRLTLDKA 680
Db 598 IKFNVGNGYIIVHYEDDGDWDSLTGLLKGTHTAVSSNDRASLNNAFQVLSIGKLSIEKA 657
Qy 681 LDMTYLOHETSSPALLEGSLYSLEFVHMMDRRNIIDSINLKRYLQYKPKVIDRQSW 740
Db 658 LDLSLYLKHEITMPVFOGLNELIPMYKLMKEKMDMEVETQFKAFILRLRLDLIDKQTT 717
Qy 741 DKGSVDRMLRSALLKLACDLNAPCTOKAAELFSQWMESSGKLNPTDVLKLVYSVGAQ 800
Db 718 DEGSVEQMLRSELLLACVHNYQPCVQRAEGYFRFKWKESNGNLSLPVDVTLAVFAVGAQ 777
Qy 801 TTAGNNYLLQYELSMSSAEONKILYALSTKSHOEKLLKLIELGMEGVKIKTONLAALLH 860
Db 778 STEGWDFLYSKYQSLSTESKQLEFALCRQNKKEKQWLDESFKGDKIKTQFPQLT 837
Qy 861 AIARRPKGOQLAWDFVRENWTHLLKFDGLGSYDIRMIISGTTAHHFSSKDKLQEVKLPFES 920
Db 838 LIGRNPVGYLAWQFLRKNWKLQKPELGSSIAHVMVGTGTFSTRTRLEEVKGFSS 897
Qy 921 LEAQSGLHDIFQTVLETTITKNIKLEKNLPLRTWL 956
Db 898 LKENGSQLRCVQQTETIEENIGWMDKNFKIRVWL 933

RESULT 7
ART1_MOUSE STANDARD; PRT; 930 AA.
AC Q9EQH2; Q9ET63;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-
DE LAP) (ARTS-1) (aminopeptidase Pfam) (Puromycin-insensitive leucyl-
DE specific aminopeptidase) (PILS-AP) (VEGF induced aminopeptidase).
GN Name=Artel; Synonyms=Appils;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hattori A., Kitatani K., Matsumoto H., Mizutani S., Tsujimoto M.;
RT "Molecular cloning of murine adipocyte-derived leucine aminopeptidase
RT and its expression in adipocyte cell line 3T3-L1 cells."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
```

RX MEDLINE-21961541; PubMed-11964289; DOI=10.1182/blood.V99.9.3241;  
 RA Miyashita H., Yamazaki T., Akada T., Niihaki O., Ogawa M.,  
 RA Nishikawa S., Sato Y.;  
 RT "A mouse orthologue of puromycin-insensitive leucyl-specific  
 RT aminopeptidase is expressed in endothelial cells and plays an  
 RT important role in angiogenesis.";  
 RL Blood 99:3241-3249(2002).  
 CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.  
 CC May be involved in the regulation of blood pressure through the  
 CC inactivation of angiotensin II and/or the generation of bradykinin  
 CC in the kidney (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid. Xaa-|-  
 CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.  
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- SIMILARITY: Belongs to the peptidase M1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF227511; AAC44260.1; -;  
 DR EMBL; AB047552; BAB11982.1; -;  
 DR MEROPS; M01.018; -;  
 DR MGD; MGI:1933403; Artsl.  
 DR GO; GO:0005829; Cytozol; ISS.  
 DR GO; GO:0005783; C:cytoplasmic reticulum; ISS.  
 DR GO; GO:0005576; C:extracellular; ISS.  
 DR GO; GO:0016021; C:integral to membrane; ISS.  
 DR GO; GO:0005138; P:interleukin-6 receptor binding; ISS.  
 DR GO; GO:0004178; P:leucyl aminopeptidase activity; ISS.  
 DR GO; GO:0004239; P:methionyl aminopeptidase activity; ISS.  
 DR GO; GO:0005164; P:tumor necrosis factor receptor binding; ISS.  
 DR GO; GO:0008270; F:zinc ion binding; ISS.  
 DR GO; GO:0045444; P:adipocyte differentiation; ISS.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . ; ISS.  
 DR GO; GO:0005509; P:membrane protein ectodomain proteolysis; ISS.  
 DR GO; GO:00050714; P:positive regulation of protein secretion; ISS.  
 DR GO; GO:0008217; P:regulation of blood pressure; ISS.  
 DR GO; GO:0045088; P:regulation of innate immune response; ISS.  
 DR InterPro; IPR006025; Pept\_Mn\_BS.  
 DR InterPro; IPR001930; Peptidase\_M1.  
 DR InterPro; IPR003163; Yeast\_DNA\_bind.  
 DR Pfam; PF01433; Peptidase\_M1; 1.  
 DR PRINTS; PR00756; ALADIPTASE.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Aminopeptidase; Glycoprotein; Hydrolase; Metalloprotease; Protease;  
 KW Signal; Zinc.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 930 Adipocyte-derived leucine aminopeptidase.  
 FT METAL 342 342 Zinc (catalytic) (By similarity).  
 FT ACT\_SITE 343 343 By similarity.  
 FT METAL 346 346 Zinc (catalytic) (By similarity).  
 FT METAL 465 465 Zinc (catalytic) (By similarity).  
 FT ACT\_SITE 427 427 Proton donor (Potential).  
 FT CARBOHYD 59 59 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 143 143 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 403 403 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 540 540 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 655 655 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 749 749 N-linked (GlcNAc . .) (Potential).  
 FT CARBOHYD 890 890 N-linked (GlcNAc . .) (Potential).  
 FT CONFLICT 540 541 NA -> KG (in Ref. 2).  
 SQ SEQUENCE 930 AA; 106598 MW; 17430D8E5EAD7668 CRC64;

Query Match 49.1%; Score 2480; DB 1; Length 930;  
 Best Local Similarity 51.2%; Pred. No. 1.7e-138;  
 Matches 462; Conservative 167; Mismatches 263; Indels 10; Gaps 4;

QY	56	ATNGERFPWQELRPSVVVPIHLYFVHPNUTSLDFVASEKIEVLVSNATOFIILHSKDL	115
DB	30	ASNGDSFPWNMRLPEYMTPIHYDLMIHANLSTLTFMGKTEVEIIASRPTSTIIMHSHL	89
QY	116	EITWATLQSEBDSRYMKPGKELKVLSPAHQIALLVPEKLTPLHLYVYVMDFOAKLGDG	175
DB	90	QISKATUR--RGAGEMLSEELKVLZEPAHQVQALLAAOPLLAGSLYTVIIDYANLSES	147
QY	176	PEGYKSTYRTLGGETRILAVTDEPTQARMAFFCFDEPLFKANFSIKIRRESRIALS	235
DB	148	PHGYKSTYRTQEGEMRILAATQFEPTAARMAFFCFDEPALKASFSIKIKRDPRLAISN	207
QY	236	MPKVTTLEBGLLEDPETTVKXSTYLVAIVCDPHSLSGFTSSGVKVSIVASDPKRNQ	295
DB	208	MPLVKSVNVAEGLIEDHFDITVKMSTYLVAIFIIDPKSVSVMKSGVSVYAVDPKINQ	267
QY	296	THYLAQSLKLLDFEYKFDIYVPLSKLLDLTAIPDFAPGAMENWGLTIYRTSLLPDPKT	355
DB	268	ADYALDAAVTLLEFYEDYFNIPYLPKQDLAAIPDFQSGAMENWGLTIYRTSLLPDPKT	327
QY	356	SSASDKLWTVRIAHQLAHQWFGNLVTMEWMDIWLKEGFAKYMELIAVNATYPELQDD	415
DB	328	SSASSKLGITIVSHELAHQWFGNLVTMEWMDIWLKEGFAKYMELIAVNATYPELQDD	387
QY	416	YFLNVCEVITKDSLSRPIKSPAEPTQIQEHFDEVSYNKGACILNMLKDFLGEKFO	475
DB	388	YFFGKCFNAMEVDALNSHPVSTVENPAQIREMPDDVSYEKGACILNMLKDFLGEKFO	447
QY	476	KGIIOYLKFSYRNKNDLWSSLNSNC--LESDFTSVSGVCHSDPKMTSNMLAFGENAEV	534
DB	448	RGIYOYLKFSYRNKNDLWSSLNSNC--LESDFTSVSGVCHSDPKMTSNMLAFGENAEV	506
QY	535	KEMTTTTLQKGIPLLVVVKQDGCRLRQERFQGVQEDPEWRALQRYLWHIPLTYST	594
DB	507	KTMNTTTLQKGFPLIITVSGRNVHMKQEHY-----NASRFPETGYLWHVPLTIT	560
QY	595	SSSVIHRHILKSTDTLDLPEKTSWVKFNVDNSNGYIIVHYEGHGWDLITQLNQHTLL	654
DB	561	SKSDSVORFLKTKTDVLILPEAVQWIKFNVMGNGYIIVHYADGWSLGLLKEAHTTI	620
QY	655	RPKRVGLIHDVFLVAGAGRLTLKALDMTYVLOHETSSPALLEGSLYLESFYHMDRRN	714
DB	621	SSNDASLINNAFQVLSIEKUSIEKALDITLYLKNETEIMPIFQALNELIPYKLMKRD	680
QY	715	ISDISENLKRYLQVFKPVIDRQSDSKSGVYDRLRSALLKACDLNHPICQKAELEF	774
DB	681	MEIVETQPKFLKLLKDLIDKQWTDGVSYSERMLRSQLLLLACVRNYPQVQRAERYF	740
QY	775	SQWMESSGKLNIPDVLKIVSVGAQTAGWNYLLEQYELSSNAEQNKILYALSTXHQ	834
DB	741	REWKSSNGNMSIPIDVTLAVFAVGAQNTGWDPLYSKYQSSLSSTSEKSIQIEFSLCTSDP	800
QY	835	EKLKLLIELGMEGVIKITQNLALHAIARRPKQQLAWDFVRENWTHLLKKFLDGLGSDI	894
DB	801	EKLQWLLDQSPKGEIITKQEPHILTLIGRNPVGVPLAWKFLRENWTHLLKKFLDGLGSDI	860
QY	895	RMIISGTTAHPSSKDKLQEVKLPFLESBAQSHLIDIFQVLETITKIKWLEKRLPTLRT	954
DB	861	AHMVMTDQFSTRARLEEVKGFSSLKENGSQLRCVQQTETIETIENIRWMDKPKRL	920
QY	955	WL 956	
DB	921	WL 922	
RESULT 8			
ARTI	RAT	STANDARD;	PRT; 930 AA.
ID	ARTI_RAT	AC Q9J22; Q9J23;	
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	25-OCT-2004	(Rel. 45, Last annotation update)	



QY 887 FOLGSDYDRIIMISCTTAHSSKDKLOEVKLPFESLEAQSGLDIPQVLETTIKWKLE 946  
 Db 853 FELGSSSTAHVMYGTNOPTSTRARLEEVKGFSSLKQNGSQLRCVQQTETIEENIRWMD 912  
 QY 947 KXLPTLRTWL 956  
 Db 913 KNFKDKRLWL 922

RESULT 9  
 Q6PE23  
 ID ID6PE23 PRELIMINARY; PRT; 1003 AA.  
 AC Q6PE23;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein zgc:66103.  
 CN ORFNames=zgc:66103;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]\_TaxID=7955;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Strausberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC059317, RAH59317.1; zgc:66103.  
 DR ZFIN, ZDB-GENE-030131-1534; zgc:66103.  
 DR GO, GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.  
 DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro, IPR001930; Peptidase M1.  
 DR InterPro, IPR006025; Pept M.Zn\_BS.  
 DR Pfam, PF01433; Peptidase\_M1; 1.  
 DR PRINTS, PRO0756; ALADIPTASE.  
 DR PROSITE, PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1003 AA; E2209CE4B753E978 CRC64;

Query Match 40.3%; Score 2034; DB 2; Length 1003;  
 Best Local Similarity 43.8%; Pred. No. 5.5e-112;  
 Matches 407; Conservative 170; Mismatches 293; Indels 60; Gaps 10;

QY 33 CICSQFSPVSHYFTEDPCAFVATNGERFPQELRPSVPLHYDLFVPHNLTSLOFV 92  
 Db 128 CQKSNSSMSISY-----PISISGELFPFTDLRLPVSVPVHYNTSLHPDLNSMTFQ 178  
 QY 93 ASEKIEVLVSNATQFIILHSKDLEITNATLQSEEDSRYNKPKELKVLSPAPAEQIALIV 152

Db 179 GNVSIWLVVHETKNIVLHSSDMNIIKVTFFD-----KEYRLEYKPMQOIAIKF 228  
 QY PEKLTPLHKYVAMDFQAKLDGDFEGFYKSTYRTLGGETRILAVTDFEPTQARMAFPCCF 212  
 Db 229 PEDLKKG-QYVLKFSYKANLSYDGFYNSSVDTAGTKRVLAATQFPEPLAARAKAPCCF 287  
 QY EPLFKANFSIKIRRESRHIALSNPKVKTIEL-EGGLEDHPETTVKSTYLVVAIVCDF 271  
 Db 288 EPAPKSTFVVRWMTREKYISLSNMPKIKTTDLNENGLQEDFESSVKMSTYLVAFIVAEF 347  
 QY HSLSGFTSSGVKVIYASPKRNOTHYALQASLKLLDPYKVEDIYYPLSKLDLIAIPDF 331  
 Db 348 SSHSKNVSK-TTVSVIAPVDDKKQVHALETACKLLKFTNTFFLEYPLSKLDLVIAIPDF 406  
 QY APGAMENWGLITYRETSLLFPDKTSSASDKLWTVRIAHELAHQWFGNLVMEWMDIWL 391  
 Db 407 LAGAMENWGLITPRETILLVG-NQSSRFDKQLVTSVIAHELAHQWFGNLVTRWMDLWL 465  
 QY KEGFAKYMELIATVATPELQFDYFLNVCPVITKOSLSNRRPISKPAETPTQIQEHPD 451  
 Db 466 NEGFAITYQVMSIENVPDLIDIEFLNVRPKALAKOALNSSHPVSTFVSTPEQVEEMFD 525  
 QY EVSYNKGACILNMLKDFLGEKFKOGIIQYLKFSYRNKNDLWSSLSNCSLESDFTS 511  
 Db 526 SVSYEKGASILLMLNATLRDGEFHKGVIEYQNTNLSNTESKDLWNSLSQVSKS----- 580  
 QY GVCHSDPKMTSNMLAFGLGNAEVKEMTTTWTLOKGIPLLVVVKQDGCSURLQOERFLOGVF 571  
 Db 581 -----LNVSEMMNTWTVHKGFPLTVKRNQGPQVTLQSEHPLLNA- 619  
 QY QEDPEWRALQRYLWHLPTVYSTSSNVIHR-----HILKSKTDTLDLPEKTSVWKFVND 626  
 Db 620 -----ENGTDSDSLWHIPLTVYVNDSCVLSCKQVHF-LKDKEATLQLPGQVKNLKFNR 673  
 QY SNGYVIHYEHGCHDQILITQLNQNHLLRPDRVGLIHDVQLVQAGAGRLTLDKALDMTY 686  
 Db 674 SDGYVIHYHQGWSDLISALKVNVNVLPSDDKALINNIIFALSRGKVSFRQVJNLMDY 733  
 QY LQHTSSPALLEGSLVSEFYHMMDRRINISBNLKYLLQYFKPVIDROSWSKGVW 746  
 Db 734 IRNETEAPLTEALSQGLQIYVLLDKRDLNASSMTTYIESHFGSLMESQSWETSVS 793  
 QY DRMLRSALLKLACDLNHPACTOKAELFQSMWSSGKLNIPITDVLKIVYSGAQTAGN 806  
 Db 794 KWTLSALLEATACALNRPCTTQARRLFDOWLASNKTQIPSDLMRTVFKVAAKTDEGS 853  
 QY YLLEQYELSSSAEQNKLYALSTSKHQEKLLKLELGMGKVIKTONLAALLHAIARRP 866  
 Db 854 KLGSYKHSIYDTEKRWLEALASTQDVVKIWIWLQKSLDGEIQNGEPLVHTVCRDF 913  
 QY KGQQLAWDFVRENWTHLLKKFDLGSYDIRMIISGTTAHFSSKDKLQEVKLPFESLEAQS 926  
 Db 914 AGLYVANDFMKENKEKITQKEPIGSPAQSIITSTTSQFSTKTHLAEVQNFSSILGAKGS 973  
 QY HLDIFQTVLETTIKNWKLEKNLPLRTWL 956  
 Db 974 QMRIVQEAETIKHNRWMEKNLTLQSWL 1003

RESULT 10  
 LCAP\_RAT  
 ID LCAP\_RAT STANDARD; PRT; 1025 AA.  
 AC P97629; Q11009;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)  
 DE (Oxytocinase) (OTase) (Insulin-regulated membrane aminopeptidase)  
 DE (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine  
 aminopeptidase) (P-LAP) (Vesicle protein of 165 kDa) (Vp165) (GP160).  
 GN Name=Lape; Synonyms=Irap, Otase;  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
RA MEDLINE=96007507; PubMed=755927; DOI=10.1074/jbc.270.40.23612;  
RX Keller S.R., Scott H.M., Mastick C.C., Aebersold R., Lienhard G.E.,  
RT "Cloning and characterization of a novel insulin-regulated membrane  
RT aminopeptidase from Glut4 vesicles";  
RL J. Biol. Chem. 270:23612-23618(1995).  
RN [2]  
RP SEQUENCE OF 168-176; 387-399; 731-740 AND 893-905.  
RX MEDLINE=94164972; PubMed=8119954;  
RA Mastick C.C., Aebersold R., Lienhard G.E.;  
RT "Characterization of a major protein in GLUT4 vesicles. Concentration  
RT in the vesicles and insulin-stimulated translocation to the plasma  
RT membrane";  
RL J. Biol. Chem. 269:6089-6092(1994).  
CC -!- FUNCTION: Release of an N-terminal amino acid, cleave before  
CC cysteine, leucine as well as other amino acids, degrades peptide  
CC hormones such as oxytocin, vasopressin and angiotensin III, and  
CC plays a role in maintaining homeostasis during pregnancy. May be  
CC involved in the inactivation of neuronal peptides in the brain.  
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may  
CC be the angiotensin IV receptor in the brain (By similarity).  
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-  
CC Xaa, in which the half-cysteine residue is involved in a disulfide  
CC loop, notably in oxytocin and vasopressin.  
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -!- SUBUNIT: Homodimer. Binds tankyrases 1 and 2 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Localized mainly  
CC in intracellular vesicles together with GLUT4. Relocalizes to the  
CC plasma membrane in response to insulin. The dileucine  
CC internalization motif and/or the interaction with tankyrases may  
CC be involved in intracellular sequestration.  
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, spleen,  
CC lung, kidney and white adipose tissue. Detected at lower levels in  
CC skeletal muscle and liver.  
CC -!- PTM: N-glycosylated.  
CC -!- SIMILARITY: Belongs to the peptidase M1 family.  
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
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DR EMBL; U76997; AAB19066.1; -;  
DR EMBL; U32990; AAB38021.1; -;  
DR PIR; I55441; I55441.  
DR MEKOPS; M01.011; -;  
DR InterPro; IPR001930; Peptidase M1.  
DR InterPro; IPR006025; Pept M Zn BS.  
DR Pfam; PF01433; Peptidase M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Aminopeptidase; Direct protein sequencing; Glycoprotein; Hydrolase;  
KW Metal-binding; Metalloprotease; Protease; Signal-anchor;  
KW Transmembrane; Zinc.  
FT DOMAIN 1 109  
FT TRANSMEM 110 131  
FT Signal-anchor for type II membrane  
FT protein (Potential).  
FT Extracellular (Potential).  
FT Dileucine internalization motif  
FT (Potential).  
FT Dileucine internalization motif  
FT (Potential).  
FT Tankyrase binding (By similarity).  
FT Zinc (catalytic) (By similarity).  
FT ACT\_SITE 464 465  
By similarity.

FT METAL	468	468	Zinc (catalytic) (By similarity).
FT METAL	487	487	Zinc (catalytic) (By similarity).
FT CARBOHYD	145	145	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	184	184	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	215	215	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	256	256	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	266	266	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	368	368	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	374	374	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	447	447	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	525	525	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	578	578	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	664	664	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	682	682	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	695	695	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	758	758	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	834	834	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	850	850	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	989	989	N-linked (GlcNAc. . .) (Potential).
FT CONFLICT	909	916	LMKSSLDG -> YGTTQRAW (in Ref. 1; AAB38021).
FT CONFLICT	916	1025	Missing (in Ref. 1; AAB38021).
SQ SEQUENCE	1025 AA;	11701 MW;	8AD3BA3A446FB5EF CRC64;
Query Match 40.1%; Score 2027; DB 1; Length 1025;			
Best Local Similarity 44.4%; Pred. No. 1.5e-111;			
Matches 402; Conservative 158; Mismatches 310; Indels 36; Gaps 5;			
Qy	54	PVATNGRFPQBELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNTQPIILHSK	113
Db	153	PIATNGKVFVPAQITLPTAIIPQRYELSLHPNTSMTFRGSVTISLQALQDTRDIILHST	212
Qy	114	DLEITNATLQSEBDSRYMKGKELKVLSPAHQIALLVPEKTLPHLKYVVMDFQAKG	173
Db	213	GHNISSVTFMSVSSQ-----EKQVEILEYPHQIAVAVAPESLLTGHNYLKIEYSANIS	268
Qy	174	DGFEFGYKTYRTLGGETRILAVTDFPPTQARMAFCDFEPLFKANFSIKIRRESRHIAL	233
Db	269	NSYVGFYGITVTDKSNKKNFAATQPEPLAARSAFFCPDFEPAPKATFIKITRDEHHTAL	328
Qy	234	SNMPKVTIEGLELDEHFTVTVMSTYLVAIVCDPHSLSGFTSSGKSVKSVYASDKR	293
Db	329	SNMPKSSVPTTEGLIQDFESVSKMSTYLVAIVGEMRLSQ-DVNGTLVSVVAVPEKI	387
Qy	294	NOHYALQASLKLLDFEYKFDIYVPLSKDLTAIPDFAPGAMENWGLITVYRSTSLFDP	353
Db	388	DQYHALDTTVKLEFFQNYFEIQYPLKLDLVAIPDFEAGAMENWGLITFRETLIDYN	447
Qy	354	KTSSADKLWTVRIAHQAHQWFGNLTVMWMDIWLKEGFAKYMELIAVNATYPQLQF	413
Db	448	ATSSVADRLVTKIIAHQAHQWFGNLTVMWMDIWLKEGFAKYMELIAVNATYPQLQF	507
Qy	414	DDYFLNVCFEVITKDSLNSSRPISKPAETPTQEMPEDEVSYNKGACILNKLKDFLEEK	473
Db	508	YEDFLDARFPTMRKDSLNSSHPISSSVSQSESEQEEMFDSLSYFKGASLLMLKSYLSEDV	567
Qy	474	FOKGIQYKKFSVRNAKNDLWLSNLSNCSLESDFTSGGCVCHSDPKMTSNMLAFLGNAE	533
Db	568	FQHAIIYLHNHSAVAIQSDDLWDSFNE-----VTGKTL	602
Qy	534	VKEMMTWTTLQKGIPLLVKQDCSLRLQOERFLQGVQEDPEWRALQERYLHPIPTYS	593
Db	603	VKKMKMTWTTLQKGFPLTVQRKGTLLQLQERFPFSM--QPEIQSDSTSLHPIPTISYV	659
Qy	594	TSSSNVTHRH---ILKSKTDTLDPKTSWVKVNDVNSGYIVHYEGHGDQILITOLNQN	650
Db	660	TGGRNYSYSESVSLDKKSDVINLTQGVQVQVNTNMTGYIIVHYAHGDAALINQLKRN	719
Qy	651	HTLLRPKDRVGLIHDFVQLVGAGRLTLDKALDMMTYTLQHTETSSPALLEGSLYESFYHMM	710
Db	720	PYVLSDKORANLNNFELAGLCKVPLQMAFDLIDYLRNETHAPITEALFQTDLIYNLL	779
Qy	711	DRRNISISENLKRYLLQYFKPVIHQSDWSKSGVMDRLRSALLKLACDLNHAPCIQKA	770

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Db 780 EKLGHMDLSRLVTRVHKLQNOIQOQWTWDEGTSFMRRLRSLLEFACAHLENCTTWA 839
Qy 771 AELFSOMESSGKLAIPDVLKIVSVGAQTAGNNYLLQYELSMSSAEQNKILYALST 830
Db 840 TKLFDGWMASNGTSLPTDVTMTVPKVGARTKGLFLFSMYSSMGSEAKDKILEALAS 899
Qy 831 SXHQEKLLKLELHGEGKVIKTONLAALLHATARPCKGOOLAWDFVRENWTHLLKKFDLG 890
Db 900 SADAHLKYLWLMKSSLDGDIIRTKLSLIIRTVGRQPPGHLAWDFVKNWNKLVHKPHLG 959
Qy 891 SYDIRMISGTTAFHSSKDKLEVKLFPSLEAQSHLDIFOTVLETTIKNIKLEKNLP 950
Db 960 STIOSIVAGSTHLFSTKTHLSEVQEFENQSEATLQRCVQAEFVIELNLOMWARNLK 1019
Qy 951 TLRTWL 956
Db 1020 TLTLWL 1025

RESULT 11
Q8C129
AC Q8C129 PRELIMINARY; PRT; 1025 AA.
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732490P18 product:INSULIN-REGULATED MEMBRANE
DE AMINOPEPTIDASE IRAP homolog.
GN Name=Lmep;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:683-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ighii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishihara T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imocani K., Ighii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kachi H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK029094; BAC26293.1; --
DR MEROPS: M01.011; --
DR MGD: MGI:2387123; lmpcp.
DR GO: GO:0005624; C:membrane fraction; IMP.
DR GO: GO:0004177; P:aminopeptidase activity; IMP.
DR GO: GO:0030163; P:protein catabolism; IMP.
DR InterPro: IPR000150; Hypothet cof.
DR InterPro: IPR001930; Peptidase_M1.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam: PF01433; Peptidase_M1; 1.
DR PRINTS: PR00756; ALADIPTASE.
DR PROSITE: PS01228; COF 1; UNKNOWN 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN 1.
KW Amino-peptidase.
SQ SEQUENCE 1025 AA; 117303 MW; AD6F98196EBA683B CRC64;

Query Match 40.0%; Score 2022; DB 2; Length 1025;
Best Local Similarity 44.7%; Pred. No. 2.9e-111;
Matches 405; Conservative 153; Mismatches 312; Indels 36; Gaps 6;

Qy 54 PVATNGERFPWQELRLPSVWPLHYDLFVHNLNLSLDVASEKIEVLVSNATQFILLHSK 113
Db 153 PVATNGKVPWPAQIRLPTAIIPLCYELSLHNLNLSMTFRGVSITSLQALQDTRDILHST 212
Qy 114 DLEITNATLQSEDSRYMKPKELVLSYPAHEQIALVPEKLTPLHLYVYVAMDFOAKLG 173
Db 213 GHNLSRVTFMSAVSQ-----EKQVEILEYPHEQIAVVAPEPLLTGCHNYTLKIEYSNIS 268

Qy 174 DGFEGFYKSTYRTLGGTRILAVTDPEPTQARMAPCFDEPLFKANFISKIRRESRHIAL 233
Db 269 NSYGYGYGITVTDKSNKKYFAATQFEPLEAARSAPCFDEPAFKATFIKITRNEHHTAL 328

Qy 234 SNMPKVTIELEGGLEDHFTTVMSTYLVAYIVCDPHSLSGFTSSGVKVIYASPKR 293
Db 329 SNMPKSSVPAEGLIQIDEFSESVKMSYLVAFIVGEMRNLSQ-DVNGTLVSVYAVPEKI 387

Qy 294 NOTHVALQASLKLDDEYKEDIYVPLSKLDLIAIPDPFAGMENVGLITVRETSLLFDP 353
Db 388 GQVHHAIDTTIKLEFFYQTYFEIQYPLKLDLVAIPDFEAGMENVGLITFREETLLYDN 447

Qy 354 KTSSASDKLWTRVIAHELAHQWFGNVLVTEWMDNIMLKEGFYKYMELIAYNATYPELQF 413
Db 448 ATSSVADRKLVTIKIAHELAHQWFGNVLVTEWMDNIMLNEGFATFMEYFSEKIFKELNS 507

Qy 414 DDYFLNVCFEVITKDSLNSSRPIKPAETPTQIEMDFEVSYNKACILNMLKDLGEEK 473
Db 508 YEFDLDAFRTMRKDSLNSHPISSSVQSSQISEMFDLSLYFGASLLMLKSLSDV 567

Qy 474 FQKGIIOYKKFSYRNKNDLWSSLNSCLESDFTSQGVCHSDPKMTSNMLAFIGENAE 533
Db 568 FRHAVILYLNHNSYAAIQSDDLWDSFN-----EVTDKTL-----D 602

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QY 534 VKEMMTTTLQKGIPLLVKODGSLRLOQERFLQGVFOEDPEWRALQERYLWHIPLTYS 593  
D 534 VKEMMTTTLQKGIPLLVKODGSLRLOQERFLQGVFOEDPEWRALQERYLWHIPLTYS 593  
Db 603 VKKMKTTTLQKGIPLLVKODGSLRLOQERFLQGVFOEDPEWRALQERYLWHIPLTYS 659  
QY 594 TSSNNVIRH---ILKSKTDLTDLPEKTSWYKFNVDNSNGYIYVHYEGHGWDLITQLNQ 650  
D 594 TSSNNVIRH---ILKSKTDLTDLPEKTSWYKFNVDNSNGYIYVHYEGHGWDLITQLNQ 650  
Db 660 TDGRNYSYRVSLSLDKSDVINLQTEQVQWVKVNSMTGYIYVHYAHDWDTALLINQLKRN 719  
QY 651 HTLLRPKDRVGLIHDVFLVAGRLTLDKALDMYTYLQHEHSSPALLBGLSYLESFYHMM 710  
D 651 HTLLRPKDRVGLIHDVFLVAGRLTLDKALDMYTYLQHEHSSPALLBGLSYLESFYHMM 710  
Db 720 PYVLSDKDRANLNNIFELAGLVKPLRMAFDLLDKNETHHTAPITFALFQTNLIYNLL 779  
QY 711 DRNIDISLENLRYLLQYFYPVDRQSWDKGSVMDRLRSALLKLACDLNHPACQKA 770  
D 711 DRNIDISLENLRYLLQYFYPVDRQSWDKGSVMDRLRSALLKLACDLNHPACQKA 770  
Db 780 EKLGHMDLSRLVARVHKLLQNLQOQQTWDEGTPSMRLRSALLFACAHLENCTMA 839  
QY 771 AELFSQWMESSGKLNIPDVLKIVYSGAQTAGNNYLLQYELSMGSAEQNKILYALST 830  
D 771 AELFSQWMESSGKLNIPDVLKIVYSGAQTAGNNYLLQYELSMGSAEQNKILYALST 830  
Db 840 TNLFDNMWASNGTQSLPTDVMVTVKVGARTEKGLWFLFSYSSWMSGSAEQNKILEALAS 899  
QY 831 SKHQEKLKLIELGMEGVKVTQNLALALLHAIARRPKQQLAWDFVENWTHLLKKFDLG 890  
D 831 SKHQEKLKLIELGMEGVKVTQNLALALLHAIARRPKQQLAWDFVENWTHLLKKFDLG 890  
Db 900 SEDVHKLWLMKSSLDGDIIRTKLSLIRTVGRHFGHLLAWDFVENWTHLLKKFDLG 959  
QY 891 SYDIRMIISGTTAFSSKDKQEVKLPFPELEAQSGLHLDIFQTVLETTIKNKKLEKNLP 950  
D 891 SYDIRMIISGTTAFSSKDKQEVKLPFPELEAQSGLHLDIFQTVLETTIKNKKLEKNLP 950  
Db 960 SYTQISVAGSTHLPSTKTHLSEVQAFENQSEATLKCRCQEALEVLQNLQWVRNLK 1019  
QY 951 TLRTWL 956  
D 1020 TLSQWL 1025

## RESULT 12

LCAP HUMAN STANDARD; PRT: 1025 AA.  
ID LCAP HUMAN STANDARD; PRT: 1025 AA.  
AC Q9UIQ6; O00769; Q15145; Q9UIQ7;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)  
DE (Oxytocinase) (Otrase) (Insulin-regulated membrane aminopeptidase)  
DE (Insulin)-responsive aminopeptidase (IRAP) (Placental leucine  
DE aminopeptidase) (P-LAP).  
GN Name=LNPEP; Synonyms=OTASE;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 160-168; 319-332; 615-624;  
RP 633-647; 798-814 AND 870-880.  
RC TISSUE=Placenta;  
RX MEDLINE=96132882; PubMed=8550619; DOI=10.1074/jbc.271.1.56;  
RA Rogi T., Tsujimoto M., Nakazato H., Mizutani S., Tomoda Y.;  
RT "Human placental leucine aminopeptidase/oxytocinase. A new member of  
RT type II membrane-spanning zinc metalloproteinase family.";  
RL J. Biol. Chem. 271:56-61(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Placenta;  
RX MEDLINE=97320624; PubMed=9177475; DOI=10.1016/S0167-4781(97)00036-5;  
RA Laustsen P.G., Rasmussen T.E., Petersen K., Pedraza-Diaz S.,  
RA Moestrup S.K., Gliemann J., Sottrup-Jensen L., Kristensen T.;  
RT "The complete amino acid sequence of human placental oxytocinase.";  
RL Biochim. Biophys. Acta 1352:1-7(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).  
RX MEDLINE=2022264; PubMed=10759854;  
RA Rasmussen T.E., Pedraza-Diaz S., Hardre R., Laustsen P.G.,  
RA Carrion A.G., Kristensen T.;  
RT "Structure of the human oxytocinase/insulin-regulated aminopeptidase

gene and localization to chromosome 5q21.";  
Eur. J. Biochem. 267:2297-2306(2000).  
[4]  
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
MEDLINE=21286092; PubMed=11389728;  
RA Matsumoto H., Nagasaka T., Hattori A., Rogi T., Tsuruoka N.,  
RA Mizutani S., Tsujimoto M.;  
RT "Expression of placental leucine aminopeptidase/oxytocinase in  
RT neuronal cells and its action on neuronal peptides.";  
Eur. J. Biochem. 268:3259-3266(2001).  
[5]  
CHARACTERIZATION.  
MEDLINE=92117646; PubMed=1731608;  
RA Tsujimoto M., Mizutani S., Adachi H., Kimura M., Nakazato H.,  
RA Tomoda Y.;  
RT "Identification of human placental leucine aminopeptidase as  
RT oxytocinase.";  
Arch. Biochem. Biophys. 292:388-392(1992).  
[6]  
FUNCTION.  
MEDLINE=21623680; PubMed=11707427; DOI=10.1074/jbc.C100512200;  
RA Albiston A.L., McDowall S.G., Matsacos D., Sim P., Clune E.,  
RA Mustafa T., Lee J., Mendelsohn F.A., Simpson R.J., Connolly L.M.,  
RA Chai S.Y.;  
RT "Evidence that the angiotensin IV (AT(4)) receptor is the enzyme  
RT insulin-regulated aminopeptidase.";  
J. Biol. Chem. 276:48623-48626(2001).  
CC -!- FUNCTION: Release of an N-terminal amino acid, cleave before  
CC cysteine, leucine as well as other amino acids. Degrades peptide  
CC hormones such as oxytocin, vasopressin and angiotensin III, and  
CC plays a role in maintaining homeostasis during pregnancy. May be  
CC involved in the inactivation of neuronal peptides in the brain.  
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may  
CC be the angiotensin IV receptor in the brain.  
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-  
CC Xaa, in which the half-cystine residue is involved in a disulfide  
CC loop, notably in oxytocin and vasopressin.  
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -!- SUBUNIT: Homodimer. Binds tankyrase 1 and 2.  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted.  
CC During pregnancy serum levels are low in the first trimester, rise  
CC progressively during the second and third trimester and decrease  
CC rapidly after parturition. In brain only the membrane-bound form  
CC is found. The protein resides in intracellular vesicles together  
CC with GLUT4 and can then translocate to the cell surface in  
CC response to insulin and/or oxytocin. Localization may be  
CC determined by dileucine internalization motifs, and/or by  
CC interaction with tankyrase.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Experimental confirmation may be lacking for some  
CC isoforms;  
CC Name=1;  
CC IsoId=Q9UIQ6-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9UIQ6-2; Sequence=VSP\_005448;  
CC Name=3;  
CC IsoId=Q9UIQ6-3; Sequence=VSP\_005449;  
CC -!- TISSUE SPECIFICITY: Highly expressed in placenta, heart, kidney  
CC and small intestine. Detected at lower levels in neuronal cells in  
CC the brain, in skeletal muscle, spleen, liver, testes and colon.  
CC -!- PTM: The pregnancy serum form is derived from the membrane-bound  
CC form by proteolytic processing.  
CC -!- PTM: N-glycosylated.  
CC -!- SIMILARITY: Belongs to the peptidase M1 family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))





Db 534 GNDFLYKYSQSSTKESQIFSLCTSKDPKQLWLLDQSKFGKGIKQEPHILTLIG 593  
Qy 864 RRPKQOQLAWDFVRENWTHLLKKFDLGSYDIRMIISGTTAHFSSKDKLQEVKLPFFESLEA 923  
Db 594 RNPVGYPALAKFLRENWNLVKQFELGSSSIAHWMTGTTDQFSTRALKEEVKGFSSSLKE 653  
Qy 924 QCSHLDFQTVLETTIKNKLKLEKLPULRTWL 956  
Db 654 NGSQRLRCVQOQTETIETIENIRWMDKNPDKIRLWL 686

## RESULT 14

ID Q6PCG5 PRELIMINARY; PRT; 997 AA.  
AC O6PCG5;  
DT 05-JUL-2004 (trEMBLrel. 27, Created)  
DT 05-JUL-2004 (trEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (trEMBLrel. 27, Last annotation update)  
DE MGC69084 protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Klein S., Strausberg R.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC059334; AAH59334.1; -  
DR GO; GO:0004179; Fmembrane ananyl aminopeptidase activity; IEA.  
DR GO; GO:0006508; Proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001930; Peptidase M1.  
DR InterPro; IPR006025; Pept M Zn Bs.  
DR Pfam; PF01433; Peptidase M1; 1.  
DR PRINTS; PR00756; ALADIPTASE;  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
SQ SEQUENCE 997 AA; 113619 MW; 460E0EC895D0A14 CRC64;

Query Match 36.6%; Score 1847; DB 2; Length 997;  
Best Local Similarity 41.7%; Pred. No. 6.8e-101; Indels 88; Gaps 16;  
Matches 383; Conservative 161; Mismatches 287;  
Qy 53 PPVATNGRRFPQOELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNAQPIIHLHS 112  
Db 150 YPIARNGKVPFPAWLSRLPNSIKPIHYILTLHPNMTMSFTGTQVQINLNTARSKNIVLHS 209  
Qy 113 KDLBITNATLOSBEEDSRMKPG---KELKVIISYPAHQIALLVPEKLPKLPKLYVYVAMDFQ 169  
Db 210 SDLRITKANV-----LVPGGTTMDAEVLEYPREFEIAIISPESL-PKGNCLLTIEYT 260  
Qy 170 AKLGDGPEGYKSTYRTLGGETRILAVTDPPTOARMAPPCFDEPLFKANESIK-IRRES 228  
Db 261 SNFSSSYGYFKIDYMDKGSK-RSLAATQFEPFAKAPCFDEPAFASFTQINIRKDE 319  
Qy 229 RHIALSNMPKVTIELEGGLLEDFETTVKMSHTVLVAVIVCDFHSLSGFTSSGVKUSIYA 288  
Db 320 SMISLSNMPKAKTSTNDGLLDLDFSTSVKMSVILVAFIVGDIKNTTRETNDTL-VSVYT 378  
Qy 289 SPDKNQTHYALQASLKLLDFEYKFDIYYPLSKLDLIAIPDFAPGAMENGLIITYRETS 348  
Db 379 VPEKTDQVKYALDSAVKLLDFSYNYGKYPLEKLDLVAIPDFQAAAMENMGLITFRETS 438  
Qy 349 LLPDPKTSASDKLWTVRVIAHSLAHQWFGNLTWEMNDIWLKEGFAKYMELIIVNATY 408  
Db 439 LLYNEDSSIKDKQTITIAIAHELTHQWFGNLTWEMNDIWLKEGFAKYMELIIVNATY 498  
Qy 409 PELQFDDYFLNVCPEVITKDSLSRPTSKAETPTQIQEMFDEVSYNKGACILNMLKDF 468  
Db 499 PELNSENDFLOVPWALKKDSLSNASHPISTDIRSPEQIEEMFNDSYIKGASILLMLKTF 558  
Qy 469 LGEKFKGIIQYLKFSYRNAKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAF 528  
Db 559 LSEDMFHLIRSLSHQSHQYGGTSDSLWDSLN-----VVT 593  
Qy 529 GENAEVKEMTTWILQKIPILVVKQDCSLRLOQERFLOGVFQEDPEWALQERYLWHI 588  
Db 594 KENPNVNMKMTWTKAGYPLVTLARKGEEITVQERFLRST---KPD-HATNASTVWHI 649  
Qy 599 PLTVSTSSNVIHR-----HILKSTDTLDLPEKTSWVKFNVDNSNGYIVHYEGHGDOL 643  
Db 650 PLTVTKKNGVDPDCVKYLLKAPTGTINVSSEFPWVKFNVMNTGYIIVDYGADWDAL 709  
Qy 644 ITQLNQNTLARPDRVGLIHDVFLQVAGRLTLDKALDMTYIYLQHETSSPALLBGLSYL 703  
Db 710 IEQLHRDHTVLHSSDRANLIHDIWLAGVGVPLAKAFKLLGLVNETDSAPIQA--L 766  
Qy 704 ESPTH---MDDRNISDISENLKRYLQYFKPVDTRQSWSDKGSVWDRMLRSALKLACD 760  
Db 767 HQFYHIRGILLKRGDLDDSLKMERGLDNLNTLIKQTKDEGLTAEERLTSLLDPACS 826  
Qy 761 LNHAPCLOKAAELFSQWMESSGKLNIPTDVLKIYVVGQAQTTAGWNLYLEOVELSSSAE 820  
Db 827 NGVNLCDRLATLFSNW--RNETRIPSDVINIVFKVGTKTTEGTFPLRRRVDSIIYSE 884  
Qy 821 QNKILYALSTSKHQEKLLKLIELGMEGVKVIKTQNLAAALLHAIARRPKQQLAWDFVRENW 880  
Db 885 KSKILEALSTDNAKDLQGLMQESLAGGSIRSQELPNVISFICRRSPGVLLAWNPKQNW 944  
Qy 881 THLLKKFPLGSDYIRMIISGTTAHP--SSKOKLQEVKLPFESLEAQGSHLDIFQTVLETI 938  
Db 945 NLITQKL-----LHFFNSTKEKSRVWYVKEA-----LETI 975  
Qy 939 TKNIKWLKELNPLTARTWLM 957  
Db 976 KLINIKWMKNLSDLSKTWLL 994

## RESULT 15

Q8WVJ4  
ID Q8WVJ4 PRT; 350 AA.  
AC Q8WVJ4;

Search completed: September 26, 2005, 06:10:34  
Job time : 188 secs

```
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE LRAP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017927; AAH17927.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR PRINTS; PR00756; ALADIPTASE.
SQ SEQUENCE 350 AA; 4060 MW; 5234F40276A81253 CRC64;

Query Match          33.5%; Score 1690; DB 2; Length 350;
Best Local Similarity 99.1%; Pred. No. 3.3e-92;
Matches 322; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFHSSAMVNSHRKPMFNIRHGFYCLTALPQICICQSFSPSSYHFTDPGAFPVATNGE 60
Db 1 MFHSSAMVNSHRKPMFNIRHGFYCLTALPQICICQSFSPSSYHFTDPGAFPVATNGE 60

QY 61 RPPQQLRLPSVPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSQLEITNA 120
Db 61 RPPQQLRLPSVPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHKSQLEITNA 120

QY 121 TLQSEDSRYMKPGKELVSLVPAHEQIALVPEKLTPLHLYVYVAMDFOAKLGDGEGFY 180
Db 121 TLQSEDSRYMKPGKELVSLVPAHEQIALVPEKLTPLHLYVYVAMDFOAKLGDGEGFY 180

QY 181 KSTYRTLGGTRILAVTDPEPTQARMAPFCDEPLFKANFSIKIRRESRHIALSNMPKV 240
Db 181 KSTYRTLGGTRILAVTDPEPTQARMAPFCDEPLFKANFSIKIRRESRHIALSNMPKV 240

QY 241 TIEEGGLLEHFFETVVKMSTYLVAYIVCDFHSLSGFTSSGVKYSIYASDPKRNQTHYAL 300
Db 241 TIEEGGLLEHFFETVVKMSTYLVAYIVCDFHSLSGFTSSGVKYSIYASDPKRNQTHYAL 300

QY 301 QASLKLLDFYKYFDIYYPLSKLDL 325
Db 301 QASLKLLDFYKYFDIYYPLSKLGM 325
```

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 06:03:26 ; Search time 170 Seconds  
(without alignments)  
2184.059 Million cell updates/sec

Title: US-10-039-073-1  
Perfect score: 5052  
Sequence: 1 MFHSAMVNSHRKPNFTHR.....NIKWLKRLPTLRTWLMVNT 960

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	100.0	960	4	AAB60299 Human ami
2	5052	100.0	960	4	AAB60299 Human pro
3	5048	99.9	960	5	Abp69122 Human pol
4	4141	82.0	785	5	Abp63022 Human pol
5	3799	75.2	728	4	Abb10338 Human CDN
6	3799	75.2	728	5	Abp66925 Human pol
7	3770	74.6	722	4	Aau22999 Novel hum
8	3770	74.6	722	4	Abb10511 Human CDN
9	3770	74.6	722	5	Abp67098 Human pol
10	3763	74.5	722	5	Adr41453 Human CD-
11	2516.5	49.8	941	4	Aau07829 Human ART
12	2515.5	49.8	941	5	Abp90347 Human pol
13	2515.5	49.8	941	6	Adh56820 Human sec
14	2515.5	49.8	941	6	Abp67098 Human pol
15	2515.5	49.8	941	6	Abp67098 Human pol
16	2515.5	49.8	941	7	Abp67098 Human pol
17	2515.5	49.8	941	7	Abp67098 Human pol
18	2515.5	49.8	941	7	Abp67098 Human pol
19	2515.5	49.8	941	7	Abp67098 Human pol
20	2515.5	49.7	941	3	Aay66736 Membrane-
21	2512.5	49.7	941	3	Aab24422 Human PRO
22	2512.5	49.7	941	4	Aau12403 Human PRO
23	2512.5	49.7	941	4	Aau12403 Human PRO
24	2512.5	49.7	941	4	Abp65259 Human PRO
25	2512.5	49.7	941	6	Abu58074 Human PRO
26	2512.5	49.7	941	6	Abu59152 Novel hum

ALIGNMENTS

RESULT 1  
AAB60299  
ID AAB60299 standard; protein; 960 AA.

AC AAB60299;  
XX  
XX  
DT 06-APR-2001 (first entry)  
DE Human aminopeptidase 17867.  
XX  
KW Human aminopeptidase 17867; neutral zinc metalloproteinase;  
KW zinc-binding region; M1 aminopeptidase family; lung disorder;  
KW colon disorder; lung cancer; colon cancer; breast cancer; tumour;  
KW squamous cell carcinoma; insulin-related disorder; diabetes;  
KW drug screening.  
XX  
OS Homo sapiens.  
XX  
PN WO200100811-A2.  
XX  
PD 04-JAN-2001.  
XX  
PF 30-JUN-2000; 2000WO-US018250.  
XX  
PR 30-JUN-1999; 99US-00345650.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Kapeller-Libermann R, Williamson M;  
XX  
DR WPI; 2001-137953/14.  
DR N-ESDB; AAF27148.  
XX  
PT Novel human aminopeptidase polypeptide and polynucleotide useful as  
PT target for diagnosis and treatment in aminopeptidase-related disorders  
PT and for identifying modulators of therapeutic use.  
XX  
XX Claim 9; Fig 1; 92pp; English.  
XX  
CC The invention relates to a novel human aminopeptidase, designated  
CC aminopeptidase 17867 (AAB60299) and to cDNA encoding aminopeptidase 17867  
CC (AAF27148). Human aminopeptidase 17867 contains a neutral zinc  
CC metalloproteinase zinc-binding region signature motif at residues 367-376,  
CC and an M1 aminopeptidase signature motif at residues 334-338. The  
CC invention also relates to host cells comprising human aminopeptidase  
CC 17867 DNA, the preparation of the protein, an antibody which binds to the  
CC protein, methods of detection of the protein, methods of modulating  
CC activity of the protein, and methods of identifying modulators of protein

CC activity. Aminopeptidase 17867 proteins and nucleic acids are useful as  
CC targets for diagnosis and treatment in aminopeptidase- related diseases.  
CC Such diseases include a wide variety of lung disorders (e.g., pulmonary  
CC embolism, pulmonary hypertension, emphysema, bronchial asthma) and colon  
CC disorders (e.g., diarrhoea, dysentery, Crohn's disease, ulcerative  
CC colitis). In particular, they may be used in the diagnosis and treatment  
CC of breast and colon carcinoma, lung carcinoma (especially squamous cell  
CC carcinoma), and insulin-related disorders such as diabetes. The  
CC aminopeptidase 17867 proteins are also useful in drug screening methods  
CC to identify modulators of activity, and for raising antibodies for use in  
CC diagnosis and treatment. The present sequence represents human  
CC aminopeptidase 17867  
XX  
SQ

Query Match 100.0%; Score 5052; DB 4; Length 960;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFHSSAMVNSHRKPMFNTHRGFYCLTAILPQICCSQFSVPSSVHFTDPCGAPFVATNGE 60  
Db |||||  
Qy 1 MFHSSAMVNSHRKPMFNTHRGFYCLTAILPQICCSQFSVPSSVHFTDPCGAPFVATNGE 60  
Db |||||  
Qy 61 RPPMQELRLPSVPIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHASKOLEITNA 120  
Db |||||  
Qy 121 TLQSEDSRYMKPGKELKVLSPYAEHQIALLVPEKLTPLHLKYVYVNDPQAKLGDFGEGFY 180  
Db |||||  
Qy 121 TLQSEDSRYMKPGKELKVLSPYAEHQIALLVPEKLTPLHLKYVYVNDPQAKLGDFGEGFY 180  
Db |||||  
Qy 181 KSTYTLGGETRILAVTDFEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPKVK 240  
Db |||||  
Qy 181 KSTYTLGGETRILAVTDFEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPKVK 240  
Db |||||  
Qy 241 TIELEGGLEDHFFETVTKMSTYLVAYIVCDFHSLSGFTSSGKVSIVASPDKRNQTHYAL 300  
Db |||||  
Qy 241 TIELEGGLEDHFFETVTKMSTYLVAYIVCDFHSLSGFTSSGKVSIVASPDKRNQTHYAL 300  
Db |||||  
Qy 301 QASLKLLDFEYKFDIYYPLSKLDLIAIPDFAPGAMENWGLITVRETSLLDPKTSASD 360  
Db |||||  
Qy 301 QASLKLLDFEYKFDIYYPLSKLDLIAIPDFAPGAMENWGLITVRETSLLDPKTSASD 360  
Db |||||  
Qy 361 KLWTRVIAHELAWHGFNLVTMEWNDIWLKEGFAKYMELIANVATYPELQFDYFLNV 420  
Db |||||  
Qy 361 KLWTRVIAHELAWHGFNLVTMEWNDIWLKEGFAKYMELIANVATYPELQFDYFLNV 420  
Db |||||  
Qy 421 CFEVITKDSLSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIQ 480  
Db |||||  
Qy 421 CFEVITKDSLSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKEFKGIQ 480  
Db |||||  
Qy 481 YLKFSYRNAKNDLLWSLSNSCLESDFTSGGVCHSDPKMTSNMLAFIAGENAEVKEMWTT 540  
Db |||||  
Qy 481 YLKFSYRNAKNDLLWSLSNSCLESDFTSGGVCHSDPKMTSNMLAFIAGENAEVKEMWTT 540  
Db |||||  
Qy 541 WTLQKGIPLLVKQDCSLRQLQERFLQGVQEDPWRALQERYLWHIPLTYSTSSNVI 600  
Db |||||  
Qy 541 WTLQKGIPLLVKQDCSLRQLQERFLQGVQEDPWRALQERYLWHIPLTYSTSSNVI 600  
Db |||||  
Qy 601 HRHLKSKTDLTDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQNHLLRPKDRV 660  
Db |||||  
Qy 601 HRHLKSKTDLTDLPEKTSWVKFNVDNSNGYIYVHVEGHGWDLITQLNQNHLLRPKDRV 660  
Db |||||  
Qy 661 GLIHDVFLVAGRLTDLKALDNTYLLQHEFTSSPALLGLSYLSFYHMDRRNISDISE 720  
Db |||||  
Qy 661 GLIHDVFLVAGRLTDLKALDNTYLLQHEFTSSPALLGLSYLSFYHMDRRNISDISE 720  
Db |||||  
Qy 721 NLKRYLQVFKPVIDRQSWSDKGSVWDRMLASALLKLACDLNHPACIOKAELFSQWMS 780  
Db |||||  
Qy 721 NLKRYLQVFKPVIDRQSWSDKGSVWDRMLASALLKLACDLNHPACIOKAELFSQWMS 780  
Db |||||  
Qy 781 SGKLNIPDVLKIVYSGAQTTFAGWNYLLLEQYELSMSSAEQNKILYALSTSKHOEKLKL 840  
Db |||||

Db 781 SGKLNIPDVLKIVYSGAQTTFAGWNYLLLEQYELSMSSAEQNKILYALSTSKHOEKLKL 840  
Qy 841 IELGMEGKVIKTQNLALALHAIARRPKGOQLANDFVRENWTHLLKKFDLGSYDIRMIISG 900  
Db |||||  
Qy 841 IELGMEGKVIKTQNLALALHAIARRPKGOQLANDFVRENWTHLLKKFDLGSYDIRMIISG 900  
Db |||||  
Qy 901 TTAHFSSKDKLQEVKLFESLEAQQSHLDIFQTVLETTITNKNWLEKNLPLTRTLMWNT 960  
Db |||||  
Qy 901 TTAHFSSKDKLQEVKLFESLEAQQSHLDIFQTVLETTITNKNWLEKNLPLTRTLMWNT 960  
Db |||||  
RESULT 2  
AAE04879  
ID AAE04879 standard; protein; 960 AA.  
XX  
AC AAE04879;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human protease protein-6 (PRTS-6).  
XX  
DE Human; protease protein-6; PRTS-6; cytostatic; hypotensive; gene therapy;  
KW gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;  
KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;  
KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;  
KW acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;  
KW developmental disorder; epithelial disorder; eczema; dementia; neotropic;  
KW neurological disorder; reproductive disorder; infertility; teratogenesis;  
KW immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;  
KW anaemia; antitumour; antiviral; antibacterial.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..35  
FT Protein /label= Signal\_peptide  
FT /note= "Mature human PRTS-6"  
FT Binding-site 367..377  
FT /label= Zinc\_binding\_region  
FT Binding-site 367..376  
FT /label= Zinc\_binding\_region  
XX  
PN WO200146443-A2.  
XX  
PD 28-JUN-2001.  
XX  
PF 19-DEC-2000; 2000WO-US034811.  
XX  
PR 23-DEC-1999; 99US-0172055P.  
PR 21-JAN-2000; 2000US-0177334P.  
PR 28-JAN-2000; 2000US-0178884P.  
PR 02-FEB-2000; 2000US-0179903P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;  
PI Yue H, Nguyen DB, Tang YT, Yao MG, Lal P;  
XX  
DR WPI; 2001-418080/44.  
DR N-PSDB; AAD09543.  
XX  
PT Novel human protease proteins (PRTS) useful for diagnosing, treating,  
PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,  
XX cell proliferative disorders associated with abnormal expression of PRTS.  
PS Claim 1; Page 110-112; 129pp; English.  
XX  
CC The present sequence is human protease protein (PRTS-6). Human PRTS and  
CC its nucleic acid molecule are useful for the diagnosis, treatment and  
CC prevention of disorders associated with increased or decreased expression  
CC of PRTS. Examples of such disorders include, gastrointestinal disorder  
CC such as anorexia, dysphagia; cardiovascular disorder such as

CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as  
CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative  
CC disorder such as actinic keratosis, cirrhosis; developmental disorder  
CC such as epilepsy, anaemia; epithelial disorder such as allergic contact  
CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,  
CC dementia and reproductive disorder such as infertility and teratogenesis.  
CC PRS DNA is useful for creating 'knockin' humanised animals (pigs) or  
CC transgenic animals (mice or rats) to model human disease. PRS DNA is  
CC also useful in gene therapy. PRS and its immunogenic fragments are  
CC useful for screening libraries of compounds in several drug screening  
CC assays. PRS is useful for analysing the proteome of a tissue or cell  
CC type  
XX  
SQ Sequence 960 AA;  
Query Match 100.0%; Score 5052; DB 4; Length 960;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFHSAMVNSHRKPMFNHRRFYCLTALPQICISQSPVSSVHYFTBDPGAPPVATNGE 60  
Db 1 MFHSAMVNSHRKPMFNHRRFYCLTALPQICISQSPVSSVHYFTBDPGAPPVATNGE 60  
Qy 61 RPPQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSKOLEITNA 120  
Db 61 RPPQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSKOLEITNA 120  
Qy 121 TQSEEDSRYPKPKELVSLYPANHEQIALVPEKLTPLHLYVYVAMDFQAKLGDFEGFY 180  
Db 121 TQSEEDSRYPKPKELVSLYPANHEQIALVPEKLTPLHLYVYVAMDFQAKLGDFEGFY 180  
Qy 181 KSTVTLGGETRILAVTDFEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPVK 240  
Db 181 KSTVTLGGETRILAVTDFEPTQARMAPPCDEPLFKANFSIKIRRESRHIALSNMPVK 240  
Qy 241 TIELEGGLEHFFETVKNSTYLVAYIVCDPHSLSGFTSSGVKSIYASPKRNQTHVAL 300  
Db 241 TIELEGGLEHFFETVKNSTYLVAYIVCDPHSLSGFTSSGVKSIYASPKRNQTHVAL 300  
Qy 301 QASKLDFEYKYFDIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLPDKPTSSASD 360  
Db 301 QASKLDFEYKYFDIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLLPDKPTSSASD 360  
Qy 361 KLWTRVIAHELAWQFNLVTMEWNDIWLKEGPAKYMELIANVATYPELQFDYFLNV 420  
Db 361 KLWTRVIAHELAWQFNLVTMEWNDIWLKEGPAKYMELIANVATYPELQFDYFLNV 420  
Qy 421 CFEVITKDSLSRRPISPKAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGIIQ 480  
Db 421 CFEVITKDSLSRRPISPKAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGIIQ 480  
Qy 481 YLKXPSYRNKNDLWSLSNCSLESDFTSGGVCHSDPKMTSNMLAFLGNAEVKEMMTT 540  
Db 481 YLKXPSYRNKNDLWSLSNCSLESDFTSGGVCHSDPKMTSNMLAFLGNAEVKEMMTT 540  
Qy 541 WTLQKGIPLLVKQDGSRLRQERFLQGVQEDPEWALQERYLWHIPLTYSTSSNVI 600  
Db 541 WTLQKGIPLLVKQDGSRLRQERFLQGVQEDPEWALQERYLWHIPLTYSTSSNVI 600  
Qy 601 HRHILKSTDTLDLPEKTSWKNFVNSNGYIVVHYEGHWDLITQLNQNHTLLRPKDRV 660  
Db 601 HRHILKSTDTLDLPEKTSWKNFVNSNGYIVVHYEGHWDLITQLNQNHTLLRPKDRV 660  
Qy 661 GLIHDFVQLVAGRITLTKALDMTYLQHETSSPALLEGLSYLESFYHMDRRNISDISE 720  
Db 661 GLIHDFVQLVAGRITLTKALDMTYLQHETSSPALLEGLSYLESFYHMDRRNISDISE 720  
Qy 721 NLKRYLLQYFKPIDRQSWDKGSVWDRMLRSALLKLACDLNHPACIQKAAELFSQWMS 780  
Db 721 NLKRYLLQYFKPIDRQSWDKGSVWDRMLRSALLKLACDLNHPACIQKAAELFSQWMS 780  
Qy 781 SGKLNIPDVLKIVYVSGAQTAGNVLLEQYELSMSSAEQNKILYALSTSKHQEKLKL 840  
Db 781 SGKLNIPDVLKIVYVSGAQTAGNVLLEQYELSMSSAEQNKILYALSTSKHQEKLKL 840

Db 781 SGKLNIPDVLKIVYVSGAQTAGNVLLEQYELSMSSAEQNKILYALSTSKHQEKLKL 840  
Qy 841 IELGMECKVIKTQNLQALALHAIARRPKGQQLANDFVRENWTHLLKKFPLDGSYDIRMIISG 900  
Db 841 IELGMECKVIKTQNLQALALHAIARRPKGQQLANDFVRENWTHLLKKFPLDGSYDIRMIISG 900  
Qy 901 TTAHFSSKDKLOEVKLPFESLEAGSHLDIFQTVLETITKNIKWLKLNPLTLRTWLMVNT 960  
Db 901 TTAHFSSKDKLOEVKLPFESLEAGSHLDIFQTVLETITKNIKWLKLNPLTLRTWLMVNT 960  
RESULT 3  
ABP69122  
ID ABP69122 standard; protein; 960 AA.  
XX  
AC ABP69122;  
XX AC  
XX 20-JAN-2003 (first entry)  
XX  
XX Human polypeptide SEQ ID NO 1169.  
DE Human; genome mapping; gene therapy; food supplement; virus; fungus;  
XX cell-proliferative disorder; neurodegenerative disease; bacterial;  
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;  
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
XX arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
XX haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
XX antiarthritic.  
XX  
XX Homo sapiens.  
XX  
XX WO200270539-A2.  
XX  
XX 12-SEP-2002.  
XX  
XX 05-MAR-2002; 2002WO-US005095.  
XX  
XX 05-MAR-2001; 2001US-00799451.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
XX Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
XX WPI; 2002-759812/82.  
XX  
XX N-PSDB; ABZ11339.  
XX  
XX New polynucleotides comprising sequences assembled from expressed  
XX sequence tags (ESTs), useful for treating cell-proliferative,  
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
XX or coagulation disorders.  
XX  
XX Claim 9; SEQ ID NO 1169; 1012pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) comprising a  
XX nucleotide sequence selected from any of 948 sequences (ABZ11119-  
XX ABZ12066) or their mature protein coding portion, active domain coding  
XX protein or complementary sequences. The polynucleotides are useful for  
XX identifying expressed genes or for physical mapping of human genome. The  
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight  
XX markers, as a food supplement, for generating antibodies, in medical  
XX imaging, screening and diagnostic assays and for treating cell-  
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
XX arthritis, etc. Note: The sequence data for this patent did not form part  
XX of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SQ		Sequence 960 AA;					
Query Match		99.9%; Score 5048; DB 5; Length 960;					
Best Local Similarity		99.9%; Pred. No. 0;					
Matches 959; Conservative 1; Mismatches 0; Indels 0; Gaps 0;							
Qy	1	MFHSSAMVNSHRKPMFNHRGFYCLTALPQICISQFSVPSSYHFTEDPGAFVATNGE	60	Qy	1	MFHSSAMVNSHRKPMFNHRGFYCLTALPQICISQFSVPSSYHFTEDPGAFVATNGE	60
Db	1	MFHSSAMVNSHRKPMFNHRGFYCLTALPQICISQFSVPSSYHFTEDPGAFVATNGE	60	Db	1	MFHSSAMVNSHRKPMFNHRGFYCLTALPQICISQFSVPSSYHFTEDPGAFVATNGE	60
Qy	61	RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDLEITNA	120	Qy	61	RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDLEITNA	120
Db	61	RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDLEITNA	120	Db	61	RFPWQELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSDLEITNA	120
Qy	121	TLOSEEDSRVMKPGKELKVLSPAHEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGFGFY	180	Qy	121	TLOSEEDSRVMKPGKELKVLSPAHEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGFGFY	180
Db	121	TLOSEEDSRVMKPGKELKVLSPAHEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGFGFY	180	Db	121	TLOSEEDSRVMKPGKELKVLSPAHEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGFGFY	180
Qy	181	KSTYRTLGGETRILAVTDFEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK	240	Qy	181	KSTYRTLGGETRILAVTDFEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK	240
Db	181	KSTYRTLGGETRILAVTDFEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK	240	Db	181	KSTYRTLGGETRILAVTDFEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK	240
Qy	241	TIELEGGLLEDHFTTVMKSTYLVAVIYVCDPHSLSGFTSSGKVSIIYASDPKRNQTHYAL	300	Qy	241	TIELEGGLLEDHFTTVMKSTYLVAVIYVCDPHSLSGFTSSGKVSIIYASDPKRNQTHYAL	300
Db	241	TIELEGGLLEDHFTTVMKSTYLVAVIYVCDPHSLSGFTSSGKVSIIYASDPKRNQTHYAL	300	Db	241	TIELEGGLLEDHFTTVMKSTYLVAVIYVCDPHSLSGFTSSGKVSIIYASDPKRNQTHYAL	300
Qy	301	QASLKLDJFYFYDIYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLPDKTSSASD	360	Qy	301	QASLKLDJFYFYDIYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLPDKTSSASD	360
Db	301	QASLKLDJFYFYDIYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLPDKTSSASD	360	Db	301	QASLKLDJFYFYDIYPLSKLDLIAIPDFAPGAMENWGLITYRETSLLPDKTSSASD	360
Qy	361	KLWTRVIAHELAWHGFNLVMEWMDIWLKEGFAKYMELIAVNATYPELQFDYDFLNV	420	Qy	361	KLWTRVIAHELAWHGFNLVMEWMDIWLKEGFAKYMELIAVNATYPELQFDYDFLNV	420
Db	361	KLWTRVIAHELAWHGFNLVMEWMDIWLKEGFAKYMELIAVNATYPELQFDYDFLNV	420	Db	361	KLWTRVIAHELAWHGFNLVMEWMDIWLKEGFAKYMELIAVNATYPELQFDYDFLNV	420
Qy	421	CFEVITKDSLNSSRPISKPAETPTQIQEMFEVSYNKGACILNMLKDFLGEERFKQGIQ	480	Qy	421	CFEVITKDSLNSSRPISKPAETPTQIQEMFEVSYNKGACILNMLKDFLGEERFKQGIQ	480
Db	421	CFEVITKDSLNSSRPISKPAETPTQIQEMFEVSYNKGACILNMLKDFLGEERFKQGIQ	480	Db	421	CFEVITKDSLNSSRPISKPAETPTQIQEMFEVSYNKGACILNMLKDFLGEERFKQGIQ	480
Qy	481	YLKGFVSNKNDLWSLSNCSLESDFTSGVCHSDPKMTSNMLAFGENAEVKNMTT	540	Qy	481	YLKGFVSNKNDLWSLSNCSLESDFTSGVCHSDPKMTSNMLAFGENAEVKNMTT	540
Db	481	YLKGFVSNKNDLWSLSNCSLESDFTSGVCHSDPKMTSNMLAFGENAEVKNMTT	540	Db	481	YLKGFVSNKNDLWSLSNCSLESDFTSGVCHSDPKMTSNMLAFGENAEVKNMTT	540
Qy	541	WTLQKGIPLLVVKQDGSRLRQERFLQGVQEDPEWRALQERYLWHPITYSTSSNVI	600	Qy	541	WTLQKGIPLLVVKQDGSRLRQERFLQGVQEDPEWRALQERYLWHPITYSTSSNVI	600
Db	541	WTLQKGIPLLVVKQDGSRLRQERFLQGVQEDPEWRALQERYLWHPITYSTSSNVI	600	Db	541	WTLQKGIPLLVVKQDGSRLRQERFLQGVQEDPEWRALQERYLWHPITYSTSSNVI	600
Qy	601	HRHILKSTDTLDLPEKTSWVKFNVDNSNGYIVHYEGHGDQLITQLNQHTLLRPKDRV	660	Qy	601	HRHILKSTDTLDLPEKTSWVKFNVDNSNGYIVHYEGHGDQLITQLNQHTLLRPKDRV	660
Db	601	HRHILKSTDTLDLPEKTSWVKFNVDNSNGYIVHYEGHGDQLITQLNQHTLLRPKDRV	660	Db	601	HRHILKSTDTLDLPEKTSWVKFNVDNSNGYIVHYEGHGDQLITQLNQHTLLRPKDRV	660
Qy	661	GLIHDVQLVAGRLTLDKALDWTYIQLHETSSPALLGSLYSLSFYHMDRRNISDISE	720	Qy	661	GLIHDVQLVAGRLTLDKALDWTYIQLHETSSPALLGSLYSLSFYHMDRRNISDISE	720
Db	661	GLIHDVQLVAGRLTLDKALDWTYIQLHETSSPALLGSLYSLSFYHMDRRNISDISE	720	Db	661	GLIHDVQLVAGRLTLDKALDWTYIQLHETSSPALLGSLYSLSFYHMDRRNISDISE	720
Qy	721	NLKEYLLQYKFPVIDRQSWSDKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS	780	Qy	721	NLKEYLLQYKFPVIDRQSWSDKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS	780
Db	721	NLKEYLLQYKFPVIDRQSWSDKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS	780	Db	721	NLKEYLLQYKFPVIDRQSWSDKGSVMDRLRSALLKLACDLNHAPCIQKAELFSQWMS	780
Qy	781	SGKUNIPDVLKIVYSGAQTAGNVLLEYELSMSSABONKILYALSTSKHQEKLLKL	840	Qy	781	SGKUNIPDVLKIVYSGAQTAGNVLLEYELSMSSABONKILYALSTSKHQEKLLKL	840
Db	781	SGKUNIPDVLKIVYSGAQTAGNVLLEYELSMSSABONKILYALSTSKHQEKLLKL	840	Db	781	SGKUNIPDVLKIVYSGAQTAGNVLLEYELSMSSABONKILYALSTSKHQEKLLKL	840
Qy	841	IELWMEGVKIKTONLAALLHAIARRPKQQLAWDFVRENTHLLKDFLGSYDIRMLIISG	900	Qy	841	IELWMEGVKIKTONLAALLHAIARRPKQQLAWDFVRENTHLLKDFLGSYDIRMLIISG	900
Db	841	IELWMEGVKIKTONLAALLHAIARRPKQQLAWDFVRENTHLLKDFLGSYDIRMLIISG	900	Db	841	IELWMEGVKIKTONLAALLHAIARRPKQQLAWDFVRENTHLLKDFLGSYDIRMLIISG	900
Qy	901	TTAHFSSKDLQEVKLFESLEAQSGLDIFQTVLETTITKNIKWLEKNLPLTRTLMVNT	960	Qy	901	TTAHFSSKDLQEVKLFESLEAQSGLDIFQTVLETTITKNIKWLEKNLPLTRTLMVNT	960
Db	901	TTAHFSSKDLQEVKLFESLEAQSGLDIFQTVLETTITKNIKWLEKNLPLTRTLMVNT	960	Db	901	TTAHFSSKDLQEVKLFESLEAQSGLDIFQTVLETTITKNIKWLEKNLPLTRTLMVNT	960
RESULT 4		ABP63022					

ID	ABP63022	standard; protein; 785 AA.
XX	AC	ABP63022;
XX	DT	14-OCT-2002 (first entry)
XX	DE	Human polypeptide SEQ ID NO 459.
XX	KW	Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX	OS	Homo sapiens.
XX	PN	WO200218424-A2.
XX	PD	07-MAR-2002.
XX	PF	31-AUG-2001; 2001WO-US027093.
XX	PR	01-SEP-2000; 2000US-00654935.
XX	PA	(HYSE-) HYSEQ INC.
XX	PI	Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX	PI	Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
XX	XX	WPI; 2002-583321/62.
DR	DR	N-PSDB; ABQ93501.
XX	XX	New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
PT	PT	Claim 20; SEQ ID NO 459; 284pp + Sequence Listing; English.
XX	XX	The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
CC	CC	(I), (II) and (III) are useful for diagnostic evaluation of disorders.
CC	CC	(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	XX	Sequence 785 AA;
XX	XX	Query Match 82.0%; Score 4141; DB 5; Length 785;
XX	XX	Best Local Similarity 99.7%; Pred. No. 0;
XX	XX	Matches 782; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1	MFHSSAMVNSHRKPMFNHRGFYCLTALPQICISQFSVPSSYHFTEDPGAPVATNGE 60
DB	1	MFHSSAMVNSHRKPMFNHRGFYCLTALPQICISQFSVPSSYHFTEDPGAPVATNGE 60
QY	61	RFPWQELRLPSVVIPLHYDLFVHPNLTSDFVASEKIEVLVSNATQFIILHSDLEITNA 120
DB	61	RFPWQELRLPSVVIPLHYDLFVHPNLTSDFVASEKIEVLVSNATQFIILHSDLEITNA 120
QY	121	TLOSEEDSRVMKPGKELKVLSPAHEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGFGFY 180
DB	121	TLOSEEDSRVMKPGKELKVLSPAHEQIALLVPEKLTPLHLKYVYVAMDFOAKLGDGFGFY 180

Qy	181	KSTYRTLGGETRILAVTDEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK	240	PR	17-MAR-2000;	2000US-0190076P.
Db	181	KSTYRTLGGETRILAVTDEPTQARMAPCFDEPLFKANFSIKIRRESRHIALSNMPKVK	240	PR	18-APR-2000;	2000US-0198123P.
Qy	241	TIELEGGLEDHFETTVMKSTYLVAYIVCDPHSLSGFTSSGVKVIYASPKKNQTHYAL	300	PR	19-MAY-2000;	2000US-0205515P.
Db	241	TIELEGGLEDHFETTVMKSTYLVAYIVCDPHSLSGFTSSGVKVIYASPKKNQTHYAL	300	PR	07-JUN-2000;	2000US-0209467P.
Qy	301	QASLKLLDPFYKFIYIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLFLDPKTTSSASD	360	PR	28-JUN-2000;	2000US-0214886P.
Db	301	QASLKLLDPFYKFIYIYPLSKLDLIAIPDPAPGAMENWGLITYRETSLFLDPKTTSSASD	360	PR	30-JUN-2000;	2000US-0215135P.
Qy	361	KLMVTRVIAHELAHQFGLNVTMEWNNDIWLKEGFAKYMELIAVNATYPELOFDDYFLNV	420	PR	07-JUL-2000;	2000US-0216647P.
Db	361	KLMVTRVIAHELAHQFGLNVTMEWNNDIWLKEGFAKYMELIAVNATYPELOFDDYFLNV	420	PR	07-JUL-2000;	2000US-0216880P.
Qy	421	CPEVITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGIIQ	480	PR	11-JUL-2000;	2000US-0217487P.
Db	421	CPEVITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGEKFKGIIQ	480	PR	11-JUL-2000;	2000US-0217496P.
Qy	481	YLKFSYRNKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFLGENAEVKEMMTT	540	PR	14-JUL-2000;	2000US-0218290P.
Db	481	YLKFSYRNKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSNMLAFLGENAEVKEMMTT	540	PR	26-JUL-2000;	2000US-0220963P.
Qy	541	WTLOKGIPLLVKQDGCSLRLOERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSNVI	600	PR	26-JUL-2000;	2000US-0220964P.
Db	541	WTLOKGIPLLVKQDGCSLRLOERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSNVI	600	PR	14-AUG-2000;	2000US-0224518P.
Qy	601	HRHILKSKTDTLDLPEKTSWKFNVDSNGYIIVHYEGHGDQITQLNQNHHTLLRPKRV	660	PR	14-AUG-2000;	2000US-0225213P.
Db	601	HRHILKSKTDTLDLPEKTSWKFNVDSNGYIIVHYEGHGDQITQLNQNHHTLLRPKRV	660	PR	14-AUG-2000;	2000US-0225266P.
Qy	661	GLIHDFVLVGAGRLTLDKALDMTYTLQHETSSPALLEGLSYLESFYHMDRRNIDISE	720	PR	14-AUG-2000;	2000US-0225267P.
Db	661	GLIHDFVLVGAGRLTLDKALDMTYTLQHETSSPALLEGLSYLESFYHMDRRNIDISE	720	PR	14-AUG-2000;	2000US-0225268P.
Qy	721	NLKRYLLQYFKPVIDRQSWDKGSDVMDRLRSALLKLACDLNHAPCIQKAABLFPQWMS	780	PR	14-AUG-2000;	2000US-0225270P.
Db	721	NLKRYLLQYFKPVIDRQSWDKGSDVMDRLRSALLKLACDLNHAPCIQKAABLFPQWMS	780	PR	14-AUG-2000;	2000US-0225447P.
Qy	781	SGKL 784		PR	14-AUG-2000;	2000US-0225757P.
Db	781	SGKL 784		PR	14-AUG-2000;	2000US-0225758P.
RESULT 5						
ABB10338						
ID	ABB10338	standard; protein; 728 AA.				
XX	AC	ABB10338;				
XX	DT	10-JAN-2002 (first entry)				
XX	DE	Human cDNA SEQ ID NO: 646.				
Kw	Kw	Human; gene therapy; neural disorder; immune system disorder;				
Kw	Kw	muscular disorder; reproductive disorder; gastrointestinal disorder;				
Kw	Kw	pulmonary disorder; cardiovascular disorder; renal disorder;				
Kw	Kw	proliferative disorder; inflammation.				
XX	XX	Homo sapiens.				
XX	XX	WO200154474-A2.				
XX	PD	02-AUG-2001.				
PF	17-JAN-2001;	2001WO-US001349.				
XX	31-JAN-2000;	2000US-0179065P.				
PR	04-FEB-2000;	2000US-0180628P.				
PR	24-FEB-2000;	2000US-0184664P.				
PR	02-MAR-2000;	2000US-0186350P.				
PR	16-MAR-2000;	2000US-0189874P.				

PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241825P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

XX (HUNA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI, 2001-476161/51.

XX N-PSDB; ABA06560.

DR Isolated nucleic acid molecule encoding an inflammation-associated  
PT polypeptide is used in preventing, treating or ameliorating a medical  
XX condition.

PS Claim 11; SEQ ID NO 646; 859pp + Sequence Listing; English.

XX The present invention provides human cDNAs, proteins and related genomic  
XX

CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence  
CC is a protein of the invention  
XX  
SQ Sequence 728 AA;

	Query Match	75.2%;	Score 3799;	DB 4;	Length 728;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 722;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	239	VKTIELEGGLEDHFETTVKMSYLVAYIVCDPHLSLGSFTSSGVKVIYASPDKRNQTHY	298		
Db	7	VKTIELEGGLEDHFETTVKMSYLVAYIVCDPHLSLGSFTSSGVKVIYASPDKRNQTHY	66		
Qy	299	ALQASLKLLDPYKYFDIYYPLSKLDLIAIPDPFAPGAMENWGLITYRETSLLFPKTS	358		
Db	67	ALQASLKLLDPYKYFDIYYPLSKLDLIAIPDPFAPGAMENWGLITYRETSLLFPKTS	126		
Qy	359	SDKLWTRVIAHELAHQWFGNLTVMWWDIWLKEGFAKYMELIAVNATYPQLQDDYFL	418		
Db	127	SDKLWTRVIAHELAHQWFGNLTVMWWDIWLKEGFAKYMELIAVNATYPQLQDDYFL	186		
Qy	419	NVCFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGESEKFKGI	478		
Db	187	NVCFEVITKDSLNSRRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGESEKFKGI	246		
Qy	479	IQYLKFSYRNAXNDDLLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFGENAEVKEMM	538		
Db	247	IQYLKFSYRNAXNDDLLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFGENAEVKEMM	306		
Qy	539	TTWTLOKGIPLLVKQDGCRLRQOERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN	598		
Db	307	TTWTLOKGIPLLVKQDGCRLRQOERFLOQVQEDPEWRALQERYLWHIPLTYSTSSN	366		
Qy	599	VIHRHLKSKTDLTDLPEKTSWVKFNVDNSGYIVHYEGHGWDLITOLNQNHLLRPKD	658		
Db	367	VIHRHLKSKTDLTDLPEKTSWVKFNVDNSGYIVHYEGHGWDLITOLNQNHLLRPKD	426		
Qy	659	RVGLIHDVFLVAGRLTLDKALDNTYYLQHETSSPALLEGLSVLESFYHMDRRNISDI	718		
Db	427	RVGLIHDVFLVAGRLTLDKALDNTYYLQHETSSPALLEGLSVLESFYHMDRRNISDI	486		
Qy	719	SENKRYLLQYFKPVIDRQSWDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM	778		
Db	487	SENKRYLLQYFKPVIDRQSWDKGSVWDRMLRSALLKLACDLNHAPCIQKAAELFSQWM	546		
Qy	779	ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQVELSMSAEOQNKILYALSTSKHQEKLL	838		
Db	547	ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQVELSMSAEOQNKILYALSTSKHQEKLL	606		
Qy	839	KLIELGMEGKVIKTONLAALLHAIAREPKGOOLAWDFVRENWTHLLKFKDLSYDIRMII	898		
Db	607	KLIELGMEGKVIKTONLAALLHAIAREPKGOOLAWDFVRENWTHLLKFKDLSYDIRMII	666		
Qy	899	SGTTAHFSSKDKLQEVKLPFESLEAOGSHLIDIFQTVLETITTKIKLWLEKNLPTLRTLMV	958		
Db	667	SGTTAHFSSKDKLQEVKLPFESLEAOGSHLIDIFQTVLETITTKIKLWLEKNLPTLRTLMV	726		
Qy	959	NT 960			
Db	727	NT 728			

RESULT 6

ABP66925

ID ABP66925 standard; protein; 728 AA.

XX AC ABP66925;

XX DT 09-DEC-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 646.

XX Human, neotropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnery;  
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX US2002090672-A1.  
XX  
XX 11-JUL-2002.  
XX  
XX 17-JAN-2001; 2001US-00764853.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 28-JUN-2000; 2000US-0214886P.  
XX 07-JUL-2000; 2000US-0215647P.  
XX 07-JUL-2000; 2000US-0215880P.  
XX 11-JUL-2000; 2000US-0217487P.  
XX 11-JUL-2000; 2000US-0217496P.  
XX 14-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
XX 26-JUL-2000; 2000US-0220964P.  
XX 14-AUG-2000; 2000US-0224518P.  
XX 14-AUG-2000; 2000US-0224519P.  
XX 14-AUG-2000; 2000US-0225267P.  
XX 14-AUG-2000; 2000US-0225268P.  
XX 14-AUG-2000; 2000US-0225270P.  
XX 14-AUG-2000; 2000US-0225447P.  
XX 14-AUG-2000; 2000US-0225757P.  
XX 14-AUG-2000; 2000US-0225758P.  
XX 22-AUG-2000; 2000US-0226868P.  
XX 30-AUG-2000; 2000US-0228924P.  
XX 01-SEP-2000; 2000US-0229287P.  
XX 01-SEP-2000; 2000US-0229343P.  
XX 01-SEP-2000; 2000US-0229344P.  
XX 01-SEP-2000; 2000US-0229345P.  
XX 05-SEP-2000; 2000US-0229509P.  
XX 05-SEP-2000; 2000US-0229513P.  
XX 08-SEP-2000; 2000US-0231413P.  
XX 21-SEP-2000; 2000US-0234223P.  
XX 21-SEP-2000; 2000US-0234274P.  
XX 25-SEP-2000; 2000US-0234997P.  
XX 27-SEP-2000; 2000US-0235834P.  
XX 29-SEP-2000; 2000US-0236327P.  
XX 29-SEP-2000; 2000US-0236367P.  
XX 29-SEP-2000; 2000US-0236368P.  
XX 29-SEP-2000; 2000US-0236369P.  
XX 29-SEP-2000; 2000US-0236370P.  
XX 02-OCT-2000; 2000US-0236802P.  
XX 02-OCT-2000; 2000US-0237037P.  
XX 02-OCT-2000; 2000US-0237038P.  
XX 02-OCT-2000; 2000US-0237039P.  
XX 02-OCT-2000; 2000US-0237040P.  
XX 13-OCT-2000; 2000US-0239935P.  
XX 20-OCT-2000; 2000US-0240960P.  
XX 20-OCT-2000; 2000US-0241783P.  
XX 01-NOV-2000; 2000US-0244617P.  
XX 17-NOV-2000; 2000US-0249299P.  
XX 08-DEC-2000; 2000US-0251856P.  
XX 08-DEC-2000; 2000US-0251868P.  
XX 08-DEC-2000; 2000US-0251869P.  
XX  
XX (ROSE/) ROSEN C A.  
XX (RUBE/) RUBEN S M.  
XX (BARA/) BARASH S C.  
XX  
XX Rosen CA, Ruben SM, Barash SC;

XX WPI; 2002-681727/73.  
DR N-PSDB; ABV83897.  
XX  
XX Novel polypeptide useful for diagnosis, prognosis, prevention, and  
PT treatment of immune, hyperproliferative, renal, respiratory,  
PT cardiovascular, reproductive, endocrine, gastrointestinal and  
PT neurological disorders.  
XX  
XX Claim 11; SEQ ID NO 646; 369pp + Sequence Listing; English.  
XX  
XX The invention relates to novel genes (ABV83682-ABV84101) and proteins  
CC (ASP66710-ABP67129) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 728 AA;  
XX  
XX Query Match 75.2%; Score 3799; DB 5; Length 728;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 239 VKTIEGGLLEDFHFTTVKMTYLVAYIVCDHSLSGFTSSGVKVTYASPDKNQTHY 298  
XX DB 7 VKTIEGGLLEDFHFTTVKMTYLVAYIVCDHSLSGFTSSGVKVTYASPDKNQTHY 66  
XX  
XX QY 299 ALQASLKLLDFYKYFYIYVPLSKLDLIAIPDFAPGAMENGLITYRETSLLFPKTS 358  
XX DB 67 ALQASLKLLDFYKYFYIYVPLSKLDLIAIPDFAPGAMENGLITYRETSLLFPKTS 126  
XX  
XX QY 359 SDKLWTRVIAHQLAHQWFGNLTVMWWDIWLKGFAYKYMELIAVNAVATYDELQDDYFL 418  
XX DB 127 SDKLWTRVIAHQLAHQWFGNLTVMWWDIWLKGFAYKYMELIAVNAVATYDELQDDYFL 186  
XX  
XX QY 419 NVCEVITKDSLSSRRPISKPAETPTQIQEMFDEVSYNKGACIILNMLKDFLGEKFKQGI 478  
XX DB 187 NVCEVITKDSLSSRRPISKPAETPTQIQEMFDEVSYNKGACIILNMLKDFLGEKFKQGI 246  
XX  
XX QY 479 IQYLKFSYRNKNDLWSSLSNCSLESDFTSBGVCHSDPKMTSNMLAFLGENAEVKEMM 538  
XX DB 247 IQYLKFSYRNKNDLWSSLSNCSLESDFTSBGVCHSDPKMTSNMLAFLGENAEVKEMM 306  
XX  
XX QY 539 TTWTLQKGIPLLVKQDGCSLRLOQERFLOQVFOEDPEWRALQERYLWHIPLTYSTSSN 598  
XX DB 307 TTWTLQKGIPLLVKQDGCSLRLOQERFLOQVFOEDPEWRALQERYLWHIPLTYSTSSN 366  
XX  
XX QY 599 VIHRHILKSTDTLDLPEKTSWKFNVDNGYITVHYEGHGWDLITQLNQNHLLRPKD 658  
XX DB 367 VIHRHILKSTDTLDLPEKTSWKFNVDNGYITVHYEGHGWDLITQLNQNHLLRPKD 426  
XX  
XX QY 659 RVGLIHDFVQLVAGRLTLDKALDWTYIYLOHETSSPALLEGLSYLESFYHMDRNRNISI 718  
XX DB 427 RVGLIHDFVQLVAGRLTLDKALDWTYIYLOHETSSPALLEGLSYLESFYHMDRNRNISI 486  
XX  
XX QY 719 SENLKYLLQYFKPVIDRQSWSDKGSVWDRMLASALLKLACDLNHAPCIQKAAELFQWM 778  
XX DB 487 SENLKYLLQYFKPVIDRQSWSDKGSVWDRMLASALLKLACDLNHAPCIQKAAELFQWM 546  
XX  
XX QY 779 ESSGKNIPTDVLKIVYVGAQTAGHNYLLEQVELSMSSAEQNKIYALSTSHOEKLL 838  
XX

Db	547	ESSGKLNIPDVLKIVYSGAQTTAGMNYLLEQVELSMSSAEQNKILYALSTSKHQEKLL	606	PR	22-AUG-2000;	2000US-0227182P.
				PR	23-AUG-2000;	2000US-0227009P.
Qy	839	KLIELGHEGKVIKTONLAALHAIAARRPKGOOLAWDFVRENWTHLLKKFDLGSYDIIRMI	898	PR	30-AUG-2000;	2000US-0228924P.
				PR	01-SEP-2000;	2000US-0229287P.
Db	607	KLIELGHEGKVIKTONLAALHAIAARRPKGOOLAWDFVRENWTHLLKKFDLGSYDIIRMI	666	PR	01-SEP-2000;	2000US-0229343P.
				PR	01-SEP-2000;	2000US-0229344P.
Qy	899	SGTTAHFSSKDLQEVKLFFESLEAQSGSHLDIFQTVLETTITKNIKWLEKNLPTLRTWLMV	958	PR	01-SEP-2000;	2000US-0229345P.
				PR	05-SEP-2000;	2000US-0229509P.
Db	667	SGTTAHFSSKDLQEVKLFFESLEAQSGSHLDIFQTVLETTITKNIKWLEKNLPTLRTWLMV	726	PR	05-SEP-2000;	2000US-0229513P.
				PR	06-SEP-2000;	2000US-0230437P.
Qy	959	NT 960		PR	06-SEP-2000;	2000US-0230438P.
				PR	08-SEP-2000;	2000US-0231242P.
Db	727	NT 728		PR	08-SEP-2000;	2000US-0231243P.
				PR	08-SEP-2000;	2000US-0231244P.
				PR	08-SEP-2000;	2000US-0231413P.
				PR	08-SEP-2000;	2000US-0231414P.
				PR	08-SEP-2000;	2000US-0232080P.
				PR	08-SEP-2000;	2000US-0232081P.
				PR	12-SEP-2000;	2000US-0231968P.
				PR	14-SEP-2000;	2000US-0232397P.
				PR	14-SEP-2000;	2000US-0232398P.
				PR	14-SEP-2000;	2000US-0232399P.
				PR	14-SEP-2000;	2000US-0232400P.
				PR	14-SEP-2000;	2000US-0232401P.
				PR	14-SEP-2000;	2000US-0233063P.
				PR	14-SEP-2000;	2000US-0233065P.
				PR	21-SEP-2000;	2000US-0234223P.
				PR	21-SEP-2000;	2000US-0234274P.
				PR	25-SEP-2000;	2000US-0234997P.
				PR	25-SEP-2000;	2000US-0234998P.
				PR	26-SEP-2000;	2000US-0235484P.
				PR	27-SEP-2000;	2000US-0235834P.
				PR	27-SEP-2000;	2000US-0235836P.
				PR	29-SEP-2000;	2000US-0236327P.
				PR	29-SEP-2000;	2000US-0236367P.
				PR	29-SEP-2000;	2000US-0236368P.
				PR	29-SEP-2000;	2000US-0236369P.
				PR	29-SEP-2000;	2000US-0236370P.
				PR	02-OCT-2000;	2000US-0236802P.
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				PR	02-OCT-2000;	2000US-0237038P.
				PR	02-OCT-2000;	2000US-0237039P.
				PR	02-OCT-2000;	2000US-0237040P.
				PR	13-OCT-2000;	2000US-0239935P.
				PR	13-OCT-2000;	2000US-0239937P.
				PR	20-OCT-2000;	2000US-0240960P.
				PR	20-OCT-2000;	2000US-0241221P.
				PR	20-OCT-2000;	2000US-0241221P.
				PR	20-OCT-2000;	2000US-0241785P.
				PR	20-OCT-2000;	2000US-0241786P.
				PR	20-OCT-2000;	2000US-0241787P.
				PR	20-OCT-2000;	2000US-0241808P.
				PR	20-OCT-2000;	2000US-0241809P.
				PR	20-OCT-2000;	2000US-0241826P.
				PR	01-NOV-2000;	2000US-0244617P.
				PR	08-NOV-2000;	2000US-0246474P.
				PR	08-NOV-2000;	2000US-0246475P.
				PR	08-NOV-2000;	2000US-0246476P.
				PR	08-NOV-2000;	2000US-0246477P.
				PR	08-NOV-2000;	2000US-0246478P.
				PR	08-NOV-2000;	2000US-0246523P.
				PR	08-NOV-2000;	2000US-0246524P.
				PR	08-NOV-2000;	2000US-0246525P.
				PR	08-NOV-2000;	2000US-0246526P.
				PR	08-NOV-2000;	2000US-0246527P.
				PR	08-NOV-2000;	2000US-0246528P.
				PR	08-NOV-2000;	2000US-0246532P.
				PR	08-NOV-2000;	2000US-0246609P.
				PR	08-NOV-2000;	2000US-0246610P.
				PR	08-NOV-2000;	2000US-0246611P.
				PR	08-NOV-2000;	2000US-0246613P.
				PR	17-NOV-2000;	2000US-0249207P.
				PR	17-NOV-2000;	2000US-0249208P.

PR 17-NOV-2000; 2000US-0249203P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-465566/50.  
 DR N-P5DB; AAS40869.

XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,  
 PT treating neural, immune system, muscular, reproductive, pulmonary,  
 PT cardiovascular, renal, proliferative disorders and cancerous diseases.  
 XX Claim 11; SEQ ID NO 995; 1180pp; English.

XX The present invention relates to the isolation of novel human enzyme  
 CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences  
 CC encoding them. The enzyme polypeptides of the invention may comprise the  
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 CC isomerases or ligases. The sequences of the invention are useful in the  
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
 CC disorders including hyperproliferative disorders (e.g. cancer),  
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.  
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic  
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),  
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders  
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and  
 CC infectious disorders (e.g. Influenza). The polynucleotides of the  
 CC invention can also be used in gene therapy. AAU22915-AAU23814 represent  
 CC the novel human enzyme polypeptides of the invention. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 722 AA;

Query Match 74.6%; Score 3770; DB 4; Length 722;  
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QY	299	ALQASLKLDPEYKFDIYYPLSKLDLIAIPDFAPGAMENGLITYBETSLPDPKSSA	358
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QY	359	SDKLWTRVIAHSLAHQWFGNLTVMWWDIWLKEGFAKYMELIAVANATYPQLQDDYFL	418
DB	121	SDKLWTRVIAHSLAHQWFGNLTVMWWDIWLKEGFAKYMELIAVANATYPQLQDDYFL	180
QY	419	NVCFEVIITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGESEKPKQGI	478
DB	181	NVCFEVIITKDSLNSSRPISKPAETPTQIQEMFDEVSYNKGACILNMLKDFLGESEKPKQGI	240
QY	479	IQYLKFSYRNAKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFGENAEVKEMM	538
DB	241	IQYLKFSYRNAKNDLWSSLSNCSLESDFTSQGVCHSDPKMTSNMLAFGENAEVKEMM	300
QY	539	TTWTLOKGIPLLVKQDGCISLRLOQERFLOQVQFEDPEWRALQERYLWHIPLTYTSSSN	598
DB	301	TTWTLOKGIPLLVKQDGCISLRLOQERFLOQVQFEDPEWRALQERYLWHIPLTYTSSSN	360
QY	599	VIHRHILKSKTDTLDLPEKTSWVKFNVDNSGYIIVHYEGHGWDLITQLNQHTLLRPKD	658
DB	361	VIHRHILKSKTDTLDLPEKTSWVKFNVDNSGYIIVHYEGHGWDLITQLNQHTLLRPKD	420
QY	659	RVGLIHDVFOVLGAGRLTLDKALDNTYYLOHETSSPALLLEGLSYLESFYHMDRRNTSDI	718
DB	421	RVGLIHDVFOVLGAGRLTLDKALDNTYYLOHETSSPALLLEGLSYLESFYHMDRRNTSDI	480
QY	719	SENLKRYLLOVFKFVIDRQSWDKGSVWDRMLRSALLKLACDLNHPACIOKAAELFSQWM	778
DB	481	SENLKRYLLOVFKFVIDRQSWDKGSVWDRMLRSALLKLACDLNHPACIOKAAELFSQWM	540
QY	779	ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQVELSMSSAEQNKILYALSTSKHQEKLL	838
DB	541	ESSGKLNIPDVLKIVYSGAQTAGWNYLLEQVELSMSSAEQNKILYALSTSKHQEKLL	600
QY	839	KLIELGMEGVKIKTONLAALLHAIRAPKGOQLAWDFVRENWTHLLKKFDLGSVDIRMI	898
DB	601	KLIELGMEGVKIKTONLAALLHAIRAPKGOQLAWDFVRENWTHLLKKFDLGSVDIRMI	660
QY	899	SGTTAFHSSKDKLQEVKLPFESLEAQSHLIDIFQTVLETITQIKWLEKNLPTLRTWLMV	958
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QY	959	NT 960	
DB	721	XT 722	
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XX	10-JAN-2002	(first entry)	
DT	Human cDNA	SEQ ID NO: 819.	
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KW	muscular disorder; reproductive disorder; gastrointestinal disorder;		
KW	pulmonary disorder; cardiovascular disorder; renal disorder;		
KW	proliferative disorder; inflammation.		
OS	Homo sapiens.		
XX	WO200154474-A2.		
XX	02-AUG-2001.		
XX	17-JAN-2001; 2001WO-US001349.		
XX	31-JAN-2000; 2000US-0179065P.		

PR 04-FEB-2000; 2000US-0180628P.  
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PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
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PR 08-DEC-2000; 2000US-0251479P.  
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PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI; 2001-476161/51.  
XX N-PSDB; ABA06733.  
DR Isolated nucleic acid molecule encoding an inflammation-associated  
XX polypeptide is used in preventing, treating or ameliorating a medical  
PT condition.  
PT

XX Claim 11; SEQ ID NO 819; 859pp + Sequence Listing; English.  
XX  
CC The present invention provides human cDNAs, proteins and related genomic  
CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence  
CC is a protein of the invention  
XX  
SQ Sequence 722 AA;  
  
Query Match 74.6%; Score 3770; DB 4; Length 722;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 239 VKTIEGGLLDHDETTVMKSTYLVAYIVCDPHSLSGFTSGVKVSIYASDPKKNQTHY 298  
Db 1 VKTIEGGLLDHDETTVMKSTYLVAYIVCDPHSLSGFTSGVKVSIYASDPKKNQTHY 60  
  
Qy 299 ALQASLKLDIFYEKFYDIYPLSKLDLIAIPDAFAGMENWGLITYRETSLLFDPKTS 358  
Db 61 ALQASLKLDIFYEKFYDIYPLSKLDLIAIPDAFAGMENWGLITYRETSLLFDPKTS 120  
  
Qy 359 SKLWVTRVIAHELHQAQFNLVTWENNDIWLKGFPAKYMELIAVNATYPELQDDYPL 418  
Db 121 SKLWVTRVIAHELHQAQFNLVTWENNDIWLKGFPAKYMELIAVNATYPELQDDYPL 180  
  
Qy 419 NVCFEVITKDSLSNSRPTSKPAETPTQOEMFDEVSYNKGACILANLWDFLGEERFKGI 478  
Db 181 NVCFEVITKDSLSNSRPTSKPAETPTQOEMFDEVSYNKGACILANLWDFLGEERFKGI 240  
  
Qy 479 IQYKKFSYRNARNDLWSSLSNSCLESFTSGVCHSDPKMTSNMLAFGENAEVKEMM 538  
Db 241 IQYKKFSYRNARNDLWSSLSNSCLESFTSGVCHSDPKMTSNMLAFGENAEVKEMM 300  
  
Qy 539 TTWTLOKGIPLLVKQDGSRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN 598  
Db 301 TTWTLOKGIPLLVKQDGSRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN 360  
  
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Db 361 VIHRHILSKTDTLDLPEKTSWVKFNVDNSNGYIIVHGEHGWDLITQLNQNHLLRPKD 420  
  
Qy 659 RVGLIHDVQLVAGRLTLDKALDMMTYLQHETSSPALLLEGISYLFYHMDRNNISDI 718  
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Qy 719 SENLXRYLQYKPKVIDRQSWDKGSVDRMLRSALLKLACDLNHPACIQKAAELFSQWM 778  
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ID ABP67098 standard; protein; 722 AA.  
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AC ABP67098;

XX 09-DEC-2002 (first entry)  
XX Human polypeptide SEQ ID NO 819.  
XX Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; cancer;  
KW antiparkinsonian; anti-sclerotic; antianemic; antiarthritic; vulnary;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX Homo sapiens.  
XX US2002090672-A1.  
XX 11-JUL-2002.  
  
XX 17-JAN-2001; 2001US-00764853.  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 28-JUN-2000; 2000US-0214886P.  
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XX 14-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
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(ROSE/) ROSEN C A.



Query Match	74.5%;	Score 3763;	DB 5;	Length 722;
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QY	359	SDKLWVTRVIAHELHAFQGNLVTHWENDIWLKEGFAYKYMELIAVNAVYPELQDDYFL	418	
Db	121	SDKLWVTRVIAHELHAFQGNLVTHWENDIWLKEGFAYKYMELIAVNAVYPELQDDYFL	180	
QY	419	NVCFEVIKDSLSNSRPISKPAETPTQIEMFDEVSYNKGACILNMLKDFLGEERFQGI	478	
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QY	479	IQYLKFFSYRNAKNDLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFLGENAEVKEM	538	
Db	241	IQYLKFFSYRNAKNDLWSSLSNSCLESDFTSGGVCHSDPKMTSNMLAFLGENAEVKEM	300	
QY	539	TTWTLOKGIPLLVKQDGSRLQOERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN	598	
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QY	599	VHRRHILKSTDTLDLPEKTSWVKFNVDNSNGYIIVHYEGHGWDLITQLNQNHLLRPKD	658	
Db	361	VHRRHILKSTDTLDLPEKTSWVKFNVDNSNGYIIVHYEGHGWDLITQLNQNHLLRPKD	420	
QY	659	RVGLIHDVFLQVAGRLTDLKALDMMTYIQLQHETSSPALLEGISYLESFYHMDRNI	718	
Db	421	RVGLIHDVFLQVAGRLTDLKALDMMTYIQLQHETSSPALLEGISYLESFYHMDRNI	480	
QY	719	SENKRYLLQYKPKVIDRQSWSDKGSVWDRMLRSALLKACDLNHPACTQKAAELFSQW	778	
Db	481	SENKRYLLQYKPKVIDRQSWSDKGSVWDRMLRSALLKACDLNHPACTQKAAELFSQW	540	
QY	779	ESSGKLNPTDVLKIVYSGAOTTAGNVLLEQYELSMSSAQNKLVALSTSRKQEKLL	838	
Db	541	ESSGKLNPTDVLKIVYSGAOTTAGNVLLEQYELSMSSAQNKLVALSTSRKQEKLL	600	
QY	839	KLIELGMEGKVIKTQNLALHAIARRPKGQQLAWDFVRENWTHLLKFDLGSYDIRMI	898	
Db	601	KLIELGMEGKVIKTQNLALHAIARRPKGQQLAWDFVRENWTHLLKFDLGSYDIRMI	660	
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Db	661	SGTTAHFSSKDLQEVKLPFFESLEAQGSHLDIFQTVLETITIKNIKWLEKNLPTLTWLV	720	
QY	959	NT 960		
Db	721	XT 722		
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XX	XX			
AC	AAU07829;			
DT	04-DEC-2001	(first entry)		
XX	Human ARTS-1 polypeptide.			
XX	Human; aminopeptidase regulator of type I; cytokine signalling; ARTS-1;			
KW	tumour necrosis factor receptor ectodomain shedding; interleukin-1;			
KW	interleukin-6; immune disorder; TNF-mediated immune disease;			
KW	inflammatory disorder; anti arthritic; vasotropic; immunomodulator;			
XX	immunosuppressive; antibacterial; gene therapy.			
XX	XX			

OS	Homo sapiens.
XX	Key
PH	Domain
FT	350..361
FT	/label= Zinc_binding domain
FT	353..376
FT	/label= Zinc_metalloproteinase_catalytic_motif
FT	372..379
FT	/label= Zinc_binding_catalytic_site
XX	WO200164856-A2.
PN	07-SEP-2001.
PD	28-FEB-2001; 2001WO-US006464.
XX	28-FEB-2000; 2000US-0185586P.
PR	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	Levine S;
PI	WPI; 2001-550175/61.
DR	N-PSDB; AAS09227.
XX	Novel polypeptide useful for the regulation of ectodomain shedding of type I, tumor necrosis factor receptor and other cytokine receptors and for treating disorders and diseases of the immune system.
XX	Claim 2; Fig 1; 139pp; English.
CC	The present invention relates to the isolation of a novel human polypeptide, defined as aminopeptidase regulator of type I, 55 kDa tumour necrosis factor (TNF) receptor ectodomain shedding (ARTS-1), and the polynucleotide sequence encoding for ARTS-1. The invention describes compositions and methods for the regulation of cytokine signalling through the TNF pathway. The ARTS-1 polypeptide and antibodies that bind ARTS-1 are useful for regulating the shedding of the extracellular domain of a cytokine receptor such as type-1 tumour necrosis factor receptor, type I or II interleukin-1 cytokine receptor and interleukin-6 cytokine receptor alpha-chain gp80, by delivering the molecules to a tissue comprising one or more cells expressing the cytokine receptor or their plasma membrane extracellular surface. The ARTS-1 sequences are useful for treating a subject, preferably human, displaying, suspected of, or at risk of displaying a pathology resulting from abnormal cytokine activity, such as tumour necrosis factor alpha, interleukin-1alpha, lbeta or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1 or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1 is useful in gene therapy. The ARTS-1 sequences are useful in diagnostic and therapeutic regimens in treating immune disorders (e.g. TNF-mediated immune diseases) and inflammatory disorders (e.g. rheumatoid arthritis). The present sequence represents human ARTS-1 polypeptide
XX	Sequence 941 AA;
SQ	Query Match 49.8%; Score 2516.5; DB 4; Length 941;
	Best Local Similarity 51.1%; Pred. No. 4.4e-218;
	Matches 478; Conservative 171; Mismatches 268; Indels 19; Gaps 7;
QY	23 YCLTALLPQICICQFSVPSSYHFTEDPGAPFVATNGRFPWQELRLPSVVIPLHYDLFV 82
Db	15 FLLSLLALLTV----STPSWCQSTB---ASPKSGDTGTFPPWKNIRLPEYVIPHYDILLI 67
QY	83 HPNLTSLDFVASEKIEVLVSNATQFIILHSHKLEITNATLQSEDSRYMKPGKELKVLSY 142
Db	68 HANLTTLTFWGTTKVEITASOPTSTIILSHHLLQISRATLRKGAGERLSE--EPLQVLEH 125
QY	143 PAHQIALLVPEKLTPLHLYVAMDFOAKLGDGEGFYKSTYRTLGGETRILAVTDPEPT 202
Db	126 PRQEQIALLAPEPLLVGLPYTVVHYAGNLSETPHGYKSTYRTKGBSLRLASTQFEPST 185
QY	203 QARMAFCDEPFLKAFNSIKIRRESRHIALSNMPKVKTIIEGGLLEDHFETTVKMSTY 262
Db	186 AARMAFCDEPFLKAFNSIKIRRESRHIALSNMPKVKSVTVASGLIEDHFDVTVMSTY 245

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Qy 263 LVAYIVCDFHSLSGFTSSGVKSVIYASDPKRNQTHYALQALKLLDFYKDYFYPLSK 322
Dy 246 LVAFIISDFSVSKTKSVKSVYAVDPDKINQADYALDAATLLEFYEDYFSPYLPK 305
Qy 323 LDLIAIPDFAPGAMENWGLIYRETSLDPKTSASDKLWTRVIAHELAHQWFGNLVT 382
Dy 306 QDLAAIPDFQSGAMENWGLIYRESALLFDAEKSASSKLGITWTVAHELAHQWFGNLVT 365
Qy 383 MEWNDIWLKEGFAKYMELIAVNAVTPQLDFFVFNVCFEVITKDSLSNRPISKAET 442
Dy 366 MEWNDIWLNEGFAKMEFVSUVTHPELKVGDYFFGKCFDAMEVDALNSHPVSTPVEN 425
Qy 443 PTQOEMFDESVYKNGACILNMLKDFLGEERFQKGIIOYLKKFYSYNAKNDLWSSLSNS 502
Dy 426 PAQIREMFDDVSVDKGCILNMLREYLSADAFKSGIVQLKHSYKNTKNEDLWDSWASI 485
Qy 503 CLESDFTS--GVCHSDPKMTNMLAFLEGENAEVKEMMTTWLOKGPLLVVVKQDGSCLR 560
Dy 486 C-PTDGVKMGDFC-SRSQHSSSSHWHQEGVDVKTMTWNTWLOKGFPLITITVGRNVH 543
Qy 561 LQORFLAGVQEDPEWALQERLWHLPLTYSTSSNVHRLHILKSKTDTLDLPEKTSW 620
Dy 544 MKQEHYMGK-----SDGAPDTGYLWVPLTFITSKSDMVRHRLTKTDVLLIPEEVEW 597
Qy 621 VKFNVDNSGYIYVHYEGHGWDQLITQLNQNHHTLLRPKDRVGLIHDVOLFVAGRLTLDKA 680
Dy 598 IKFNVMNGYIYVHYEDDGDWLSLGLKGTHTVSSNDRASLIINNAQLVSGIKLSIEKA 657
Qy 681 LDMTYLLOHETSSPALLBGLSVLSFYHMDRRNISIDISENLKRYLQYFKPVIDRQSW 740
Dy 658 LOLSLLKHETEMFVFGNLNELIPMYKLMKRDNMNEVETQKAFRLRLDLIDKQWT 717
Qy 741 DKGSVMDWLSALLKLACDLNHPACIOKAELFSQWMESSGKLNIPDVLKIYVYVGAQ 800
Dy 718 DEGSVSEMLKSLQLLLACVHYQCVQARAGYFRKMKESNGNLSLPVDVTLAVFAVGAQ 777
Qy 801 TTAGNMYLLEQVELSMSSAEONKILYALSTSKHOKELKJLELWEGKVIKTONQLAALLH 860
Dy 778 STEGWDFLYSKYQFSLSTESKQLEFALCQNKELQWLDESPKGDKINTQFPQILT 837
Qy 861 AIARRPKQQLAWDFVRNETHLLKKFOLGSDYDIRMIIISGTHAFSSKKDLQEVKLFPES 920
Dy 838 LIGRNPVGYPLAWQFLRKNWKLKQKELGSSIAHVMVGTNQFSTRLEEVKGFSS 897
Qy 921 LEAQSGLDIDFTVLETTITKIKMLEKNLPTLRTWL 956
Dy 898 LKENGSQLRCVQQTETIENIGWMDKRNFDKIRVWL 933

RESULT 12
ABB90347
ID ABB90347 standard, protein; 941 AA.
XX
AC ABB90347;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2723.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antibacterial; antiinflammatory; antitumor;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
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XX 19-MAY-2000; 2000US-020551SP.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX WPI; 2002-122018/16.
XX N-PSDB; ABL90756.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 11; SEQ ID NO 2723; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL9449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences
XX
SQ Sequence 941 AA;
Query Match 49.8%; Score 2515.5; DB 5; Length 941;
Best Local Similarity 51.0%; Pred. No. 5.5e-218;
Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;
Qy 23 YCTAILPQICISQSPVSSSYHFTDPGAFVATNGERPFPQBELRLPVSVIPHYDLFV 82
Dy 15 FLLSLALLTLV---STPSWCQSTE---ASPKSDGTFFPMNKIRLPEVIPVHYDILL 67
Qy 83 HPNLTSLDFVASKEIVLVSNATQFILLHSDLEITNATLQSEBDSRYMKPGKELVLSY 142
Dy 68 HANLTTLTTFWGTTKVEITASQPTSTTILSHHLLQISRATLRKAGERLS--EPLQVLEH 125
Qy 143 PAHEQIALLVPEKILTPHLKYVYVAMDFOAKLGDGFEGFYKSTYRTLGGETRILAVTDEPT 202
Dy 126 PPOEQIALLAPEPLLVCLPYTVVIHYNLSEITFHGFYKSTYRTKEGELAILASTQFEPT 185
Qy 203 QARMAPCPDEPLFKANFSIKIRRESRHIALSNMPKVTTELGGLEDHFETVRKMSY 262
Dy 186 AARMAPCPDEPAFKASFISIKIRREPRHLAISNNPLKSVTVAEGLTFHDTVTKMSY 245
Qy 263 LVAYIVCDFHSLSGFTSSGVKSVIYASDPKRNQTHYALQALKLLDFYKDYFYPLSK 322
Dy 246 LVAFIISDFSVSKTKSVKSVYAVDPDKINQADYALDAATLLEFYEDYFSPYLPK 305
Qy 323 LDLIAIPDFAPGAMENWGLIYRETSLDPKTSASDKLWTRVIAHELAHQWFGNLVT 382
Dy 306 QDLAAIPDFQSGAMENWGLIYRESALLFDAEKSASSKLGITWTVAHELAHQWFGNLVT 365
Qy 383 MEWNDIWLKEGFAKYMELIAVNAVTPQLDFFVFNVCFEVITKDSLSNRPISKAET 442
Dy 366 MEWNDIWLNEGFAKMEFVSUVTHPELKVGDYFFGKCFDAMEVDALNSHPVSTPVEN 425
Qy 443 PTQOEMFDESVYKNGACILNMLKDFLGEERFQKGIIOYLKKFYSYNAKNDLWSSLSNS 502
Dy 426 PAQIREMFDDVSVDKGCILNMLREYLSADAFKSGIVQLKHSYKNTKNEDLWDSWASI 485
```





QY 681 LDMYYLOHETSSPALLEGLSYLESFYHMDERNISDIENIKRYLLQYFKPVIDRQWS 740  
Db 658 LLSLYLKHETIMPVFOGLNELIPMYKLMKRDWNEVETQKAFILRLDLIDKQWT 717  
QY 741 DKGSVDRMLRSALLKACDLNHPACIQKAAELFSQWMESSGKLNIPDVLKIVYVGAQ 800  
Db 718 DEGSYERMLRSELALLACVHNYQPCVQRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQ 777  
QY 801 TTAGWNYLLEQYELSMSSAEONKILYALSTSKHQEKLLKLIELGMWEGKVIKTONLAALLH 860  
Db 778 STEGWDPLYSKYQFSLSTESQIEFALCRTONKEKQLWLLDESFKDKIKTQEPQILT 837  
QY 861 AIAREPKGOQLAWDFRENWTHLLKFKDLGSYDIRMIISGTTAHFSSKDKLOEVKLFES 920  
Db 838 LIGRNPVGYPLAWQFLRKNWKLKVKFELGSSIAHVMYGTINQFSTRLEEVKGFSS 897  
QY 921 LEAQSHLDIFQTVLETITKNIKWKLEKNLPILRTWL 956  
Db 898 LKENGSQLRCVQQTETIETIENIGWDRKDFKIRVWL 933  
RESULT 15  
ABR00040  
ID ABR00040 standard; protein; 941 AA.  
XX ABR00040;  
AC ABR00040;  
XX  
DT 03-APR-2003 (first entry)  
XX  
DE Human gene 30 encoded secreted protein HDPBA28, SEQ ID NO:329.  
XX  
KW Human; secreted protein; digestive disorder; gastrointestinal disorder;  
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;  
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;  
KW immune disorder; inflammation; infection; wound healing; drug screening;  
KW chromosome identification; chromosome mapping; cytostatic; gene therapy;  
KW antiinflammatory; immunosuppressive; vulnerary; chromosome 5q14.3.  
XX  
OS Homo sapiens.  
XX  
PN WO200276488-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 19-MAR-2002; 2002WO-US008276.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2003-029900/02.  
DR N-PSDB; ABZ71219.  
XX  
PT New human secreted proteins and nucleic acids, useful for detecting,  
PT preventing, diagnosing, prognosticating, treating and/or ameliorating  
PT e.g. gastrointestinal diseases and disorders, or cancers.  
XX  
PS Claim 13; Page 953-955; 1216pp; English.  
XX  
CC ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted  
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.  
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The  
CC invention also encompasses antibodies specific for the secreted proteins,  
CC the use of the secreted proteins in drug screening, and recombinant  
CC vectors and host cells comprising a nucleic acid of the invention. The  
CC secreted proteins, nucleic acids encoding them, antibodies or antibody  
CC fragments specific for the secreted proteins, and modulators of protein  
CC activity are useful for diagnosing, treating, ameliorating or preventing  
CC digestive disorders. Such conditions include disorders of the mouth,

CC oesophagus, stomach, small intestine, large intestine, liver, biliary  
CC tract and pancreas, and include cancers of these organs and tissues. The  
CC secreted proteins and their nucleic acids may also be used in the  
CC treatment of immune disorders, inflammation, infection,  
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids  
CC of the invention may be used for chromosome identification, chromosome  
CC mapping, in gene therapy, for identifying individuals from minute  
CC biological samples, as hybridisation probes, and as molecular weight  
CC markers. The present sequence represents a human secreted protein of the  
CC invention  
XX  
SQ Sequence 941 AA;  
Query Match 49.8%; Score 2515.5; DB 6; Length 941;  
Best Local Similarity 51.0%; Pred. No. 5.5e-218;  
Matches 477; Conservative 172; Mismatches 268; Indels 19; Gaps 7;  
QY 23 YCLTAAILPQICICQSFVSPSSYHFTEDPGAPVPVATNGERRPQOELRLPSVVIPLHYDLFV 82  
Db 15 FLLSLLALLTV-----STPSWCQSTE---ASPKSDGTPFPWNKIRLPEYVIPVHYDILLI 67  
QY 83 HPNLTSLDFVASEKIEVLVSNATQFIILHSKDLBITNATLQSEEDSRMYKPKELKVLVS 142  
Db 68 HANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLKGAGERLSE--EPLQVLEH 125  
QY 143 PAHQIALLVPEKLTPLHLKYVAMDFOAKLGDGEGFYKSTYRTLGGSTRILAVTDPEPT 202  
Db 126 PPQEQIALLAPEPLLVGLPYTVVHYAGNLSETFHGFYKSTYRTKEGRLILASTQPEPT 185  
QY 203 QARNAFCFDEPLKAFNFSIKIRRESRHIALSNMPKVKTIIEGLGLLEDHDETTVMKSTY 262  
Db 186 AARNAFCFDEPAPKAFSFKIRREPHLALSNPLVKSVTVAEGLIEDHEDFVTVKMTY 245  
QY 263 LVAYIVCDFHSLGFTSSGVKSVIYASPKRNQTHYALQASLKLDLDFYKFDIYIPLSK 322  
Db 246 LVAIISDFESVSKITKSGVKSVYAVDPKNNQADYALDAATVLLLEFYDFSIYPLPK 305  
QY 323 LDLIAIPDFAPGAMENGLITYRETSLLFPDKTSASDKLVWTRVIAHELAHQWFGNLT 382  
Db 306 QDLAAIPDFQSGAMENGLITYRESALLFDAEKSASSKLGITMTVAHELAHQWFGNLT 365  
QY 383 MEWWDNLWKEGFRKAKYMLTAVNATYPELODFDVLNVCREVITKDSLSRSPKPAET 442  
Db 366 MEWWDNLWKEGFRKAFMEFVSVTHPELKVGDYFFGKCFDAMEVDALNSHPSTPVEN 425  
QY 443 PTQIEMFDEVSNKGACILNMLKDFLGEKFKQGIQYKKFSYRNAKNDLMSLSNS 502  
Db 426 PAQIREMFDDVSYDKGACILNMLREYLSADAFKSGIVQYLOKHSYKNTKEDLWDSMASI 485  
QY 503 CLESDFTS--GVCHSDPKMTSNMLAFGENAEVKEMMTTWTLOKGIPLLVVKQDGCCLR 560  
Db 486 C-PTDGVKMGDGC-SSQHSSSSSSHWHQEGVDVKTWMTWTLORGFPPLITTVRGRNVH 543  
QY 561 LOQERFLQGVFOEDPEWRALQERYLWHIPLTYSTSSSNVHRHILKSTDTLDLPEKTSW 620  
Db 544 MKQEHYKMG-----SDGAPDTGYLWVHVLPTFTITKSDMVHRFLTKTDLVLLPEEVEM 597  
QY 621 VKFNVDNGYIYVHVEGHGMDQLITQLNQNHLLRPKDRVGLIHDVOLFVAGARLTLDKA 680  
Db 598 IKFNVGNGYIYVHVEDDGDWDSLTGLKGTHTAVSSNDRASLINNAQOLVSGKLSIEKA 657  
QY 681 LDMTYIYLOHETSSPALLEGLSYLESFYHMDRRNISDIENIKRYLLQYFKPVIDRQWS 740  
Db 658 LLSLYLKHETIEMPVFOGLNELIPMYKLMKRDWNEVETQKAFILRLDLIDKQWT 717  
QY 741 DKGSVDRMLRSALLKACDLNHPACIQKAAELFSQWMESSGKLNIPDVLKIVYVGAQ 800  
Db 718 DEGSYERMLRSELALLACVHNYQPCVQRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQ 777  
QY 801 TTAGWNYLLEQYELSMSSAEONKILYALSTSKHQEKLLKLIELGMWEGKVIKTONLAALLH 860  
Db 778 STEGWDPLYSKYQFSLSTESQIEFALCRTONKEKQLWLLDESFKDKIKTQEPQILT 837

Qy	861	AIARRPKGQQLAWDFVRENWTHLLKKFDLGSYDIRMIISGTTAHFSSKDKLQEVKLEFES	920
Db	838	LIGRNPVGYPLAQFLRKNNKLVQKPELGSSSIAHVMGTTNQFSTRTRLEEVKGFSS	897
Qy	921	LEAGSHLDIFQTVLETITKNIKWLEKNLPTLRWL	956
Db	898	LKENGSQLRCVQQTETIETIENIGWMDKNFDKIRVL	933

Search completed: September 26, 2005, 06:07:26  
Job time : 177 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: September 26, 2005, 06:03:26 ; Search time 48 Seconds  
(without alignments)  
1924.335 Million cell updates/sec  
Title: US-10-039-073-1  
Perfect score: 5052  
Sequence: 1 MFHSSAMVNSHRKMFNTHR.....NIKMLEKNLPTLRWLWMT 960  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 79:\*  
1: piri:\*  
2: piri2:\*  
3: piri3:\*  
4: piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match	Length	DB	ID	Description			
1	1999	39.6	1006	2	A59384	oxytocinase/insuli			
2	1999	39.6	1025	2	A59383	oxytocinase/insuli			
3	1771	35.1	916	2	I55441	vp165 - rat			
4	1440	28.5	957	2	A47531	glutamyl aminopept			
5	1390.5	27.5	945	2	S30398	aminopeptidase N h			
6	1327	26.3	1025	2	I59331	thyrotropin-releas			
7	1312	26.0	965	2	A32852	membrane alanyl am			
8	1269	25.1	963	2	A53984	membrane alanyl am			
9	1264.5	25.0	967	2	A30325	membrane alanyl am			
10	1214	24.0	920	2	T10052	aminopeptidase (EC			
11	1176	23.3	805	2	S07099	membrane alanyl am			
12	1151	22.8	884	2	T29637	hypothetical prote			
13	1116	22.1	844	2	S37794	aminopeptidase ysc			
14	1067	21.1	856	2	S46750	aminopeptidase ysc			
15	1047.5	20.7	882	2	T39789	aminopeptidase - f			
16	1039	20.6	988	2	T24668	hypothetical prote			
17	1031	20.4	990	2	JC8058	laeverin - human			
18	899.5	17.8	873	2	T05189	glutamyl aminopept			
19	895.5	17.7	849	2	JC7959	lysyl aminopeptida			
20	893.5	17.7	849	2	JU0191	aminopeptidase y			
21	888.5	17.6	785	2	S73098	aminopeptidase (EC			
22	875	17.3	844	2	S47274	membrane alanyl am			
23	873	17.3	846	2	A86663	aminopeptidase N [			
24	871.5	17.3	784	2	B90442	tricorn proteinase			
25	870	17.2	843	2	S38364	membrane alanyl am			
26	868	17.2	844	2	JC4054	membrane alanyl am			
27	865	17.1	848	2	B97960	membrane alanyl am			
28	864	17.1	848	2	E95092	aminopeptidase N [			
29	856	16.9	846	2	JN0324	lysine aminopeptid			

RESULT 1  
A59384  
oxytocinase/insulin-responsive aminopeptidase, variant 2 [imported] - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 20-Apr-2001  
C:Accession: A59384  
R:Rasmussen, T.E.; Pedraza-Diaz, S.; Hardre, R.; Laustsen, P.G.; Carrion, A.G.; Kristens  
Eur. J. Biochem. 267, 2297-2306, 2000  
A:Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and 1c  
A:Reference number: A59384; MUID:20223264; PMID:10759854  
A:Accession: A59384  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1006 <STO>  
A:Cross-references: GB:CA894753; NID:G8574036; PIDN:CA894753.1  
C:Superfamily: membrane alanyl aminopeptidase

Query Match		39.6%; Score 1999; DB 2; Length 1006;	
Best Local Similarity		44.2%; Pred. No. 3.8e-118;	
Matches 400; Conservative 160; Mismatches 310; Indels 36; Gaps 6;			
Qy	54	PVATNGERFPQOELRLPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSK	113
Db	134	PFATNGKLFPAQIRLPTAVVPLRYELSLHPNLTSMTPRGSVTISVQALQVTWNILLHST	193
Qy	114	DLEITNATLQSEDSRYSMKPGKELKVLSPAHQIALLVPEKLTPLHLYKYVAMDFQAKLG	173
Db	194	GHNISRVTFMSAVSQ-----EKOAEILEYAHGQIAIIVAPALLAGHNYTLKIEYSANIS	249
Qy	174	DGFEFGYKSTYRTLGGETRILAVTDPEPTQARMAPCFDEPLFKANFSIKIRSRHIAL	233
Db	250	SSYGYGFYSYTDSENEKKYPAATQFEPLAARSAPPCDEPAFAKATFIIKIIRDQYALT	309
Qy	234	SNMPKVKTTIELEGSLLEDHFTTVKMSYTLVAVYVCDPHLSGFTSSGVKSYIYASPKR	293
Db	310	SNMPKSSVWLDDGLVQDFESVSKMSYLVAFIVGEMKNLSQ-DVNGTLVSIYAVPENI	368
Qy	294	NOTHYALQASKLDDFYEKYFDIYVPLSKLDLIAIPDFAPGAMENWGLITVRETSLLDPP	353
Db	369	QGVHYALETTVKLLEFFQNYFEIQYPLKLLDLVAIPDFEAGAMENWGLITFREETLLYDS	428
Qy	354	KTSSASDKLWTRVIAHELAHQWFGNLTVMWNNIDILWKEGFAYMEILIANVATPELOF	413
Db	429	NTSSMAADRKLVTKIIAHELAHQWFGNLTVMWNNIDILWKEGFATFMEYFSLKIFKELSS	488
Qy	414	DDYFLNVCFEVITKDSLNSSRPISKPAETPQIQEMPEDEVSYNKGCACILNMLKDFLGEK	473
Db	489	YEDFLDARFRTMKKDSLNSSHPISSSVQSSQIEMFDSLSYFKGSSLLMLKTYLSEDV	548
Qy	474	FOKGIIOYLLKKFYSYRNANNDLWSSLSNCSLEDSFTSGGVCHSDPKPMTNNMLAFGENAE	533
Db	549	FQHAVVLYLHNHSTASIOSDDLWDSFN-----EVTNQLT-----D	583





Db 847 TQDVFTVIRYISYNGKNMANNIQLNWDVLYNRYTINNRLGRIVT-IAEPNTEIQL 905  
Qy 912 QEVKLFRESLEAQSGLDIFQTVLETITKNIKWLKELNPLTLRTW 955  
Db 906 WQMESFFAKYPQAGAGKPREQVLETQKNINLWKLQHRNTIREW 949  
RESULT 5  
S30398  
aminopeptidase N homolog BP-1/6C3 - mouse  
A;Alternate names: surface antigen BP-1/6C3  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: S30398  
R;Wu, Q.; Lahti, J.M.; Air, G.M.; Burrows, P.D.; Cooper, M.D.  
Proc. Natl. Acad. Sci. U.S.A. 87, 993-997, 1990  
A;Title: Molecular cloning of the murine BP-1/6C3 antigen: a member of the zinc-dependent  
A;Reference number: S30398; MUID:90139003; PMID:1689065  
A;Accession: S30398  
A;Molecule type: mRNA  
A;Residues: 1-945 <WUQ>  
A;Cross-references: UNIPROT:P16406; EMBL:M29961; NID:g191947; PIDN:AAB47732.1; PID:g3091  
C;Superfamily: membrane alanyl aminopeptidase  
C;Keywords: disulfide bond; glycoprotein; homodimer; membrane protein; phosphoprotein; s

Query Match 27.5%; Score 1390.5; DB 2; Length 945;  
Best Local Similarity 34.0%; Pred. No. 9.6e-80;  
Matches 322; Conservative 168; Mismatches 373; Indels 85; Gaps 20;

Qy 26 TAILPOICISQSFVPSYHFTDPGAPPVATNGERFPWQELRPSVVIPLHYDLFVHPN 85  
Db 60 TALPPQ----DQNVCPDS----ED-----ESGE---WKQFLRPDFINPVHYDLEVKAL 101  
Qy 86 LTSDFVASEKIEVLVSNATQFIILHSDKLEITNATLQSEEDSRMYKPGKE----LKVL 141  
Db 102 MEEDRYTGIVTISYVNLKPTDLHLHIRETKITKL-----PBLRPPSGEQVPIRRCE 154  
Qy 142 YPAHEQIALLVPEKL---TPHLKYVAVMDFOAKLGDGFGFYKTYRTLTGETRILAVTD 198  
Db 155 YKQEVYVIOAEDLAATSGDSVRLTMEFGWLGNSLVGFYKTYME-DQIRSIATD 213  
Qy 199 FEPTQARMAPFCFDEPLFKANFSIKIRRESRIALSNNPKVKTIELEGGLLEHFTTVK 258  
Db 214 HEPTDARKSPFCFDEPNKSTYSIIHPKEYSALSNNPEKSEMDWNKKTTFFVKSVP 273  
Qy 259 MSTYLVAIVCDFHSLSGFTSSGVKSVIYASPKRQNTQHYALQASLKLLDFEYKYPDIY 318  
Db 274 MSTYLVCFAVHRFTAIERKSRSGKPLKYVQPNQKETAAYAAANTQAVDFYDFYFAMEY 333  
Qy 319 PLSKLDLIAIPDFAPGAMENGLITYRETSLLFPDKTSSASDKLWVTRVIAHELHQWFG 378  
Db 334 ALPKLDKIAIPDFGTGAMENGLITYRETNLLYDPLLSASNQORVASVAHELHVQWFG 393  
Qy 379 NLVTMWNMDLWKEGFAKYMELIAVNATYPELO- FDDYFLNVCFEVITKDSLNSSRPIS 437  
Db 394 NTVTMDWDDLWLNNEGFPASPEFLGVNHAERQWMLSQVLLEDVFPVQEDDLSMSSHPV 453  
Qy 438 KPASTPTQIQEMFDEVSNKACILNMLKDFLGEKFKQGIIOYLKFSYRNANKDDLWS 497  
Db 454 VTVSTPAEITSVPFGISYSGKASILRLQDWITPEKFKQCGQIYLYKKFPQANAKTSDPFD 513  
Qy 498 SLNSCLESDFTSGGVCHSDPKMTSNMLAFGENAEVKEMWTTTLOKIGIPLLVV--KQD 555  
Db 514 SLQEA-----SNLPVKEVMDWTWSQMGVPVTVSGRQV 546  
Qy 556 GCSLRLOQERFLQGVQEDPEWRALQERYLWHIPLTYSTSSN--VIHRHLKSKTDTLD 613  
Db 547 -----ITOKRFLD-SKADPSQPPSELGYTNIPVRWADNDSRITVYNRLDKGGITLNA 600  
Qy 614 LPEKTSWKNVDSNGYIVHVEGHGWDLITQLNQHTLLRPKDRVGLIHDVQLVAG 673  
Db 601 NLSGDAFLIKNPDIHGFYRVNYEGTMDWIAEALSSNHRFSAAADRSSFIDDAFALAAQ 660

Qy 674 RLTLDKALDMTYTYLOHETSS---PALLEGLSYLESFYHMMDDRRNISISENLKRYLLQYF 730  
Db 661 LLNYKIALNLTWYKSEEDFLPWERVISSVYIISPEE--DDRELYPMIET---YFQGV 715  
Qy 731 KPVIDRQSWSDKGSVMDRLRSALLKILACDLNAPCTQKAAELFSQMSSESGKLNIPD 790  
Db 716 KPVADLIGMDTGSHITKLLRASILGFPACKGDRREALGNASQLFDSWLK--GSASIPVNL 773  
Qy 791 LKIVYSUGAQT---AGWNYLLBQYELSMSSAQNKILYALSTSKHQEKLKLTIELGMEG 847  
Db 774 RLIVRYGMQNSGNEAAWNTLLEQYKTSLAQEKELLYGLASVKQVKKLLARYLEMLKDP 833  
Qy 848 KVIKTQNLAAALLHAIARRPKGOQLAMDVFRENTHLILKFPDLGSDYDIRMIISGTTAHFSS 907  
Db 834 NIKTQDVFTVIRYISYNSYKTMANNWILQNLWDVLSRFTINDRYLGRIVT-IAEPNT 892  
Qy 908 KDKLQEVKLPFESLEAQSGLDIFQTVLETITKNIKWLKELNPLTLRTW 955  
Db 893 ELQLWQMOSFFAKYPNAGAGKPREQVLETQKNINLWLNVRQSIREW 940  
RESULT 6  
I59331  
thyrotropin-releasing hormone degrading enzyme (EC 3.4.11.-) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I59331  
R;Schauder, B.; Schomburg, L.; Kohrle, J.; Bauer, K.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9534-9538, 1994  
A;Title: Cloning of a cDNA encoding an ectoenzyme that degrades thyrotropin-releasing ho  
A;Reference number: I59331; MUID:95023946; PMID:7937801  
A;Accession: I59331  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1025 <RES>  
A;Cross-references: UNIPROT:Q10836; EMBL:X80535; NID:g558636; PIDN:CAA56675.1; PID:g5586  
A;Note: in Genbank entry RRTHRD, release 113.0, the source is designated as Rattus ratt  
C;Superfamily: membrane alanyl aminopeptidase  
C;Keywords: aminopeptidase

Query Match 26.3%; Score 1327; DB 2; Length 1025;  
Best Local Similarity 32.3%; Pred. No. 1.1e-75;  
Matches 302; Conservative 171; Mismatches 399; Indels 62; Gaps 16;

Qy 50 PGAPPVATNGER--FPWQELRPSVVIPLHYDLFVHPNLTSLDFVASEKIEVLVSNATOF 107  
Db 121 PSAPHPSEEEQEQWQWPTQRLSGHLKPLHYNLMTAFMENFTFSGEVNVEIACQNAIRY 180  
Qy 108 IILHSDKLEITNATLQSEEDSRMYKPKELKVLSPYPAHEQIALLVPEKLTPLHLYKYVAMD 167  
Db 181 VVLHARVAVEK--VQVAED-RAFQAVPVAGFFLYPQTQVLVVVNLNRTLDAQRHYNLKII 237  
Qy 168 FOAKLGDGFGFYKTYRTLTGETRILAVTDFTPTQARMAPFCFDEPLFKANFSIKIRRE 227  
Db 238 YNALIENELLGFRSSY-VIHGERRFLGVTFQSPTHARKAPCFDEPIYKATFKISIKHQ 296  
Qy 228 SRHIALSNMPEKVTIELEGGLLEDHPEFTVKMSTYLVAIVCDFHSLSGFTSSGVKYSIY 287  
Db 297 ATYLSNMPETSVSEEDGWNVDHFSQTLPMSTIYLAWAICNFTYRETTKSGVVVRLY 356  
Qy 288 ASPD--KRNTHYALQASLKLLDFEYKYPDIYIYPLSKLDLIAIPDFAPGAMENGLITYR 345  
Db 357 ARPDAIRRGSDYALHITKELIEFYEDYFKVPYSLPKLDDLAVPKHPVAAEMENGLSIFV 416  
Qy 346 ETSLLFPDKTSSASDKLWVTRVIAHELHQWFGNLVTMEWMDLWKEGFAKYMELIAVN 405  
Db 417 EQRIILLDPSSVSSYLLDVTMWIVHEICHQWFGDLVTPVWMDVWLKEGFAHYFEFGTD 476  
Qy 406 ATYP--ELQDIDDVFNVCFEVITKDSLNSSRPISKPAETPTQIOMEDEVSYNKAGCILN 463  
Db 477 YLPSWNMEKQRFELTVLHEVMDLGLASSHPVSQEVLRATDDKVPDWTAYKGAALIR 536  
Qy 464 MLKDFLGEERFKQGIIOYLKFSYRNANKDDLWSSLSNSCLESDFTSGGVCHSDPKWTSN 523

Db 537 MLANFMGHSVFGQDYLTIHKYGNARNDLWLTSEALKRN----- 579  
Qy 524 MLAFENAEVEMMTTTLQKGIPLLVVQDGCs---LRQOERFLOQVQEDPEWRAL 580  
Db 580 ----GKYVQIENVQDWTQMGYPVITILGNMTAENRILITQOHFIDYIGAKTKALQLO 634  
Qy 581 QERYLWHPLTYSTSS-SNVIRHLL-----KSKDTDLDPKTSVWKNVDSNGYIVRY 635  
Db 635 NSSYLWQIPLTVVGNRSHVSEALIWVSNKSEHRIITYLDKGSWILGNINQTYGFRVNY 694  
Qy 636 EGHGWDQLITQLNQNHLLRPKDRVGLIHDVQVQLVAGRLTLDKALDWTYVLQHETSS-- 693  
Db 695 DURNWRLIDQIRNHEVLSVNSRAGLDDAFSLARAGVLPONIPLEIRYLSBEKOFPLP 754  
Qy 694 -PALLEGISYLSFHYHMDRRNISISENLKRYLLQYFKPVIDROSWSd-----RGS 744  
Db 755 WHAASRALYPLDKLDRMENYNI-----FNEYILKQVATTYSLKGPKNNGSVVQAS 808  
Qy 745 VDRMLRALLKACLNLHAPICIAAELFSQWMESSKLNIPDVLKIVYSVGQATTAG 804  
Db 809 YQHEELREVINLACSGFKHCHQOASTLISDWI--SSNRNRIPLNVRDVIYCTGVSLDE 867  
Qy 805 --WNYLLQYELSMSSAQNKILYALSTSKQEKLLKLELGMECKVIKTNLAALHAI 862  
Db 868 DWVEFIWKFHSTTAVSEKKILLEALTCSDRNLSRLNLNSLSEVVDQDAIDVITHV 927  
Qy 863 ARRPQGOQLAWDFVRENTHLLKKFDLAGSYDIRMIISGTTAFHSSKDLQEVKLPFFESLE 922  
Db 928 ARNPHGRDLAWKFFDKWKILNTRYGEALFWNSKLISGVTFFLNEGELKELKNFMKSYD 987  
Qy 923 AQGSHLDIFQTVLETITITNKNLWLEKNLPLTRLTWL 956  
Db 988 GVAS--ASFSSRAVETVEANVRWRLYQDELFWL 1019

RESULT 7  
A32852  
membrane alanyl aminopeptidase (EC 3.4.11.2) - rat  
N:Alternate names: aminopeptidase N; microsomal aminopeptidase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text\_change 09-Jul-2004  
C:Accession: A32852; A32448; A61250  
R:Watt, V.M.; Yip, C.C.  
J. Biol. Chem. 264, 5480-5487, 1989  
A:Title: Amino acid sequence deduced from a rat kidney cDNA suggests it encodes the Zn-P  
A:Reference number: A32852; MUID:89174587; PMID:2564389  
A:Accession: A32852  
A:Molecule type: mRNA  
A:Residues: 1-965 <WAT>  
A:Cross-references: UNIPROT:P15684; GB:M25073; NID:G205108; PIDN:AAA41502.1; PID:G205109  
R:Malfoy, B.; Kado-Fong, H.; Gros, C.; Giros, B.; Schwartz, J.C.; Hellmiss, R.  
Biochem. Biophys. Res. Commun. 161, 236-241, 1989  
A:Title: Molecular cloning and amino acid sequence of rat kidney aminopeptidase M: a mem  
A:Reference number: A32448; MUID:89273642; PMID:2567164  
A:Accession: A32448  
A:Molecule type: mRNA  
A:Residues: 1-801,'SC',805-806,'A',808-812,'ATVPER',819-830,'VGR',834-965 <MAL>  
A:Cross-references: GB:M26710; NID:G601864; PIDN:AAA57129.1; PID:G601865  
R:Punkhouser, J.D.; Tangada, S.D.; Jones, M.; O, S.J.; Petersen, R.D.A.  
Am. J. Physiol. 260, L274-L279, 1991  
A:Title: p146 type II alveolar epithelial cell antigen is identical to aminopeptidase N.  
A:Reference number: A61250; MUID:91206591; PMID:1673322  
A:Accession: A61250  
A:Molecule type: protein  
A:Residues: 2-19,68-84;206-212,'X',214-215;286-289,291-299;364-371 <FUN>  
C:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase; glycoprotein; membrane protein  
F:114,128,234,242,264,555,606,624,780/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 26.0%; Score 1312; DB 2; Length 965;  
Best Local Similarity 32.6%; Pred. No. 9e-75; Indels 96; Gaps 26;  
Matches 326; Conservative 165; Mismatches 413;

RESULT 8

A53984  
membrane alanyl aminopeptidase (EC 3.4.11.2) - pig

Qy 20 RGFY-----CLTAILPOICICSFSPSPSHFTED-----PGAPPVATN--- 58  
Db 3 KGFYISKTLGILGLGVAACCTIIALSVVYAOEKRNAENSAIAPTLPGSTATTSTTN 62  
Qy 59 ---GERPWOELRPSVVILPHYDLFVHPNLTSLD-----FVASEKIEVLVSNATQETIL 110  
Db 63 PAIDESPKNQYRUKPTLIPDSYQVTLRPLUTPNEQGLIYIFKGSSTVFTCNETTNVILI 122  
Qy 111 HSKDLEITN-----ATLQSEEDSRMKPGKELKVLSPAH-EQIALLVPEKLTPHLKYV 164  
Db 123 HSKKLYNTKGNHRVALRALGDT---PAPNIDITTELVERTEYLVVHLQGLSVKGHQYEM 178  
Qy 165 AMDQAKLGDGFEGFYKSTYRTLTGETRILAVTDFPTQARMAPCFDEPLFKANFSKI 224  
Db 179 DSEFQGLADLAGFYRSEYME-QGNKKVATWQQAADARKSPFCFDEPAMKASFNTL 237  
Qy 225 RRESRHIALSNM-PK-VKTIIEGGLLEDPHTVTKSTYLVAIVTCDHFSLSGTSSGV 282  
Db 238 IHPNNLTALSNMLPKDSRTLQEDPSWNVTEFHTPKMSTYLLAYIVSEFKYVEAVSPNRV 297  
Qy 283 KVSIVASPDKENQTH--YALQASLKLLDFEYKYPDIYYPPLSKLDLIAIPDFAPGAMENWG 340  
Db 298 QIRIWARPSAIDEGHDYALQVTGPILNFFPAQHYNTAYPLEKSDQIALPDFNAGAMENWG 357  
Qy 341 LITVRETSLLPDKTSSASOKLWTRVIAHELAWHGFNGLVTMEWANDIWLKEGFAKME 400  
Db 358 LVTYRESALVPDPOSSISNKRVTVTIAHELAWHGFNGLVTVDWMNDLWNEGFASVYE 417  
Qy 401 LIAVNATYPELQPDYF-LAVCPVITKDSINSRPSKPA--ETPTQIOEMFDEVSYN 456  
Db 418 FLGADYABPTWNLDLVLNDVYRMAVDALSHPLSSPANENVTPAQISELFDSTIYS 477  
Qy 457 KGACILNMLDFLGEERFQKGIIOYLKKFSYRNAKNDLWSLSNSCLESDFTSQGVCHS 516  
Db 478 KGASVLRMLSSFLTEDLFKKGLSSYLHTFOYSNTIYLDLWEHLQAV----- 524  
Qy 517 DPKMTSNMLAPLGENAEVKEMTTWTLOKGIPLLVVQDGCsLRLQQRFLQGVQEDP- 575  
Db 525 -DSQTAIKLP-----ASVSTIMDRWILQMGFPVITVNTS--TGEIYQSHFLL-----DPT 571  
Qy 576 --EWRALQERYLWHIPLTYSTSSSNVTHRLHLSKTDLDLPEKTS-WVKFNVDNSNGYI 632  
Db 572 SKPTRPSDFNYLWILVPIPY-LKNGKEDHYWLETERNQSAEFQTSNEWLLNLINVTGYIQ 630  
Qy 633 VHYEGHGDQLITQLNQNHLLRPKDRVGLIHDVQVQLVAGRLTLDKALDWTYVLQHETS 692  
Db 631 VNYDENWRKIQNLQTDLSVIPINRAQIIHDSFNLASACKLSITLPLSNTLFLASETE 690  
Qy 693 SPALLEGLSYLESFYHMDRRNISIDISENLKRY-----LLQYFKPVIDRQSWSDK-GS 744  
Db 691 YMPWEAALSSLYNYPKLMFDR---SEVYGPMKRYLKKQVTPLFAYFK--IKTNMWDREPPT 745  
Qy 745 VMDRLRSALLKACLNLHAPICIAAELFSQWMESSKLNIPDVLKIVY--SVGAQTT 802  
Db 746 LMEQYNEINAIASCTSGLEBCDRDLVVGLYSQMMNNSDNNPIHPNLRSTVTCYNAIFGGE 805  
Qy 803 AGWNYLLEQVELSNSSAEQNKILYALSTSKHQLKLLKLELGMECKVIKTNLAALHAI 862  
Db 806 EEWNFANEQPKATLVNNEADKLRSLACSNVWILNRYLSYTLNPDYIRKODATSTIVSI 865  
Qy 863 ARRPKGOQLAWDFVRENTHLLKKFDLAGSYDIRMIISGTTAFHSSKDLQEVKLPFFESLE 922  
Db 866 ANNVVGQTLVWDFVRSNNWKKLFEDYGGGFSFANLIQGVTRFRSSEFELOQLEQKEDNS 925  
Qy 923 AQ--GSHLDIFQTVLETITITNKNLWLEKNLPLTRLTWLAVNT 960  
Db 926 ATGFGSGTRALEQALEKTKANIKWKENKDVVLKWFTEENS 965

N;Alternate names: aminopeptidase N; microsomal aminopeptidase N; surface glycoprotein C  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 09-Oct-1994 #sequence revision 15-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: A53984; S24020; S05040; S13177  
R;Delmas, B.; Gelfi, J.; Kut, E.; Sjoestrom, H.; Noren, O.; Laude, H.  
J. Virol. 68, 5216-5224, 1994  
A;Title: Determinants essential for the transmissible gastroenteritis virus-receptor interaction  
A;Reference number: A53984; MUID:94309188; PMID:7913510  
A;Accession: A53984  
A;Molecule type: mRNA  
A;Residues: 1-963 <DEL>  
A;Cross-references: UNIPROT:P15145; GB:Z39522; NID:G525286; PIDN:CAA82641.1; PID:G525287  
R;Delmas, B.; Gelfi, J.; L'Haridon, R.; Vogel, L.K.; Sjoestrom, H.; Noren, O.; Laude, H.  
Nature 357, 417-420, 1992  
A;Title: Aminopeptidase N is a major receptor for the entero-pathogenic coronavirus TGEV  
A;Reference number: S24020; MUID:92278435; PMID:1330661  
A;Accession: S24020  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 2-31 <DE2>  
R;Olson, J.; Sjoestrom, H.; Noren, O.  
FEBS Lett. 251, 275-281, 1989  
A;Title: Cloning of the pig aminopeptidase N gene. Identification of possible regulatory  
A;Reference number: S05040; MUID:89325681; PMID:2568950  
A;Accession: S05040  
A;Molecule type: DNA  
A;Residues: 1-294 <OLS>  
A;Cross-references: EMBL:X15088  
R;See, H.; Reithmeier, R.A.F.  
Biochem. J. 271, 147-155, 1990  
A;Title: Identification and characterization of the major stilbene- diisulphonate- and co  
A;Reference number: S13177; MUID:91024918; PMID:1977382  
A;Accession: S13177  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 2-40 <SEE>  
C;Genetics:  
A;Introns: 200/2; 248/1  
A;Note: the list of introns may be incomplete  
C;Superfamily: membrane alanyl aminopeptidase  
C;Keywords: aminopeptidase; glycoprotein; transmembrane protein  
F;1-8/Domain: intracellular #status predicted <INT>  
F;9-32/Domain: transmembrane #status predicted <TM>  
F;33-963/Domain: extracellular #status predicted <EXT>

Query Match 25.1%; Score 1269; DB 2; Length 963;  
Best Local Similarity 31.9%; Pred. No. 4.7e-72;  
Matches 323; Conservative 174; Mismatches 386; Indels 130; Gaps 28;  
Qy 20 RGFY-----CLTALPQICISQFSSVHFTEDPGAFPVATNG----- 59  
Db 3 KGFYISKALGILGLGVAATIALSVYAQENKNAEHPQAPSPITTTAATLD 62  
Qy 60 ERFPQELRPSVVIPLHYDLVHPNIT-SLD-----FVASEKIEVLVSNATQFIILHSD 114  
Db 63 QSKENRYRLTTLPLSDSYFVTLRPLTPNADGLYIFKGSIVRLLCQEPDVIHHSKK 122  
Qy 115 LEITN---ATLSEEDSRMKPKG-ELKVLVSYPAHQIALLVPEKLTPLHKYVVMDFQ 169  
Db 123 LNYTQGHMVLRGVDSQVEIDRTELVELT-----EYLVLKGSLOPHMYEMSEFQ 178  
Qy 170 AKLGGEGFGKSYRTLTGGSTRILAVTDFEPTQARMAFPDFPLPKANFSIKIRRES 229  
Db 179 GELADDLAGFVRSEYME-GNVKVLATQMQSTDARKSFCCDFEPAMKATFNITLIHPNN 237  
Qy 230 HIALSNPKVKTIIELEGG---LLBED-----HFPTVMSTYLVAIVCDPFHSLSGTSS 280  
Db 238 LTALSNMPP-----KGSSTPLAEDPNWSVTEFTPTVMSTYLVAIVSFQSVNETAQN 291  
Qy 281 GVKYSIVASPKRQTH---YALQASLKLDDVEKYFDIYVPLSKLDLIAIPDFAPGAWEN 338  
Db 292 GVLIRIWARPNIAEGHGMALNTGPIILNFNFANHTSYPLPKSQDALPDPFAGAWEN 351

Qy 339 WGLITYRETSLLPDPKPTSSADKLWTRVTRVIAHQLAHQWFGNLTVMEMNDIWLKEGPAKY 398  
Db 352 WGLIVTRENALLDPQSSSISNKERVVTVIAHQLAHQWFGNLTVMEMNDIWLNEGPASY 411  
Qy 399 MELIANNATYPEIQDDYFL-NVCFEYITKDSLNSSRPISKPAE---TPTQIQEMFDEVS 454  
Db 412 VEYLGDHAEPTWNLKDLIVPGDVYRWAVDALASSHPLTPPAEENVTPAQISEMFDNIS 471  
Qy 455 YNKGACILANMLDPLGEEKFKGLIIQYKLFYSYRNKNDLWSLSNCSLESDFTSGGVC 514  
Db 472 YSKGASVIRMLSNFLTEDEKGLASLYAHAFAYQNTTYLDLWEHLQKAV----- 520  
Qy 515 HSDPKMTNNMLAFUGENAEKEMWTTTLOKGPILIVKODGCSLRQQRFLQGVFOED 574  
Db 521 ---DAQTSIRLP-----DTVRIMDRWTLONGPPIV---DTKGNISQKHFL---LDS 568  
Qy 575 PEWRALQERYLWHIPITYSTSSNVHRR-----ILKSKTDTLDLPEKTSWVK 622  
Db 569 NVTRSSAFDYLWIVPI--SSIKGVMDHYWLRDVSQAQNDLFKTASD-----DWVL 618  
Qy 623 FNVDSNGYIVHYEGHGWDLITQLNQNHLLRPKORVGLIHVDVQLVGAGRLTLDKALD 682  
Db 619 LNVNVTGYFQVNYDEDNRMQIQLQNLNVIPVIRNAQVIYDSFNLAATAHMPVPTLALD 678  
Qy 683 MTYLQHETSSPALLEGSLYLESFYHMDRRNTSDISENKRLLYLOVFKPVDIR-----Q 737  
Db 679 NTLFLNGEKEYMPQAALSLSYSLMFDR--SEVYGPMMKYLRQVDFLQHFETLTK 735  
Qy 738 SWSDK-GSVWDRMLRSALLKLACDLNHPACIQKAELFSQWMESSGKLNITPTDVLKIVY- 795  
Db 736 NWTPEPNLMDQYSEINAISTACSNGLPQCNENLAKTLFDQWMSDPENNPVHPNLRSTIYC 795  
Qy 796 ---SVGAQTAGWNYLLEQVLSWSAQNKILYALYSTKHQEKLLKLIELGEGVKIKT 852  
Db 796 NATAQGGQDQ--WDFAWGQLQQLVNEADKLRSALACSNEVWLLNRYLYGTYLNPDDIRK 853  
Qy 853 QNLALHLHATARPKGQQLAWDFVRNWTLLKFDLGSYDIDMIISGTTAHFSSSKDLQ 912  
Db 854 QDATSINSIASNVIGQPLAWDFVQSNWKKLFQDYGGSFPSFNLIQGVTRRFSSEFELQ 913  
Qy 913 EVKLPESLEAQSHLID-----FQTVLETITKNIKWLEKNLPLTLRTWLM 957  
Db 914 QLEQF-----KKNMMDVGVSGTRALEQALEKTKANIKWKENKEVVLNWF 960  
RESULT 9  
A30325  
membrane alanyl aminopeptidase (EC 3.4.11.2) precursor - human  
N;Alternate names: aminopeptidase N; cell surface glycoprotein CD13  
C;Species: Homo sapiens (man)  
C;Date: 02-Feb-1990 #sequence revision 02-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: A30325; S01658; I39442; S35688; S56098; S56099  
R;Look, A.T.; Ashmun, R.A.; Shapiro, L.H.; Peiper, S.C.  
J. Clin. Invest. 83, 1299-1307, 1989  
A;Title: Human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminope  
A;Reference number: A30325; MUID:89198086; PMID:2564851  
A;Accession: A30325  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-967 <LOO>  
A;Cross-references: UNIPROT:P15144; UNIPROT:Q9UCE0; GB:M22324; NID:g178535; PIDN:AAAS171  
R;Olson, J.; Cowell, G.M.; Konigshofer, E.; Danielson, E.M.; Moller, J.; Laustsen, L.; H  
FEBS Lett. 238, 307-314, 1988  
A;Title: Complete amino acid sequence of human intestinal aminopeptidase N as deduced fr  
A;Reference number: S01658; MUID:89005706; PMID:2901990  
A;Accession: S01658  
A;Molecule type: mRNA  
A;Residues: 1-85,'R', 87-535,'E', 537-602,'M', 604-886,'P', 888-967 <OLS>  
R;Shapiro, L.H.; Ashmun, R.A.; Roberts, W.M.; Look, A.T.  
J. Biol. Chem. 266, 11999-12007, 1991  
A;Title: Separate promoters control transcription of the human aminopeptidase N gene in  
A;Reference number: I39442; MUID:91268079; PMID:1675638

A:Accession: I39442  
A:Molecule type: DNA  
A:Residues: 1-15 <RES>  
A:Cross-references: GB:M55522; NID:g178532; PIDN:AAA83399.1; PID:g178533  
R:Nunez, L.; Amigo, L.; Rigotti, A.; Pugliesi, L.; Mingrone, G.; Greco, A.V.; Nervi, F.  
FEBS Lett. 329, 84-88, 1993  
A>Title: Cholesterol crystallization-promoting activity of aminopeptidase-N isolated from  
A:Reference number: S35688; MUID:93359071; PMID:8102610  
A:Accession: S35688  
A:Molecule type: protein  
A:Residues: 2-18 <NUN>  
R:Watanabe, Y.; Iwaki-Rgawa, S.; Mizukoshi, H.; Fujimoto, Y.  
Biol. Chem. Hoppe-Seyler 376, 397-400, 1995  
A>Title: Identification of an alanine aminopeptidase in human maternal serum as a membra  
A:Reference number: S56098; MUID:96066273; PMID:7576235  
A:Accession: S56098  
A:Molecule type: protein  
A:Residues: 2-20 <WAT>  
A:Accession: S56099  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 70-77, 'X', 79-81 <WA2>  
C:Genetics:  
A:Gene: GDB:ANPEP; CD13; PEPN  
A:Cross-references: GDB:118728; OMIM:151530  
A:Map position: 15q25-15q26  
C:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein

Query Match 25.0%; Score 1264.5; DB 2; Length 967;  
Best Local Similarity 31.4%; Pred. No. 9.1e-72;  
Matches 325; Conservative 158; Mismatches 386; Indels 167; Gaps 26;

QY 20 RGFYCLTAI-----LPQICICQSFSSVPHTEDPGAPPVA----- 56  
DB 3 KGFYISKSLGILGVAACVITIALSVYQERKANKANSPVASTPSSASATNPASA 62  
QY 57 -TNGERFPQELRLPSVPIPLHYDLFVHPNLTSLD-----FVASKIEVLVSNATQFIIL 110  
DB 63 TTLDSQKAWNRVRLNTLKPDSYQVTLRPYLTLPNDRLGVFKGSSVTRFTCKEATDVIII 122  
QY 111 HSKOLEITNATLQSEDSRYMKPKELKVLVSY-----PAHEQIALVLP-EKLTPLK---- 161  
DB 123 HSKKLYNT-----LSQGRVRLRGVGGSQPPDIDKTELVEPTVLYLVHVLKGLS 170  
QY 162 -----YYVAMDFOAKLGDGFEQFYKSTYRTLGGETRILAVTDFEPTQARMAPPCDEPLF 216  
DB 171 VKDSQYENDSEFEGELADDLAGFYSEYWE-GNVRKVATVQMQAADARKSFPCEDEFAM 229  
QY 217 KANFSIKIRRESRHIALSNM-PKVTIIELEGGLED-----HFETTYVMSTYLVAITYVC 269  
DB 230 KAEPNITLIHPKDLTALSMLPKGPSSTLP-----EDPNMNVTEFHTTPKMSTYLLAFIVS 285  
QY 270 DPHLSLGGTSSQVKSVIYASPKRNQTH--YALQASLKLLDFYKCYFDIYVPLSKLDLIA 327  
DB 286 EFDYVEKQASNGVIRIWARPSAIAAGHDYALANTGPIILNFFAGHYDTPYLPKSDQIG 345  
QY 328 IDPAPGAMENGLITYRETSLLFPKTSASDGLVTRVIAHELAHQFNGLVMTMWN 387  
DB 346 LPDFNAGAMENGLITYRENSLLFPKSSSSNKERVTVIAHELAHQFNGLVMTIENWN 405  
QY 388 DIWLKEGFAKYMELIAVNATYPELOFDYF-LNVCFEVIITKDSLNSSRPISKPA---ETP 443  
DB 406 DLWLNEGFPASYEYLGDYAEPTWNLKDLWLNDVYRVMAVDALASSHPLSTPASEINTP 465  
QY 444 TOIQEMFDEVSNKACILNMLKDFLGEKFKGIIQYILKPSYNAKNDLWSSL----- 499  
DB 466 AQISELFDIAISYKSGASVRLMLSSELSDVFPKGLASYLHTPAYQNTIYLNLDHQLQAV 525  
QY 500 SNCSLESDFTSQGVCHSDPKMTSNMLAFI GENAEVKEWMTTWTLQKGIPLLVKDGCSL 559  
DB 526 NNRSIQLPPT-----VRDINRWTLQMGFPVITV---DTSTG 559

QY 560 RLQERFLQGVFQEDPE---WRALQERYLWHIPLT-----YST 594  
DB 560 TLSQEHFLL-----DPDSNVTRPSEFNFVMTVPTISIRDSGRQQQDYWLIDVRAQNDLFST 614  
QY 595 SSSNVIRHILKSKTDTLDLPEKTSWKFNVDNGYIYVHYEGHGDOLITQLNQNHTLL 654  
DB 615 SGN-----EWULLNUNVTGYRVNVDENWRKIQTQLQDHSAI 653  
QY 655 RPKDRVGLIHDVQLVGAGRLTDLKALDMTYLLOHETSSPALLGLSYLESFYHMMDRRN 714  
DB 654 PVINRAQIINDAFNLASAHKVPVTLALNNTLFLIEERQYMPWEAALSLSYFKLMFDR-- 711  
QY 715 ISDISENLKRYLLQYFKPVI-----DRQSWSD-KGSVWDRMLRSALLKLACDLNHPACIQ 768  
DB 712 -SEYVGMKNYLLKQVTPFLTHFRNNTNNMREIPENLMDQYSEVNAISTACNGVPECEE 770  
QY 769 KAELFSOMESSGKLNIPTDVLKIVY--SVGAQTTAGWNYLLEQYELSMSSAEONKILY 826  
DB 771 MVSLGFKQWMPNPNPNPIHNLRTVYCNALTAQGEEDWDFAWQFRNATLVNEADKLRA 830  
QY 827 ALSTSKHQEKLLKLIELGMEGKVIKTONLAALLHAIARRPKGQQLAWDFVRENTHLLKK 886  
DB 831 ALACSKELWILNRYLSYTLNPDLRKQDATSTIISITNNVIGQGLVMDVQSNWKKLPND 890  
QY 887 PDLGSYDIRMISGTTAHSKOKLQEVKLPFESLEAQ--GSHLDIFQTVLETITTKNIKW 944  
DB 891 YGGGSFSLNIQAVTRFRFSTEYELQQLQEQPKDNEETGFGSGTRALQALEKTKANIKW 950  
QY 945 LEKXLPILTIRLWLMVNT 960  
DB 951 VKENKEVVLQWFTENS 966

RESULT 10  
TI0052  
aminopeptidase (EC 3.4.11.-) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: TI0052  
R:Constam, D.B.; Tobler, A.R.; Rensing-Ehl, A.; Kemler, I.; Hersh, L.B.; Fontana, A.  
J. Biol. Chem. 270, 26931-26939, 1995  
A>Title: Puromycin-sensitive aminopeptidase sequence analysis, expression, and functiona  
A:Reference number: 216922; MUID:96070789; PMID:7592939  
A:Accession: TI0052  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-920 <CON>  
A:Cross-references: UNIPROT:Q11011; EMBL:U35646; NID:g1184160; PIDN:AAC52409.1; PID:g118  
A:Note: puromycin-sensitive  
C:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase; metalloprotein; zinc

Query Match 24.0%; Score 1214; DB 2; Length 920;  
Best Local Similarity 32.2%; Pred. No. 1.3e-68;  
Matches 305; Conservative 167; Mismatches 353; Indels 122; Gaps 26;

QY 55 VATNGERFPQELRLPSVPIPLHYDLFVHPNLTSLDFVASEKIEVL--VSNATQFIILHS 112  
DB 43 LAAMPEKRPPE--RLPAEVSPIYSLCKPDL--LDPTFEGKLEAAAQVRQATNQIVMNC 98  
QY 113 KDLBITNATLQSEDSRYMKPG-----KELKLVSYPAHEQIALLVPEKLTPLHLYYVAM 166  
DB 99 ADIDIITASVAPEGDEEIHATGFNYQNEDEKVTLSFPSTLQTG-----TGTLK----- 147  
QY 167 DFOAKLGDGFEQFYKSTYRTLGGETRILAVTDFEPTQARMAPPCDEPLFKANFSIKLRR 226  
DB 148 DFGELNDKMGKGYRSRYTTPAGRYAAVYQFRTDPRRAPPCDEPDAIKATDLSLVV 207  
QY 227 ESRIHALSNMPKV--KTIELEGGLLEDHFETTYVMSTYLVAIYVCDHSLSGFTSSGVKV 284  
DB 208 PKDRVALSNMNVDRKPYPDENLVKFKARTPMYSTYLVAIVVGEVDFVETRSKQGVV 267  
QY 285 SIYASPKRNQTHVALQASLKLLDFYKCYFDIYVPLSKLDLIAIPDFAPGAMENWGLITY 344

Db 268 RVYTPVKGAEQCKFALEVAAKTLPEYKDYFNVVPEPLPKIDLIAADFAAGAMENWGLVTV 327  
Qy 345 RETSILLDPKTSASDKLWTVRTVAHELAHQWFGNLTVMHWNDIWLKEGPAKYNELIAV 404  
Db 328 RETALLDPKNSCSSRQWVALVGVGHELAHQWFGNLTVMHWNDIWLKEGPAKYNELIAV 387  
Qy 405 NATPELQFDYDFNLNCFEVITK-DSLNSSRPISKPAETPTQIOEMFEDEVSYNGAGILN 463  
Db 388 DHCFPEVDIWTQFVSADYTRAQELDALDNSHIPISVGVHPSEVDIEIDFALSISKGASVIR 447  
Qy 464 MLKDFLGEKFKGIIQYLLKFSYRNKNDLWSSLSNCSLESDFTSGGVCHSDPKMTSN 523  
Db 448 MLHDYIGDKPKKGWNYLTKFQCKNAATEDLWESLESA----- 486  
Qy 524 MLAFGENAENKEMMTWTLOKGIPLLVVK-----ODGCSLRLOQERF-LQGVF--QEDPE 576  
Db 487 -----SGKPTAAVNNTWTQMGFPLIYVEAEQVEDDRVLKLSQKKFCASGPYGEDCPQ 540  
Qy 577 WRALQERYLWHIPLTYSTSS-NVTHRHILKSKTD---TLDLPKTSWVKFNVDSNGYII 632  
Db 541 WM-----VPIITISEDPNQAOKILMDKPEMSVVLXNVKPDQWVKNLGTGVGYR 591  
Qy 633 VHYEGHWDQIITOLNQNHLLRDKRVGLIHDVFLVQVAGRLTDLKALDWTYYLQHETS 692  
Db 592 TOYSSAMLESLLPGIRD--LSLPPVDRGLQNDLFLSLARAGII----- 632  
Qy 693 SPALLEGLSYLESFYHMDRRNI SDIS-----ENLKRYLLOYKPKVIDR 736  
Db 633 --STVEVLKVNFAFNPEPNTYVWSDLSNGLSTLASHDTDFYEEIOEFKVDVESPGER 690  
Qy 737 QSWSDK--GSVDMRLRSALLKLACDLNHPACIQKAAELFSQWESSGKLNIPDVLKI 793  
Db 691 LGWDPKGEGLH-DALLGLVLGKLGKAGHKATLEARRRKEVE--GKQILSADRSP 747  
Qy 794 VYVGAQTTAG--WNYLLEQVELSMSAEQNKILYALSTSKHQBLKLKLIELGMEGVK 851  
Db 748 VYLVKLGHDGATLIDMLKLHQADMQEENRIERVGLGATLSPELIQKVLTFALSEEV-R 806  
Qy 852 TONLAALLHATARRPK-CQQLAWDFVRENWTHLLKLPDLSYDIIRMIISGTTAHHFSSKDK 910  
Db 807 PQDVTVGVGAGSGKGRKAANKFIKDNBELNRYQ-GGFLSRILKLSVGEFAVDKM 865  
Qy 911 LQEVKLPFESLEAQGSHLIDIFQTVLETITTKNIKWLKNLPLRLTWLM 957  
Db 866 AGEVKAFESHAPSAERTI-QCCENILLNAAMLKRDADSIHQYLL 911  
RESULT 11  
S07099  
membrane alanine aminopeptidase (EC 3.4.11.2) - rabbit (fragments)  
N:Alternate names: leukemia antigen CD13; microsomal aminopeptidase N  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 30-Sep-1991 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
C:Accession: S07099; B25985  
R:Noren, O.; Dabelsteen, E.; Hoyer, P.E.; Olsen, J.; Sjoestrom, H.; Hansen, G.H.  
FEBS Lett. 259, 107-112, 1989  
A:Title: Onset of transcription of the aminopeptidase N (leukemia antigen CD 13) gene at  
A:Reference number: S07099; PMID:90092508; PMID:2574692  
A:Accession: S07099  
A:Molecule type: mRNA  
A:Residues: 15-805 <NOR>  
A:Cross-references: UNIPROT:P15541; EMBL:X51508; NID:g1447; PIDN:CRAA35873.1; PID:g1448  
R:Faracci, H.; Maroux, S.; Bonicel, J.; Desnuelle, P.  
Biochim. Biophys. Acta 684, 133-136, 1982  
A:Title: The amino acid sequence of the hydrophobic anchor of rabbit intestinal brush bo  
A:Reference number: A90640; PMID:82113673; PMID:6120002  
A:Accession: B25985  
A:Molecule type: protein  
A:Residues: 1-14 <FER>  
A>Note: this sequence represents the detergent-released form; a proteinase-released form  
C:Superfamily: membrane alanine aminopeptidase  
C:Keywords: aminopeptidase; glycoprotein; membrane protein; surface antigen; zinc

F;70,98,391,409,463,487,573,656/Binding site: carboxyhydrate (Aen) (covalent) #status pred  
F;223,224,227/Binding site: zinc (His, Glu, His) #status predicted  
Query Match 23.3%; Score 1176; DB 2; Length 805;  
Best Local Similarity 33.6%; Pred. No. 2.7e-66;  
Matches 279; Conservative 147; Mismatches 326; Indels 78; Gaps 22;  
Qy 168 FOAKLGDGPGFVKYKTVRTLGGETRIILAVT--DFEPTQARMAPPCDEPLFKANFSKIR 225  
Db 16 FOELADLLAGFTRSEYME-GNVRKVATTQMOMQAADARKSPCFDEPASKATFNLTIL 74  
Qy 226 RESRHIALSNM-PKVKITIELEGGLED-----HFETTVMSTYLVAYIVCDHSLSGFT 278  
Db 75 HPRDYTALSNNLRSST-----ALPEDPNVTVEFTTPKMYSTYLLAYIVSEPTNIEAQS 129  
Qy 279 SSGVKSYIYASPKRQWOTH--YALQASLKLLDFEYKFDIYPLSKLDLIAIDPFARCAM 336  
Db 130 PNVQIIRIWARPSAISSEGHQYALNVTGPILNFANHYNTPYPLEKSDQIGLDPFNAGM 189  
Qy 337 ENMGLITYRETSLLPKPTSSASDKLWTVRTVAHELAHQWFGNLTVMHWNDIWLKEGPA 396  
Db 190 ENMGLITYRESALLFDFLVSSISNKERVTVVAHELAHQWFGNLTVDWANDLWNEGPA 249  
Qy 397 KYMELIAVNATYPPELOFDDYF-LNVCFEVTIKDSLNSRPI SKPAE---TPTQIOEMFDE 452  
Db 250 SYVEYLGA DYAEPTWNLKDLI LVLNLSHVMVDA LASSHPLSSPADEVNTPAQISELFD 309  
Qy 453 VSTNKGACILNMLKDFLGEKFKGIIQYLLKFSYRNKNDLWSSLSNCSLESDFTSGG 512  
Db 310 ITYSKGA SVLRMLSFTLDEFLFEGSLASYLHTFAYQNTIYLDLWEHLQQAV----- 360  
Qy 513 VCHSDPKMTSNMLAFGENAENKEMMTWTLOKGIPLLVVK-ODGCSLRLOQERFLOGVF 571  
Db 361 -----NSQSAQLPASVRDIIMDRWILQNGFPVTVNTNGI---ISQHHFL--- 404  
Qy 572 QEDPE---WRALQERYLWHIPLTYSTSSNVIHRH-----ILKSKTDTLDLPKTSWVK 622  
Db 405 --DPTSNVTRPSDFNYLWIPV---SSMRNGVQQQBFWLEGVETQNSLPRVEGDNNWIL 459  
Qy 623 FNVDSNGYIIVHYEGHWDQIITOLNQNHLLRDKRVGLIHDVFLVQVAGRLTDLKALD 682  
Db 460 ANLNVTGYQVNVDEGNWKKLQLOTPNPSVPIVIRNAQIIHDAFNALASQKAPVPTLALD 519  
Qy 683 MTYLQHEITSSPALLEGLSYLESFYHMDRRNI SDISENKLRYLLOVFKPEVIDR-----Q 737  
Db 520 NTLFLIRETEYMPQAAALSSNLYFKLPDR--SEVYGPKNYLSKQVRPLFEHFKNITN 576  
Qy 738 SWSDK-GSVDMRLRSALLKLACDLNHPACIQKAAELFSQWESSGKLNIPDVLKIVY- 795  
Db 577 DWTRRPDTLMDQYNEINASTAGSNGIQECETLVSDLFQKQMDPSPNNIHPNLTVTVC 636  
Qy 796 ---SVGAQTTAGNYLLEQVELSMSAEQNKILYALSTSKHQBLKLKLIELGMEGVKIKT 852  
Db 637 NATALGGERE--WDFAWQEPNATLVNEADKLRSALACSNEVWILNRYLSYTLNPDYIRR 694  
Qy 853 QNLAAALLHATARRPKGQQLAWDFVRENWTHLLKLPDLSYDIIRMIISGTTAHHFSSKDKLQ 912  
Db 695 QDATSTINSIASNVIGTLVWDFVQSNWKKLPDFGGSGSFANLIRAVTRRSTEVLELQ 754  
Qy 913 EVKLF-FESLEAQ-GSHLIDIFQTVLETITTKNIKWLKNLPTLRLTWLMVNT 960  
Db 755 QLEQFRLNLDITFGSGTQRALEQEQTRANIKWQENKEAVLWFTANS 804  
RESULT 12  
T29637  
hypotheical protein F49B8.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29637  
R:Murray, J.; Wohlmann, P.  
submitted to the EMBL Data Library, June 1996  
A:Description: The sequence of C. elegans cosmid F49B8.

A;Reference number: Z20657  
A;Accession: T29637  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-884 <MUR>  
A;Cross-references: UNIPROT:Q20627; EMBL:U61949; PIDN:AAB03152.1; GSPDB:GN00022; CESP:F4  
A;Experimental source: strain Bristol N2; clone F49E8  
C;Genetics:  
A;Gene: CESP:F49E8.3  
A;Map position: 4  
A;Introns: 35/2; 248/2; 326/3; 636/2; 856/3  
C;Superfamily: membrane alanyl aminopeptidase

Query Match 22.8%; Score 1151; DB 2; Length 884;  
Best Local Similarity 32.6%; Pred. No. 1.2e-64;  
Matches 300; Conservative 157; Mismatches 362; Indels 100; Gaps 25;

Qy 68 RLPSVVPLHYDLFVHPNLTSLDFVASEKIEVLVSNATQFIILHSKDLIEITNATLQSEED 127  
Db 15 RLPTFAEPHYNVRSLSPCLNQSFQGHATIDVTKEATDVLKVAHQSLIQSVSLITQ-- 72  
Qy 128 SRYMKGKELKVLSPAPAEQIALL--VPEKLTPLHLYKYVAMDFOAKLGDGFGFYSKTY 184  
Db 73 -----PGDASKSLETSYDDKNILIKLPTTMOPO-KVQLDFKFKVGLNDKMGFYRSQY 126  
Qy 185 RTLGETRILAVTDEPTOARVAPCFDPEPLFKANFSIKIRRESRHIALSNPKV-KTIE 243  
Db 127 KDKNGTEKFLASTQFESTVARVAPCFDPEIYKATFDVTLEVENHLTALSNNVISEPT 186  
Qy 244 LEGGLEDHFETVQMSYLYAVIYCDPFSLSGFTSSGVKSYIYASPKRQTHYALQAS 303  
Db 187 ADGKRKAVTFATSPKSSLYAFVAFGELEYISAQTKSGVEMRVYTPVPGKQGGQVSLDLS 246  
Qy 304 LKLLDFEYKPYDIYPLSKLDLIAIDPAPGAMENGLITTYRETSLLPDKPTSSASDKLW 363  
Db 247 VCIIDWYNEWFDIKPLPKCDLIALPDFSGMAMENGLVTVREIALLVDPGVSTTRQSR 306  
Qy 364 VTRVIAHELAWFGNLTVMENWINDILKEGFKAKTMELIYVATYPELQFDYPLN-VCF 422  
Db 307 VALVVAHELAWLWFGNLTVMKWTDLWLKEGFASPMFYMGANCPFKWLHFLNDEL 366  
Qy 423 EVITKDSLNSSHPISKPAETPQIQEMDEVSYNKACILNMLKDFLEEFKQGILOYL 482  
Db 367 SGMGLDALRNSHPIVEIDNPNELDEIYDSITYAKSNSVNRMLCYLSEPFQKGLRLYL 426  
Qy 483 KKFYSYRNKNDLWSLSNCSLESFTSGGVCHSDPKMTSNMLAFGLNAEYKEMMTWT 542  
Db 427 KRFQYSNAVTQDLWTALSEAS-----GQN--VNELMSGWT 459  
Qy 543 LQKGIPLLV--KQDGCS--LRLQERFLQGVQEDPEWRALQERYLWHIPUTYS--TSS 596  
Db 460 QQMGGFVLKVSQRQDGNRRILTVQRRFISD-GGEDP-----KNSQWQVPIITVAVGSSP 512  
Qy 597 SNVIRHLKSKTD--TLDLPKTSWKFVNDNSGYIYVHVEGHWQDLITQLNQHTLL 654  
Db 513 SDVKARFLKKEKQOEFTIEGVAPGSEWVKLNSGTTGTYRVEYS-----DEMLTAMLPDIASR 568  
Qy 655 RPK--DRVGLIHDFQVLCAGRLTDLKALDMTYLYLQHTSSP-----ALLGLGYL 703  
Db 569 RNPVLDRFGLINDLALLNTGRVSI-----AQFVQVAASSAKEDYVWGAIDGMSKL 622  
Qy 704 ESFYHMDRRNISDISNKLRYLLQYKFPV-----IDRQSWSDKGSVMDRLRSALLKLA 758  
Db 623 LACAREMS-----EDTLKSAQLVVMVMEQTGAELGFAEQAGEDSKM--MLRSLVQARL 675  
Qy 759 COLNAPCIQKAAELFSQWMESSGKLNPTDVLKLYVSGAQ--TTAGNYLLEQYELSM 816  
Db 676 ARAGQPTIDKFTOMFNDFLERTGPIH--PDRLATFGVARYGKGEGDFDKLMLNRETIT 733  
Qy 817 SSAEQNKILYALSTSKHOKLKLKELGWEGKVIKTONLAALLHAIARRPKGQQLAWDFV 876  
Db 734 FOEIERQTVAMVSQTPESLLAQLFEYGFYKPKVRPDQOLYFLGTGATHMGQQYAWKYF 793

Qy 877 RENTHLLKKF-DLGSYDIRMIISGTTAHFSSKKDLQEVKLPF-----ESLEAQGSHLD 929  
Db 794 CEHIKEFLDKYGGANSSLFQRLXAFAGESFGNEKRAVEFQDFPCNVLSDTRQTLARP 853  
Qy 930 IFQTVLETITKNIKWLEKN 948  
Db 854 IGQTV-EAIRLNARLLESN 871

RESULT 13  
S37794  
aminopeptidase yscII (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae)  
A;Alternate names: protein YKL157w; protein YKL611  
C;Species: Saccharomyces cerevisiae  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: S37794; S37987; S44571; S19642  
R;Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the EMBL Data Library, September 1993  
A;Description: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci  
A;Reference number: S37786  
A;Accession: S37794  
A;Molecule type: DNA  
A;Residues: 1-844 <VAN>  
A;Cross-references: UNIPROT:P32454; EMBL:Z26877; NID:G407482; PIDN:CAA81497.1; PID:G4074  
A;Experimental source: strain S288C  
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the Protein Sequence Database, March 1994  
A;Reference number: S37976  
A;Accession: S37987  
A;Molecule type: DNA  
A;Residues: 1-844 <VA2>  
A;Cross-references: EMBL:Z28157; NID:G486272; PIDN:CAA81999.1; PID:G486273; MIPS:YKL157  
A;Experimental source: strain S288C  
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
Yeast 10, 35-40, 1994  
A;Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci of  
A;Reference number: S44563  
A;Accession: S44571  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-844 <VA3>  
A;Cross-references: EMBL:Z26877; NID:G407482; PIDN:CAA81497.1; PID:G407491  
A;Experimental source: strain S288C  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993  
R;Garcia-Alvarez, N.; Cueva, R.; Suarez-Renduelse, P.  
Eur. J. Biochem. 202, 993-1002, 1991  
A;Title: Molecular cloning of soluble aminopeptidases from Saccharomyces cerevisiae. Seq  
A;Reference number: S19642; MUID:92111552; PMID:1765107  
A;Accession: S19642  
A;Molecule type: DNA  
A;Residues: 1-163,'V',165-441,'E',443-843,'VNRDRDVNKKYKNGYY' <GAR>  
A;Cross-references: EMBL:X63998; NID:G3367; PIDN:CAA45403.1; PID:G3368  
C;Genetics:  
A;Gene: SGD:AP2; LAPI  
A;Cross-references: SGD:S0001640; MIPS:YKL157w  
A;Map position: 11L  
C;Superfamily: membrane alanyl aminopeptidase  
C;Keywords: aminopeptidase; glycoprotein; metalloprotein; zinc  
P;290,622/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;305,309/Binding site: zinc (His) #status predicted  
F;306/Active site: Glu #status predicted

Query Match 22.1%; Score 1116; DB 2; Length 844;  
Best Local Similarity 31.4%; Pred. No. 1.8e-62;  
Matches 281; Conservative 171; Mismatches 372; Indels 72; Gaps 24;

Qy 63 PQWELRPLSVVPLHYDLFVHPNLTSLDFVASEKIEVLVSN-ATQFIILHSKDLIEITNAT 121  
Db 6 PNREI-LPDNVVPLHYDLTVPEPDFKTFEGSVKELKINNPAIDTVTLNVTVDTHSAK 64  
Qy 122 LQSEEDSRYPKPKGLKVLSPAPAEQIALLVPEKLTPLHLYKYVAMD--FOAKLGDGPGGF 179  
Db 65 IGDVTS-----EIISEEEQVTTFPAPKGTMSFKGNAFLDIKFTGILNDNMAGF 115



Db	781	LQSPSPVLGGVLTGLNFTSFEALEKISAFYSRKVTGKGFDTLQAQ-ALDTIRSKAQWVS	839
Qy	947	KNLFTLRTWL	956
Db	840	RDRIVATYL	849

RESULT 15

T39789

aminopeptidase - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T39789

R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1999

A:Reference number: Z21816

A:Accession: T39789

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-882 <SEE>

A:Cross-references: UNIPROT:Q9USX1; EMBL:AL122033; PIDN:CAB58971.1; GSPDB:GN00067; SPDB:1

A:Experimental source: strain 972n-; cosmid c1921

C:Genetics:

A:Gene: SPDB:SPBC11921.05

A:Map position: 2

C:Superfamily: membrane [alan] aminopeptidase

Search completed: September 26, 2005, 06:04:26  
Job time : 52 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 26, 2005, 06:10:40 ; Search time 103.689 Seconds  
(without alignments)  
6246.842 Million cell updates/sec

Title: US-10-039-073-2  
Perfect score: 5912  
Sequence: 1 ccccgctccggcatgattt.....aaaaaaaaaaaaaaaaaaaaa 3366

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool\_p/US10039073/runat\_26092005\_070410\_21316/app\_query.fasta\_1.6606  
-DB=PIR -OPWT=fastan -SUFFIX=rdr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10039073 @CNC 1 1 317 @runat\_26092005\_070410\_21316 -NCPUP=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1999	33.8	1006	2	A59384 oxytocinase/insuli
2	1999	33.8	1025	2	A59383 oxytocinase/insuli
3	1771	30.0	916	2	155441 vpl65 - rat
4	1440	24.4	957	2	A47531 glutamyl aminopept
5	1390.5	23.5	945	2	S30398 aminopeptidase N h
6	1327	22.4	1025	2	I59321 thyrotropin-releas
7	1312	22.2	965	2	A32852 membrane alanyl am
8	1269	21.5	963	2	A53984 membrane alanyl am
9	1264.5	21.4	967	2	A30325 membrane alanyl am
10	1214	20.5	920	2	T10052 aminopeptidase (BC
11	1176	19.9	805	2	S07099 membrane alanyl am
12	1151	19.5	884	2	T29637 hypothetical prote
13	1116	18.9	844	2	S37794 aminopeptidase ysc
14	1067	18.0	856	2	S46750 aminopeptidase AAP

15	1047.5	17.7	882	2	T39789 aminopeptidase - f
16	1039	17.6	988	2	T24668 hypothetrical prote
17	1031	17.4	990	2	JC8058 laeverin - human
18	899.5	15.2	873	2	T05189 glutamyl aminopept
19	895.5	15.1	849	2	JC7959 lysyl aminopeptida
20	893.5	15.1	849	2	JU0191 aminopeptidase Y (
21	888.5	15.0	885	2	S73098 aminopeptidase (BC
22	875	14.8	844	2	S47274 membrane alanyl am
23	873	14.8	846	2	A86663 aminopeptidase N (
24	871.5	14.7	784	2	B90442 tricorn proteinase
25	870	14.7	843	2	S38364 membrane alanyl am
26	868	14.7	844	2	JC4054 membrane alanyl am
27	865	14.6	848	2	B97960 membrane alanyl am
28	864	14.6	848	2	E35092 aminopeptidase N (
29	856	14.5	846	2	JN0324 lysine aminopeptid
30	856	14.5	846	2	S23157 membrane alanyl am
31	837.5	14.2	1016	2	T30942 aminopeptidase (BC
32	832.5	14.1	1016	2	T30943 aminopeptidase (BC
33	820.5	13.9	1009	2	T18533 CryIAC toxin-bindi
34	810.5	13.7	783	2	T37457 Tricorn proteinase
35	774.5	13.1	780	2	T37456 Tricorn proteinase
36	705	11.9	747	2	T23882 hypothetrical prote
37	702	11.9	786	2	T23883 hypothetrical prote
38	692	11.7	899	2	H88572 protein T16G12.1 (
39	683	11.6	885	2	S42841 T16G12.1 protein -
40	630	10.7	1071	2	T18597 hypothetrical prote
41	626	10.6	919	2	S42842 T16G12.2 protein -
42	498	8.4	946	2	S48397 hypothetrical prote
43	450	7.6	862	2	G87094 probable aminopept
44	425	7.2	861	2	B70866 probable aminopept
45	404	6.8	613	4	C40201 artifact-warning s

#### ALIGNMENTS

##### RESULT 1

A59384 oxytocinase/insulin-responsive aminopeptidase, variant 2 [imported] - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 20-Apr-2001  
C:Accession: A59384  
R:Ramussen, T.E.; Pedraza-Diaz, S.; Hardre, R.; Laustsen, P.G.; Carrion, A.G.; Kristensen, J. J. Biochem. 267, 2297-2306, 2000  
A>Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and l  
A:Reference: GB:CA894753; NID:98574036; PIDN:CA894753.1  
A:Accession: A59384  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1006 <STO>  
A:Cross-references: GB:CA894753; NID:98574036; PIDN:CA894753.1  
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:  
Pred. No.: 6, 84e-128 Length: 1006  
Score: 1999.00 Matches: 400  
Percent Similarity: 61.81% Conservative: 160  
Best Local Similarity: 44.15% Mismatches: 310  
Query Match: 33.81% Indels: 36  
DB: 2 Gaps: 6

US-10-039-073-2 (1-3366) x A59384 (1-1006)

QY	305	CCAGTAGCCACTAATGGGAAACGATTTCTTTGGAGGAGCTAAGCTCCCGAGTGTGTC	364
DB	134	ProphealaThraenGlyLysLeuPheProTrpAlaGlnIleArgLeuProThraVal	153
QY	365	ATTCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCCTCTCGACTTGTGCA	424
DB	154	ValProLeuAArgTyGluLeuSerLeuHisProLeuThraSerMetThraPheArgGly	173
QY	425	TCTGAGAGATCGAAGCTTGTGTCAGCAATCTCAGCAATCTTATCATCTTTCACAGCAAA	484
DB	174	SerValThrIleSerValGlnAlaLeuGlnValThrTrpAenIleIleLeuHisSerThr	193



Db	881	SerGluAspValArgLysLeuTyrTrpLeuMetLysSerSerLeuAsnGlyAspAsn	900
Qy	2696	AAGACACAGAACTTGGCAGCTCTCTTCATGCGATTGGCAGCGCTCCAAAGGGCGAGCAA	2755
Db	901	ArgThrGlnLysLeuSerPheIleIleArgThrValGlyArgHisPheProGlyHisLeu	920
Qy	2756	CTAGCATGGGATTTGTAAAGAGAAAATTTGGACCCATCTCTGAAAAAATTTGACTTGGGC	2815
Db	921	LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly	940
Qy	2816	TCATATGACATGAAGATGATCATCTCTGGCACACAGCTCACTTTCTTCCAAAGGATAAG	2875
Db	941	SerTyrThrIleGlnAsnIleValIleArgSerThrTyrLeuPheSerThrLysThrHis	960
Qy	2876	TTGCAAGAGGTGAACACTATTTTGAATCTCTTGAGGCTCAAGGATCATCTGGATATT	2935
Db	961	LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrPheArgLeuArgCys	980
Qy	2936	TTTCAAACTGTTCTGGAACGATACACCAAAATATAAATGCTGGAGAGAAATCTTCG	2995
Db	981	ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetGluLysAsnLeuLys	1000
Qy	2996	ACTCTGAGGACTTGGCTA	3013
Db	1001	SerLeuThrTrpTrpLeu	1006
RESULT 2			
A59383			
oxytocinase/insulin-responsive aminopeptidase, variant 1 [imported] - human			
C:Species: Homo sapiens (man)			
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004			
R:Accession: A59383			
R:Ragmussen, T.E.; Pedraza-Diaz, S.; Hardre, R.; Laustsen, P.G.; Carrion, A.G.; Kristsen			
Eur. J. Biochem. 267, 2297-2306, 2000			
A:Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and lo			
A:Reference number: A59383; PMID:20223264; PMID:10759854			
A:Accession: A59383			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-1025 <STO>			
A:Cross-references: UNIPROT:O9UI06; GB: CAB61646; NID: g6468766; PIDN: CAB61646.1			
C:Superfamily: membrane alanyl aminopeptidase			
Alignment Scores:			
Pred. No.:	6.87e-128	Length:	1025
Score:	1999.00	Matches:	400
Percent Similarity:	61.81%	Conservative:	160
Best Local Similarity:	44.15%	Mismatches:	310
Query Match:	33.81%	Indels:	36
DB:	2	Gaps:	6
US-10-039-073-2 (1-13366) x A59383 (1-1025)			
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Db	153	ProPheAlaThrAsnGlyLysLeuPheProTrpAlaGlnIleArgLeuProThrAlaVal	172
Qy	365	ATTCTCTCCTCATTTAGCTCTTTGTCACCCCAATCTCACCTCTCTGGACTTGTGCA	424
Db	173	ValProLeuArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly	192
Qy	425	TCTGAGAAGATCGAAGTCTTGCTGACGAATGCTACCCAGTTTATCATCTTGCACAGCAA	484
Db	193	SerValThrIleSerValGlnAlaLeuGlnValThrTrpAsnIleIleLeuHisSerThr	212
Qy	485	GATCTTGAATCCAGATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAACCA	544
Db	213	GlyHisAsnIleSerArgValThrPheMetSerAlaValSerSerGln	228
Qy	545	CGAAAAGAACTGAAAGTTTGGATTACCTGCTCATGAACAATTTGCACTGCTGTTCCA	604
Db	229	GluLysGlnAlaGluLeuGluTyrAlaTyrHisGlyGlnIleAlaIleValAlaPro	248

Qy	605	GAGAACTTACGCTCACCTGAAATACTATGTGGCTATGAGCTTCCAAAGCCCAAGTTAGT	664
Db	249	GluAlaLeuLeuAlaGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer	268
Qy	665	GATGGCTTTGAAGGCTTTTATAAAGCACATACAGAACTCTTGGTGGTGAACAAGAAATT	724
Db	269	SerSerTyrTyrGlyPheTyrGlyPheSerTyrThrAspGluSerAsnGluLysLysTyr	288
Qy	725	CTTCAGTAAACAGATTTTGAAGCAACCCAGCAGCATGGCTTTCCCTTGTCTTGCATGAA	784
Db	289	PheAlaIaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu	308
Qy	785	CCGTTGTTCAAGCAACTTTTCAATCAAGATACGAGAGAGAGAGAGAGCATATTGCACTA	844
Db	309	ProAlaPheLysAlaThrPheIleIleLysIleIleArgAspGluGlnTyrThrAlaLeu	328
Qy	845	TCCAACATGCCAAAGTTTAAAGCAATGAACCTTGAAGGAGCTTTTTCGAAGATCACATTT	904
Db	329	SerAsnMetProLysLysSerSerValLeuAspAspGlyLeuValGlnAspGluPhe	348
Qy	905	GAAGACTACTGTAAAAATGAGTACATCTTGTAGCTACATAGTTTGTGATTTCCACTCT	964
Db	349	SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetLysAsn	368
Qy	965	CTGAGTGGCTTCACTTCAATCAGGGGTCAAGGTGCTCATCTATGATCCCCAGACAAACGG	1024
Db	369	LeuSerGln---AspValAsnGlyThrLeuValSerIleTyrAlaValProGluAsnIle	387
Qy	1025	AATCAAAACACATTTATGCTTTCGAGCATCACTGAAGCTTACTTTGATTTTATGAAAAGTAC	1084
Db	388	GlyGlnValHisTyrAlaLeuGluThrThrValLysLeuLeuGluPhePheGlnAsnTyr	407
Qy	1085	TTTGATATCTACTATCCACTCTCCAAACTGGAATTAATTTGCTATCTCTGACTTTGCACCT	1144
Db	408	PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla	427
Qy	1145	GGAGCCATGGAATAATGGGGCTCATACATATAGGAGAGCTCACTGCTTTTTCACCCC	1204
Db	428	GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspSer	447
Qy	1205	AAGACCTTCTCTGCTCCGATAAACTGGGTGCTCACCAGAGTCATAGCCCATGAACCTGGG	1264
Db	448	AsnThrSerSerMetAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla	467
Qy	1265	CACCAGTGGTTTGGCAACCTGGTCAATGAATGGTGAATGATATTTGGCTTAAGAGAG	1324
Db	468	HisGlnTrpPheGlyAsnLeuValThrMetLysTrpTrpAsnAspLeuTripleAsnGlu	487
Qy	1325	GGTTTTCGAAAATACATGGAACTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTT	1384
Db	488	GlyPheAlaThrPheMetGluTyrPheSerLeuGluLysIlePheLysGluLeuSerSer	507
Qy	1385	GATCACTATTTTGAATGTGTGTTTGAAGTAATACAAAAGATTCAATTCATTCATCC	1444
Db	508	TyrGluAspPheLeuAspAlaArgPheLysThrMetLysLysAspSerLeuAsnSerSer	527
Qy	1445	CGCCTATCTCCAAACCCAGCGAAACCCCGACTCAAAATACAGGAAATGTTTGTAGAGTT	1504
Db	528	HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu	547
Qy	1505	TCCTATTAACAGGAGCTTGTATTTTGATATGCTCAAGGATTTTCTGGGTGAGAGAAA	1564
Db	548	SerTyrPheLysGlySerSerLeuLeuMetLeuLysThrTyrLeuSerGluAspVal	567
Qy	1565	TTCCAGAAAGAAATAATTCAGTACTTAAAGAAGTTTCAGTATAGAAATGCTAAGATCAT	1624
Db	568	PheGlnHisAlaValLeuTyrLeuHisAsnHisSerTyrAlaSerIleGlnSerAsp	587
Qy	1625	GACTTGTGGAGCAGCTGCTCAATAGTTGTTTGTAGAAAGTGTATTTTACATCTGGTGGATT	1684
Db	588	AspLeuTrpAspSerPheAsn-----	594

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Qy 1685 TGTCAATCGGATCCCAAGATCAACAAGTAACATGCTCGCCTTTCTCGGGGAAAAATGCAGAG 1744
Db      :::::::::::GluValThrAsnGlnThrLeu-----Asp 602
Qy 1745 GTCAAAAGAGATGATGACTATACATGAGCTCTCCAGAAAAGAAATCCCTCGTGGTGGTTAA 1804
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 603 VallysArgMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
Qy 1805 CAAGACGGGTGTTCACTCCGACTCAACAGAGCGCTTCCTCCAGGGGGTTTTCCAGGAA 1864
Db      :::: ||||| ::::::::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 623 LysLysGlyLysGluLeuPheIleGlnGlnArgPhePheLeuAsnMet----- 639
Qy 1865 GACCTGAATCGAGGGCCCTCAGAGAGAGTACCTGTGGCATATCCCAATGACACTACTCC 1924
Db      ||||| ||||| :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 640 LysProGluIleGlnProSerAspThrSerTyrlLeuTrpHisIleProLeuSerTyrlVal 659
Qy 1925 ACGAGTCTCTTAATGTGATCCACAGACAC-----ATTCTAAAAATCAAGACAGAT 1975
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 660 ThrGluGlyArgAsnTyrlSerLysTyrlGlnSerValSerLeuLeuAspLysLysSerGly 679
Qy 1976 ACTCTGGATCTACCTGAAAGACCAGTTGGGTGAATTTAATGTGGACTCAATGGTTAC 2035
Db      ::::::::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 680 VallieAsnLeuThrGluGluValLeuTrpValLysValAsnIleAsnMetAsnGlyTr 699
Qy 2036 TACATCGTTCACTATGAGGGTCATGGATGGACCAACTCATTTACACAGCTGAATCAGAAC 2095
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 700 TyrlleValHisTyrlAlaAspAspTrpGluAlaLeuIleHisGlnLeuLysIleAsn 719
Qy 2096 CACACATCTTCAGACCTTAAGCAGAGTAGGTCTGATTCATGATGTGTTTCAGCTAGTT 2155
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 720 ProTyrlValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
Qy 2156 GGTCCAGGAGACTGACCCCTAGACAAAGCTCTTCACATGACTTACTACCTCCCAATGAA 2215
Db      ||||| ||||| ::::::::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 740 GlyLeuGlyLysValProLeuLysArgAlaPheAspLeuIleAsnTyrlLeuGlyAsnGlu 759
Qy 2216 ACAAGCAGCCCGCACCTTCGGAAGTCTGAGTACTTGGAAATCGTTTACCACATGATG 2275
Db      :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 760 AsnHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrlAsnLeuLeu 779
Qy 2276 GACAGAAGGAATATTTTCAGATATCTTGAAACCTCAAGCGTTACCTTCTTCAGATATTT 2335
Db      :::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 780 GluLysLeuGlyTyrlMetAspLeuAlaSerArgLeuValThrArgValPheLysLeuLeu 799
Qy 2336 AAGCCAGTGTGACAGGCAAGCTGGAGTCAAGGGCTCAGTCTGGGACAGATGCTC 2395
Db      :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 800 GlnAsnGlnIleGlnGlnIleThrTrpThrAspGluGlyThrProSerMetArgGluLeu 819
Qy 2396 CGCTCGGCTCTCTTGAAGCTCGCTGTGACCTGAACCATGCTCCTTGTCATCCAGAAAGCT 2455
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Qy 820 ArgSerAlaLeuLeuGluPheAlaCysThrHisAsnLeuGlyAsnCysSerThrThrAla 839
Qy 2456 GCTGAATCTTCTCCCGATGGAATCCAGTGGGAAAAATTAATATATACCAACAGATGTT 2515
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Qy 840 MetLysLeuPheAspAspTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
Qy 2516 TTAAGATTGTGATCTCTGGGTGCTCAGACACAGCAGATGGAATTACCTTTTAGAG 2575
Db      :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 860 MetThrThrValPheLysValGlyAlaLysThrAspLysGlyTrpSerPheLeuLeuGly 879
Qy 2576 CAATATGAATCTCAATGCTCAAGTCTGAACAAACAAAAATTCGTATGCTTTCTCAACG 2635
Db      :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 880 LysTyrlleSerIleGlySerGluAlaGluLysAsnLysIleLeuGluAlaLeuAlaSer 899
Qy 2636 AGCAAGCATCAGGAAAAGTTACTGAAGTAAATGAATCAGGAATGGAAGGAAAGGTTATC 2695
Db      ::::::::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 900 SerGluAspValArgLysLeuTyrlTrpLeuMetLysSerSerLeuAsnGlyAspAsnPhe 919
Qy 2696 AAGCACAGACTTGGCAGCTCTCTTCATCCGATGCCAGACCTCCAAAGGGGCAGCAA 2755
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Qy 920 ArgThrGlnLysLeuSerPheIleArgThrValGlyArgHisPheProGlyHisLeu 939
Qy 2756 CTAGCATGGGATTTTGAAGAAAAATTTGGACCCATCTCTCTGAAAAAATTTGACTTGGGC 2815
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Db 940 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly 959
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Qy 960 SerTyrlThrIleGlnAsnIleValAlaGlySerTyrlLeuPheSerThrLysThrHis 979
Qy 2876 TTCCAAGAGGTGAACATATTATTTTGAATCTCTTGAGGCTCAAGGATCAGATCTCGATATT 2935
Db      ||||| ||||| ::::::::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 980 LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrPheArgLeuArgCys 999
Qy 2936 TTTTCAAACTGTTCTCGAAACGATAACCAAAAAATATAAAATGGCTGGAGAAAGATCTTCG 2995
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1000 ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetGluLysAsnLeuLys 1019
Qy 2996 ACTCTGAGGACTTGGCTA 3013
Db      :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1020 SerLeuThrTrpTrpLeu 1025
Db      :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 3
I55441
vp165 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I55441
J;Keller, S.R.; Scott, H.M.; Mastick, C.C.; Aebersold, R.; Lienhard, G.E.
J; Biol. Chem. 270, 23612-23618, 1995
A;Title: Cloning and characterization of a novel insulin-regulated membrane aminopeptidase
A;Reference number: I55441; MUID:96007507; PMID:7559527
A;Accession: I55441
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-916 <RES>
A;Cross-references: UNIPROT:P97629; EMBL:U32990; NID:gl041726; PIDN:AAB38021.1; PID:gl041726
C;Superfamily: Membrane alanyl aminopeptidase

Alignment Scores:
Pred. No.: 2,09e-112 Length: 916
Score: 1771.00 Matches: 352
Percent Similarity: 61.88% Conservative: 135
Best Local Similarity: 44.73% Mismatches: 264
Query Match: 29.96% Indels: 36
DB: 2 Gaps: 5

US-10-039-073-2 (1-3366) x I55441 (1-916)
Qy 305 CCAGTAGCCACTAATGGGAAACGATTTCTTGGCAGAGACTAAGCTCCCGAGTGTGTC 364
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 153 ProIleAlaThrAsnGlyLysValPheProTrpAlaGlnIleArgLeuProThrAlaIle 172
Qy 365 ATTCTCTCCATATGACCTTTTGTCCACCCCAATCTACCTCTCTGGACTTTGTTGCA 424
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 173 IleProGlnArgTyrlGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
Qy 425 TCTGAGAAGATCGAAGTCTTTGGTCCAGCAATGCTACCCAGTTTATCATCTTTCGACAGCAA 484
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr 212
Qy 485 GATCTTGAATACAGAAATGCCACCTTCAGTCAGAGAAAGATCAAGATACATGAAACCA 544
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 213 GlyHisAsnIleSerValThrPheMetSerAlaValSerSerGln----- 228
Qy 545 GGAAGAAGACTGAAGTTTGTAGTTACCTGCTCATGAACAAATATGCACGTGCTGTTCCA 604
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 229 GluLysGlnValGlnIleLeuGluTyrlProTyrlHisGlnGlnIleAlaValAlaPro 248
Qy 605 GAGAAACTTACGGCTCACCTGAAATACTATGTGGCTATGGACTTCCAAAGCCAAAGTTAGGT 664
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 249 GluSerLeuLeuThrGlyHisAsnTyrlThrLeuLysIleGluTyrlSerAlaAsnIleSer 268
Qy 665 GATGGCTTTGAAGGTTTTATAAACGACATACAGAACTCTTGGTGGTGAACAGAAATT 724
Db      :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 269 AsnSerTyrlTyrlGlyPheTyrlGlyIleThrTyrlThrAspLysSerAsnGluLysLysAsn 288
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A:Molecule type: mRNA  
A:Residues: 1-957 <LTA>  
A:Cross-references: UNIPROT:Q07075; GB:L12468; NID:g347892; PIDN:AAAL6876.1; PID:g347893  
R:Nanus, D.M.; Engelstein, D.; Gasli, G.A.; Gluck, L.; Vidal, M.J.; Morrison, M.; Finsta  
Proc. Natl. Acad. Sci. U.S.A. 90, 7069-7073, 1993  
A:Title: Molecular cloning of the human kidney differentiation antigen gp160: human amin  
A:Reference number: A48287; MUID:93348214; PMID:8346219  
A:Accession: A48287  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-217, 'A', 219-957 <NAN>  
A:Cross-references: GB:L14721; NID:g291853; PIDN:AAA35522.1; PID:g291854  
C:Genetics:  
A:Gene: GDB:ENPEP  
A:Cross-references: GDB:L38283; OMIM:138297  
A:Map position: 1ppter-17p12  
A:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein

Alignment Scores:  
Pred. No.: 6.56e-90 Length: 957  
Score: 1490.00 Matches: 322  
Percent Similarity: 52.97% Conservative: 178  
Best Local Similarity: 34.11% Mismatches: 362  
Query Match: 24.36% Indels: 82  
DB: 2 Gaps: 19

US-10-039-073-2 (1-3366) x A47531 (1-957)

Qy	263	GTGCCATCTAGTATATCACTTCACAGGATCTCTGGGGCTTTCCAGTA-----	310
Db	60	LeuProSerSer-----ThrAlaSerProSerGlyProProAlaGlnAspGlnAsp	76
Qy	311	-----GCCACTAATGGGACGATTCCTTCGCGAGGAGCTAAGCGTCCCGAGTGTG	361
Db	77	IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe	96
Qy	362	GTCACTCTCCATTCAGCTCTCTTGTCCACCCCAATCTCACCTCTCTGGACTTGGTT	421
Db	97	ValAsnProValHisTyrAspLeuHisValLysProLeuLeuGluGluAspThrTyrThr	116
Qy	422	GCATCTGAGAGATCGAAGTCTGTGTCAGCAATGCTACCCAGTTTATCATCTTCGACAGC	481
Db	117	GlyThrValSerIleSerIleAsnSerAlaProThrArgTyrLeuTrpLeuHisLeu	136
Qy	482	AAAGATCTTGAATCAGCAATGCCACCTTCAGTCAGGAGNAGATTCAAGATACATAAA	541
Db	137	ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg	149
Qy	542	CCA---GGAAAAGAACTGAAAGTT-----TTGAGTTACCTGCTCATGAACAATTT	589
Db	150	ProSerGlyAspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal	169
Qy	590	GCATCTGTGTTCCAGAGAAACTTACGCTCCACCTG-----AAATACTATGTGCT	640
Db	170	ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr	189
Qy	641	ATGACATCCCAAGCAGTTAGTGTGCTTTGAGGGTTTATAAAGCACATACAGA	700
Db	190	MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr---	208
Qy	701	ACTCTGTGTGTGAAACAAAGAAATTTCTGCAGTACAGATTTTGAGCCAAACCGGACGC	760
Db	209	ThrGluAsnGlyArgValLysSerIleValAlaThrAspHisGluProThrAspAlaArg	228
Qy	761	ATGCTTCTCTCTTGTGATGAACCGTTGTCAAAGCCCAACTTTTCAATCAAGATACGA	820
Db	229	LysSerPheProCysPheAspGluProAsnLysLysAlaThrTyrThrIleSerIleThr	248
Qy	821	AGAGAGAGCGGCATATTGCATATCCACATGCCAAAGGTTAGACAATTTGAACTTGAA	880
Db	249	HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluLeuSerValAsp	268

Qy	881	GGAGGTCTTTTGGAGATCACTTTGAAACTACTGTAAAAATAGTACATACCTTGTAGCC	940
Db	269	AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys	288
Qy	941	TACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCATTCATCAGGGGTCAAGGTGTC	1000
Db	289	PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr	308
Qy	1001	ATCTATGCATCCCGACAGAACCGAATCAACACATATGCTTTGACGGCATCACTGAAG	1060
Db	309	IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer	328
Qy	1061	CTACTTGAATTTTATGAAAGTACTTTGATATCTACTATCTCACTCTCAAACTGGATT	1120
Db	329	ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys	348
Qy	1121	ATTGCTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1180
Db	349	IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg	368
Qy	1181	GAGACCTCACTGCTTTTGGACCCCAAGACCTCTCTGCTTCCGATAAACTGTGGTCACC	1240
Db	369	GluThrAsnLeuLeuTyrAspProLysGluSerAlaSerSerAsnGlnGlnArgValAla	388
Qy	1241	AGAGTCATAGCCCATCAACTGGCGCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1300
Db	389	ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAspTrp	408
Qy	1301	TGGAATGATATTGGCTTAAGAGGTTTTCGAAATACATGAACTATTCGCTGTTAAT	1360
Db	409	TrpGluAspLeuTrpLeuAsnGluGlyPheAlaSerPhePheGluPheLeuGlyValAsn	428
Qy	1361	GCTACATATCCAGAGCTGCNAATTT---GATGACTATTTTGAATGTGTGTTTGAAGTA	1417
Db	429	HisAlaGluThrAspTrpGlnMetArgAspGlnMetLeuLeuGluAspValLeuProVal	448
Qy	1418	ATTACAAAAGATTTCATTGAAATTCATCCGCGCTATCTCCAAACGACGCGAAACCCG	1477
Db	449	GlnGluAspAspSerLeuMetSerSerHisProIleValThrValThrProAsp	468
Qy	1478	CAAAATCAGGAATGTTTGAATGAACTTCTATACAAAGGAGCTTGTATTTGAATATG	1537
Db	469	GluIleThrSerValPheAspGlyIleSerTyrSerLysGlySerIleLeuLeuArgMet	488
Qy	1538	CTCAAGGATTTCTGCTGCTGAGGAGAAATCCACAAAGGAGTAATTCAGTACTTAAAGAAG	1597
Db	489	LeuGluAspTrpIleLysProGluAsnPheGlnLysGlyCysGlnMetTyrLeuGluLys	508
Qy	1598	TTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGCTCTGCAATAGTTGTTA	1657
Db	509	TyrGlnPheLysAsnAlaLysThrSerAspPheTipAlaAlaLeuGluAlaA----	526
Qy	1658	GAAAGTGATTTTACATCTGTGTGAGTTGTCTTCGGATCCCAAGATGACAAGTAACATG	1717
Db	526	-----	526
Qy	1718	CTCGCTTTTCGGGGGAAAATGCAGAGGTCAAAGAGATGATGACTACATGCTCTCCAG	1777
Db	527	-----SerArgLeuProValLysGluValMetAspThrTrpThrArgGln	541
Qy	1778	AAAGGAATCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1837
Db	542	MetGlyTyrProValLeuAsnVal-----AsnGlyValLys---AsnIleThrGlnLys	558
Qy	1838	CGTTCTCTCAGGGGTTTTCAGGAGACCTTGAATGAGGGCCCTGCGAGGAG-----	1891
Db	559	ArgPheLeuLeu-----AspProArgAlaAsnProSerGlnProProSer	573
Qy	1892	-----AGGTACCTGTGGCATATCCCATTCGACCTAC-----TCACGAGTCTTCT	1936
Db	574	AspLeuGlyTyrThrTrpAsnIleProValLysTrpThrGluAspAsnIleThrSerSer	593
Qy	1937	AATGTGATCCACAGACACATTTCTAAATCAAAGACAGATACTCTGGATCTACCTGAAAG	1996







655	SerSerGluAlaIleIleTrpValSerAsnLysSerGluHisHisArgIleThrTyrLeu	674
1991	GAAGAACAGCAGTGTGGGTGAAATTTAAATGTGGACATCAAAATGGTTACTACATCGTTCACTAT	2050
675	AspLysGlySerTrpIleLeuGlyAsnIleAsnGlnThrGlyTyrPheArgValAsnTyr	694
2051	GAGGGTCATGGATGGGACCAACTCATACACAGCTGAATCAGAACCAACACACACTTCTCAGA	2110
695	AspLeuArgAsnTrpArgLeuLeuIleAspGlnLeuIleArgAsnHisGluValLeuSer	714
2111	CCTAAGCAGCAGATAGTGTCTGATTCATGATCTGTTTCAGCTAGTGTGGTCAGGGAGACTG	2170
715	ValSerAsnArgAlaGlyLeuIleAspAlaPheSerLeuAlaArgAlaGlyTyrLeu	734
2171	ACCCTAGACAAAGCTCTTGACATCAGCTTACTACCTCCAACATGAAACAAGCAGC-----	2224
735	ProGlnAsnIleProLeuGluIleIleArgTyrLeuSerGluGluLysAspPheLeuPro	754
2225	---CCCAGCACTTCTCGAAGGCTCGAGTTACTTGAATCGTTTTTACCACATCATGATGCAGAGA	2281
755	TrpHisAlaAlaSerArgAlaLeuTyrProLeuAspLysLeuLeuAspArgMetGluAsn	774
2282	AGGAATATTTTCAGATATCTCTGAAAACTCAAGGTTTACCTTCTTTCAGTATTTTAAAGCCA	2341
775	TyrAsnIle-----PheAsnGluTyrIleLeuLysGlnValAlaThr	788
2342	GTGATTGACAGCAAAAGCTGGAGTGAC-----AAGGGCTCA	2377
789	ThrTyrSerLysLeuGlyTrpProLysAsnAsnPheAsnGlySerValValGlnAlaSer	808
2378	GTCGGCAGCAGATGCTCGCTCGGCTCTCTTGAAGCTGGCTGTGACCTGAACCACTGCT	2437
809	TyrGlnHisGluGluLeuArgGluValIleMetLeuAlaCysSerPheGlyAsnLys	828
2438	CCTTGCATCCGAAAGCTGCTGAACCTTCTCCAGCTGGATGGATCCAGTGGMAAATTA	2497
829	HisCysHisGlnGlnAlaSerThrLeuIleSerAspTrpIle---SerSerAsnArgAsn	847
2498	AATATACCAACAGATGTTTTAAACATTGTGTATTCTGTGGTGTCTCAGACAAACAGCAGGA	2557
848	ArgIleProLeuAsnValArgAspIleValTyrCysThrGlyValSerLeuLeuAspGlu	867
2558	-----TCGAATTACCTTTTAGACAAATGCAACTGTCAATGTCAAGTCTGCTGAACAAAC	2611
868	AspValTrpGluPheIleTrpMetLysPheHisSerThrThrAlaValSerGluLysLys	887
2612	AAAATTCGTATGCTTTGTCCACGACAGCATCAGGAAAAGTTACTGAAGTTAATTGAA	2671
888	IleLeuLeuGluAlaLeuThrCysSerAspAspAsnLeuLeuSerArgLeuLeuAsn	907
2672	CTAGGAATGGAAGGAGTTATCAACACACAGAACTTGGCAGCTCTCTTCATGCGATT	2731
908	LeuSerLeuAsnSerGluValValLeuAspGlnAspAlaIleAspValIleIleHisVal	927
2732	GCCAGACGTCCTCAAGGGGCAGCACTAGCATGGGATTTGTGAAGCAAAAATTTGGACCCAT	2791
928	AlaArgAsnProHisGlyArgAspLeuAlaTrpLysPhePheArgAspLysTrpLysIle	947
2792	CTTCTGAAAAAATTTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAACA	2851
948	LeuAsnThrArgTyrGlyGluAlaLeuPheMetAsnSerLysLysIleSerGlyValThr	967
2852	GCTCATTCTTCTCCAGGTAAGTTCGACAGGTGAACTATTATTTTTTGAATCTCTTGAG	2911
968	GluPheLeuAsnThrGluGlyGluLeuLysGlnLeuLysAsnPheMetLysSerTyrAsp	987
2912	GCTCAAGGATCACATCTGGATATTTTTTCAAACTCTTCTGGAACGATAACCAAAAATATA	2971
988	GlyValAlaSer-----AlaSerPheSerArgAlaValGluThrValGluAlaAsnVal	1005
2972	AAATGGCTGGGAAGAATCTTCCGACTCTCGAGCACTTGGCTA	3013
1006	ArgTrpLysArgLeuTyrGlnAspGluLeuPheGlnTrpLeu	1019

## RESULT 7

A32852

membrane alanyl aminopeptidase (EC 3.4.11.2) - rat

N:Alternate names: aminopeptidase N; microsomal aminopeptidase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text\_change 09-Jul-2004  
C:Accession: A32852; A32448; A61250  
R:Watt, V.M.; Yip, C.C.  
J. Biol. Chem. 264, 5480-5487, 1989  
A:Title: Amino acid sequence deduced from a rat kidney cDNA suggests it encodes the Zn<sup>2+</sup>-dependent membrane alanyl aminopeptidase  
A:Reference number: A32852; MUID:89174587; PMID:2564389  
A:Accession: A32852  
A:Molecule type: mRNA  
A:Residues: 1-965 <WAT>  
A:Cross-references: UNIPROT:P15684; GB:M25073; NID:G205108; PIDN:AAA41502.1; PID:G205109  
R:Malfroy, B.; Kado-Pong, H.; Gros, C.; Giros, B.; Schwartz, J.C.; Hellmies, R.  
Biochem. Biophys. Res. Commun. 161, 236-241, 1989  
A:Title: Molecular cloning and amino acid sequence of rat kidney aminopeptidase M: a member of the S1 family  
A:Reference number: A32448; MUID:89273642; PMID:2567164  
A:Accession: A32448  
A:Molecule type: mRNA  
A:Residues: 1-801, 'SC', 805-806, 'A', 808-812, 'ATVPER', 819-830, 'VGR', 834-965 <MAL>  
A:Cross-references: GB:M26710; NID:G601864; PIDN:AA57129.1; PID:G601865  
R:Funkhouser, J.D.; Tangada, S.D.; Jones, M.; O, S.J.; Peterson, R.D.A.  
Am. J. Physiol. 260, L274-L279, 1991  
A:Title: p146 type II alveolar epithelial cell antigen is identical to aminopeptidase N.  
A:Reference number: A61250; MUID:91206591; PMID:1673322  
A:Accession: A61250  
A:Molecule type: protein  
A:Residues: 2-19,68-84; 206-212, 'X', 214-215; 286-289, 291-299; 364-371 <FUN>  
C:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase; glycoprotein; membrane protein  
F:114,128,234,242,264,555,606,624,780/Binding site: carbohydrate (Asn) (covalent) #status

Alignment Scores:

Pred. No.:	3,28e-81	Length:	965
Score:	1312.00	Matches:	326
Percent Similarity:	49.10%	Conservative:	165
Best Local Similarity:	32.60%	Mismatches:	413
Query Match:	22.19%	Indels:	96
DB:	2	Gaps:	26

US-10-039-073-2 (1-3366) x A32852 (1-965)

Qy	203	AGAGGATTTAC-----	-----TGCTTACAGCCATCTTGCCCAATATGC	244
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Db	3	LysGlyPheTyrlleSerLysTherLeuGlylleLeuGlylleLeuGlyValAlaAla	22	
Qy	245	ATTTGTTCTCAGTGTCTCAGTGCCATCTAGTATTACTTCACTCAGGAGT-----	292	
				:::
Db	23	ValCysThrIlelleAlaLeuSerValValTyAlaGlnGluYsAsnArgAsnAlaGlu	42	
Qy	293	-----CTCGGGCTTTCCAGTAGCCACTAAT-----	319	
				:::
Db	43	AsnSerAlaIleAlaProThrLeuProGlySerThrSerAlaThrSerThrAsn	62	
Qy	320	-----GGGGAACGATTTCCTTGCCAGAGCTAAGCTCCCGAGTGTGGTTCCT	370	
				:::
Db	63	ProAlaIleAspGluSerLysProThrAsnGlnTyArgLeuProLysThrLeuIlePro	82	
Qy	371	CTCATTATGACCTTTTGTGCCACCCCAATCTCACTCTCTGGAC-----	415	
				:::
Db	83	AspSerTyrlGlnValThrLeuArgProTyrlLeuThrProAsnGluGlnGlyLeuTyrlle	102	
Qy	416	TTTCTTGTCATCGAGAGATCGAAGTCTTGTGCACAATGCTACCCAGTTTATCATCTTG	475	
				:::
Db	103	PhelysGlySerSerThrValArgPheThrCysAsnGluThrAsnValIleIleIle	122	
Qy	476	CACAGCAAGATCTTGAATCACCAGT-----GCCACCTCTCAGTCAGAG	520	
				:::
Db	123	HisSerLysLysLeuAsnTyThrAsnLysGlyAsnHisArgValAlaLeuArgAlaLeu	142	
				:::



Db 826 LysLeuArgSerAlaLeuAlaCysSerAsnGluValTrpIleLeuAsnArgTyrLeuSer 845  
Qy 2672 CTAGGAATGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATT 2731  
Db 846 TyrThrLeuAsnProAspTyrIleArgLysGlnAspAlaThrSerThrIleValSerIle 865  
Qy 2732 GCCAGAGCTCCAAAGGGCGCAACTAGCATGGGATTTTGTAAAGAAAATTTGACCCAT 2791  
Db 866 AlaAsnValValGlyGlnThrLeuValTrpAspPheValArgSerAsnTrpLysLys 885  
Qy 2792 CTTCTGAAAAAATTTGACTGGGTCTATATACATAGGATGATCATCTCTGGCACACA 2851  
Db 886 LeuPheGluAspTyrGlyGlySerPheSerPheAlaAsnLeuIleGlnGlyValThr 905  
Qy 2852 GCTCAGCTTTCTCCAGGATAAGTTGCAAGAGTGAAACTATTATTTTGAATCTCTTGAG 2911  
Db 906 ArgArgPheSerSerGluPheGluLeuGlnGlnLeuGlnPheLysGluAspAsnSer 925  
Qy 2912 GCTCAA-----GGATCAATCTCGATATTTTCAAACTGTTCTGGAACGATAAACAAA 2965  
Db 926 AlaThrGlyPheGlySerGlyThrArgAlaLeuGluGlnAlaLeuGluLysThrLysAla 945  
Qy 2966 AATATAAATCGCTGGAGAGAATCTCCGACTCTGAGGACTTGCTAATGGTTAACTACT 3025  
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RESULT 8  
A:33984  
N:Altered names: aminopeptidase (EC 3.4.11.2) - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 09-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 09-Jul-2004  
R:Accession: A53984; S24020; S05040; S13177  
R:Delmas, B.; Gelfi, J.; Kut, E.; Sjoestrom, H.; Noren, O.; Laude, H.  
J. Virol. 68, 5216-5224, 1994  
A:Title: Determinants essential for the transmissible gastroenteritis virus-receptor interaction  
A:Reference number: A53984; PMID:94309188; PMID:7913510  
A:Accession: A53984  
A:Molecule type: mRNA  
A:Residues: 1-963 <DEL>  
A:Cross-references: UNIPROT:P15145; GB:Z29522; NID:G525286; PIDN:CAA82641.1; PID:G525287  
R:Delmas, B.; Gelfi, J.; L'Hardon, R.; Vogel, L.K.; Sjoestrom, H.; Noren, O.; Laude, H.  
Nature 357, 417-420, 1992  
A:Title: Aminopeptidase N is a major receptor for the entero-pathogenic coronavirus TGEV  
A:Reference number: S24020; PMID:92278435; PMID:1350661  
A:Accession: S24020  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 2-31 <DE2>  
R:Olsson, J.; Sjoestrom, H.; Noren, O.  
FEBS Lett. 251, 275-281, 1989  
A:Title: Cloning of the pig aminopeptidase N gene. Identification of possible regulatory  
A:Reference number: S05040; PMID:89325681; PMID:2568950  
A:Accession: S05040  
A:Molecule type: DNA  
A:Residues: 1-294 <OLS>  
A:Cross-references: EMBL:X16088  
R:See, H.; Reithmeier, R.A.F.  
Biochem. J. 271, 147-155, 1990  
A:Title: Identification and characterization of the major stilbene- disulphonate- and co-  
A:Reference number: S13177; PMID:91024918; PMID:1977382  
A:Accession: S13177  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 2-40 <SES>  
C:Genetics:  
A:Introns: 200/2; 248/1  
A:Note: the list of introns may be incomplete  
C:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase; glycoprotein; transmembrane protein  
F:1-8/Domain: intracellular #status predicted <INT>  
F:9-32/Domain: transmembrane #status predicted <TM>  
F:33-963/Domain: extracellular #status predicted <EXT>

Alignment Scores:  
Pred. No.: 2,74e-78 Length: 963  
Score: 1269.00 Matches: 323  
Percent Similarity: 49.06% Conservative: 174  
Best Local Similarity: 31.89% Mismatches: 386  
Query Match: 21.46% Indels: 130  
DB: 2 Gaps: 28  
US-10-039-073-2 (1-3366) x A53984 (1-963)  
Qy 203 AGAGGATTTTAC-----TGC 217  
Db 3 LysGlyPheTyrIleSerLysAlaLeuGlyIleLeuGlyIleLeuGlyValAlaAla 22  
Qy 218 TTAACAGCCATCTTGGCCCCAAATATGCATTTGTCTTCAGTTCCTCAGTGCCATCTAGTTAT 277  
Db 23 ValAlaThrIleAlaLeuSerValValTyrAlaGlnGluLysAsnLysAlaGlu 42  
Qy 278 CACTTCAGTGGATCTGGGGCTTCCAGTAGCCACTAATGG-----322  
Db 43 HisValProGlnAlaProThrSerProThrIleThrThrAlaAlaIleThrLeuAsp 62  
Qy 323 GAACGATTTCTTGGCAGGAGCTAAGCTCCCGAGTGTGTCATCTCTCCATTATGAC 382  
Db 63 GlnSerLysProTrpAsnArgTyrArgLeuProThrThrLeuLeuProAspSerTyrPhe 82  
Qy 383 CTCTTTGTCCACCCCAATCTCACC---TCTCTGGAC-----TTTGTTCATCT 427  
Db 83 ValThrLeuArgProTyrLeuThrProAsnAlaAspGlyLeuTyrIlePheLysGlyLys 102  
Qy 428 GAGAAGATCGAAGCTCTTGGTCAGCAATGTCTACCAGTTCATCTTATCATCTTGCACAGCAAGAT 487  
Db 103 SerIleValArgLeuLeuCysGlnGluProThrAspValIleIleIleHisSerLysLys 122  
Qy 488 CTTGAAATCAGCAAT-----GCCACCCTTCAGTCAGAGGAAGATTCAAGATAC 535  
Db 123 LeuAsnTyrThrThrGlnGlyHisMetValValLeuArgGlyValGlyAspSerGlnVal 142  
Qy 536 ATCAAAACCAGGAAAA---GAACGTGAAGTTTTCAGTTTACCCTCTCATGAACAAATGCA 592  
Db 143 ProGluIleAspArgThrGluLeuValGluLeuThr-----GluTyrLeuVal 158  
Qy 593 CTGCTGGTTCAGAGAAACTTACGCTCACCTACCTGAAATACTATGTGCTATGGATTCCTCAA 652  
Db 159 ValHisLeuLysGlySerLeuGlnProGlyHisMetTyrGluMetGluSerGluPheGln 178  
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Db 179 GlyGluLeuAlaAspAspLeuAlaGlyPheTyrArgSerGluTyrMetGlu---GlyAsn 197  
Qy 713 GAAACAGGAATCTTCAGTAAACAGATTTCAGCCCAACAGGCGCATGGCTTCCCT 772  
Db 198 ValLysValValAlaThrThrGlnMetGlnSerThrAspAlaArgLysSerPhePro 217  
Qy 773 TGCTTTGATGAACCGTTGTTTCAAGCCAACTTTTCAATCAAGATACAGAGAGAGAGCAGG 832  
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Qy 833 CATATTGCATATCCAACTGCGCAAGGTTTAAAGCAATTGAACCTTGAAGAGGT-----886  
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Qy 887 ---CTTTTGAAGAT-----CACTTTGAAACTACTGTAAAAAATGAGT 925  
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Qy 986 GGGGTCAAGGTGTCCATCTATGCATCCCGACAGCAAAACGGAATCAACACAT-----TAT 1039  
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Db 292 GlyValLeuIleArgIleTrpAlaArgProAsnAlaIleAlaGluGlyHisGlyMetTyr 311  
Qy 1040 GCTTTGCGGCACTCACTGAAGCTACTTGATTTTATGAAAGTACTTTGCATATCTACTAT 1099  
Db 312 AlaLeuAenValThrGlyProIleLeuAenPheAlaAenHisTyrAsnThrSerTyr 331  
Qy 1100 CCACCTCCAACTCGATTAATTCCTATTCTGACTTTGCACCTGGAGCCATGGAATAAT 1159  
Db 332 ProLeuProLysSerAspGlnIleAlaLeuProAspPheAenAlaGlyAlaMetGluAen 351  
Qy 1160 TGGGCGCTCATTTACATATAGGAGAGCTGCTGCTTTTGGACCCCAAGACCTCTTCGCT 1219  
Db 352 TrpGlyLeuValTyrArgGluAenAlaLeuLeuPheAenProGlnSerSerSerIle 371  
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Qy 1400 ---AATGTGTGTTTGAAGTAAATACAAAAGATTCATTGAATTCATCCGCCCTATCTCC 1456  
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Qy 1457 AAACGAGCGGAA-----ACCGGACTCAATACAGGAATGTTTGTGTAAGTTTCC 1507  
Db 452 ThrProAlaGluGluValAsnThrProAlaGlnIleSerGluMetPheAspSerIleSer 471  
Qy 1508 TATACAGGAGGAGCTGTATTTTGAATGCTCAAGGATTTTCTGGGTGAGGAGAAATTC 1567  
Db 472 TyrSerLysGlyAlaSerValIleArgMetLeuSerAenPheLeuThrGluAspLeuPhe 491  
Qy 1568 CAGAAGAATAAATTCAGTACTTAAGAAGTTTCAGCTATAGAAATGCTAAGAATGATGAC 1627  
Db 492 LysGluGlyLeuAlaSerTyrLeuHisAlaPheAlaTyrGlnAenThrThrTyrLeuAsp 511  
Qy 1628 TTGTGGAGAGCTCTCAAAATAGTTGTTTGAAGAAGTATTTACATCTGGTGGAGTTGT 1687  
Db 512 LeuTrpGluHisLeuGlnLysAlaVal----- 520  
Qy 1688 CATTCCGGATCCCAAGATGACAGTAAACATGCTCGCTTCTCGGGGAAAATGCAGAGTTC 1747  
Db 521 -----AspAlaGlnThrSerIleArgLeuPro-----AspThrVal 532  
Qy 1748 AAAGAGATGATGACTACATGGAATCTCCAGAAAGGAATCCCGCTGCTGGTGTAAACAA 1807  
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Db 551 AspThrLysThrGlyAsnIleSerGlnLysHisPheLeu-----LeuAspSerGluSer 568  
Qy 1868 CTGTAATGGAGGCGCTCGCAGAGAGGTACTGTCGCATATCCCATTTGACCTACTCCAGC 1927  
Db 569 AenValThrArgSerSerAlaPheAspTyrLeuTrpIleValProIle-----SerSer 586  
Qy 1928 AGTCTCTTAATGTATCCACAGACAC----- 1954  
Db 587 IleLysAenGlyValMetGlnAspHisTyrTrpLeuArgAspValSerGlnAlaGlnAen 606  
Qy 1955 ----ATTCTAAATCAAGACAGATCTCTGGATCTACTCTGAAAGACAGTGGGTGAAA 2011  
Db 607 AspLeuPheLysThrAlaSerAsp-----AspTrpValLeu 618  
Qy 2012 TTTAATGTGACTCAATGGTTTACTACATCGTTTCACTATGAGGTCATGGATGGGACCAA 2071  
Db 619 LeuAenValAsnValThrGlyTyrPheGlnValAenTyrAspGluAspAsnTrpArgMet 638

## RESULT 9

A30325

membrane alanyl aminopeptidase (EC 3.4.11.2) precursor - human

N;Alternate names: aminopeptidase N; cell surface glycoprotein CD13

Qy 2072 CTCATTACACAGCTGAATACAGAACCCACACACTTCTCAGACCTTAAGGACAGAGTAGGTCTG 2131  
Db 639 IleGlnHisGlnLeuGlnThrAsnLeuSerValIleProValIleAenAsnAlaGlnVal 658  
Qy 2132 ATTCAATGATGTGTTTACGTAGTTGGTGCGAGGAGACTGACCCCTAGACAAAGCTCTTCAC 2191  
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Qy 2192 ATGACTTACTACCTCCCAACATGAACAGCAGCCCGCAGCTTCTCGAAGGTCTCGATTAC 2251  
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Qy 2252 TTGGAATCGTTTACCACATGATCGACAGAGGAATATTTCCAGATATCTCTGAAAACCTC 2311  
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Db 716 LysLysTyrLeuArgLysGlnValGluProLeuPheGlnHisPheGluThrLeuThrLys 735  
Qy 2357 AGCTGGAGTGCACAAG---GGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAG 2413  
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Qy 2414 CTGCGCTGTGACCTGGAACCATGCTCTTGCATCCAGAAAAGTGTGTAAGTCTTCTCCAG 2473  
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Qy 2531 -----TCTGGGCTGCTCAGACCAACAGCAGGATGGAATTAACCTTTTAGAGCAATAT 2581  
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Qy 2582 GAACGTGCAATGTCAAGTGTGAACAAACAAATCTGTATGCTTTGTCAACGAGCAAG 2641  
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C;Species: Homo sapiens (man)  
 C;Date: 02-Feb-1990 #sequence revision 02-Feb-1990 #text change 09-Jul-2004  
 C;Accession: A30325; S1658; I39442; S35688; S56098; S56099  
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 A;Title: Human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N  
 A;Reference number: A30325; MUID:89198086; PMID:2564851  
 A;Accession: A30325  
 A;Status: preliminary  
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 A;Cross-references: UNIPROT:P15144; UNIPROT:Q9UCE0; GB:M22324; NID:g178535; PIDN:AAAS171  
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 A;Title: Complete amino acid sequence of human intestinal aminopeptidase N as deduced fr  
 A;Reference number: S01658; MUID:89005706; PMID:2901990  
 A;Accession: S01658  
 A;Molecule type: mRNA  
 A;Residues: 1-85,'R',87-535,'E',537-602,'M',604-886,'P',888-967 <OLS>  
 A;Cross-references: EMBL:X13276  
 R;Shapiro, L.H.; Ashmun, R.A.; Roberts, W.M.; Look, A.T.  
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 A;Reference number: I39442; MUID:91268079; PMID:1675638  
 A;Accession: I39442  
 A;Molecule type: DNA  
 A;Residues: 1-15 <RES>  
 A;Cross-references: GB:M55522; NID:g178532; PIDN:AAAS3399.1; PID:g178533  
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 A;Title: Cholesterol crystallization-promoting activity of aminopeptidase-N isolated fro  
 A;Reference number: S35688; MUID:93359071; PMID:8102610  
 A;Accession: S35688  
 A;Molecule type: protein  
 A;Residues: 2-18 <NUN>  
 R;Watanabe, Y.; Iwaki-Egawa, S.; Mizukoshi, H.; Fujimoto, Y.  
 Biol. Chem. Hoppe-Seyler 376, 397-400, 1995  
 A;Title: Identification of an alanine aminopeptidase in human maternal serum as a membra  
 A;Reference number: S56098; MUID:96066273; PMID:7576235  
 A;Accession: S56098  
 A;Molecule type: protein  
 A;Residues: 2-20 <WAT>  
 A;Accession: S56099  
 A;Status: preliminary  
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 A;Cross-references: GDB:118728; OMIM:151530  
 A;Map position: 15q25-15q26  
 C;Superfamily: membrane alanyl aminopeptidase  
 C;Keywords: aminopeptidase; glycoprotein; transmembrane protein

Alignment Scores:  
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Qy	854	---CCAAAGGTTAAGACAATTTGAAGGAGGCTCTTTTGAAGAT-----	898
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Qy	1247	ATAGCCCATGAATCGCGCCAGTCAGTGGTTGGCAACTGGTCAATGGATGGTGAAT	1306
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R;Murray, J.; Wohlmann, P.  
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C;Superfamily: membrane alanyl aminopeptidase  
Alignment Scores:  
Pred. No.: 2,81e-70 Length: 884  
Score: 151.00 Matches: 300  
Percent Similarity: 49.73% Conservative: 157  
Best Local Similarity: 32.64% Mismatches: 362  
Query Match: 19.47% Indels: 100  
DB: 2 Gaps: 25  
US-10-039-073-2 (1-3366) x T29637 (1-884)



Db 676 AlaArgAlaGlyHisGlnProThrIleAspLysPheThrGlnMetPheAsnAspPheLeu 695  
Qy 2480 GAATCCAGTGGAAATATAATATACCAACAGATCTTTTAAAGATGTGTATCTTCGTGGT 2539  
Db 696 GluLysGlyThrProIleHis-----ProAspIleArgLeuAlaThrPheGlyValVal 713  
Qy 2540 GCTCAG-----ACAACAGCAGGATGGAATACCTTTTAGACCAATATGCACTGTAATG 2593  
Db 714 AlaArgTyrGlyGlyLysGluGlyPheAspLysLeuMetAsnLeuArgGluThrThr 733  
Qy 2594 TCAAGTCTGCAACAAACAAATCTGTATGCTTTGTTCAGGAGCAAGCATCAGGAAAG 2653  
Db 734 PheGlnGluIleGluArgGlnThrMetValAlaMetSerGlnThrProGluGluSerLeu 753  
Qy 2654 TTACTGAAGTTAATGTAAGTACAGGAAAGGTTATCAAGACACAGAACTTCGCA 2713  
Db 754 LeuAlaGlnLeuPheGluTyrGlyPheGluLysAsnLysValArgProGlnAspGlnLeu 773  
Qy 2714 GCTCTCTTCATCGGATGTCAGAGCGTCCAAAGGGCAGCAACTAGCATGGATTTTGT 2773  
Db 774 TyrLeuPheLeuGlyThrGlyAlaThrHisMetGlyGlnGlnTyrAlaTprLysTyrPhe 793  
Qy 2774 AGAGAAATGGACCATCTCTCGAAATAATTT---GACTGGGCTCATATGACATAAG 2830  
Db 794 CysGluHisIleLysGluPheLeuAspLysTyrGlyGlyAlaAsnSerSerLeuPheGln 813  
Qy 2831 ATGATCATCTCTGCGACACACAGCTCCTTTTCTCCAGGATAGTTGCAAGGTCGAA 2890  
Db 814 ArgCysLeuLysPheAlaGlyGluSerPheGlyAsnGluLysArgAlaValGluPheGln 833  
Qy 2891 CTATTTTTT-----GAATCTCTTCAGGCTCAAGGATCAGATCCTGGAT 2932  
Db 834 AspPhePheCysAsnCysAsnValLeuSerAspThrAspArgGlnThrLeuAlaArgPro 853  
Qy 2933 ATTTTTCAACTGCTCGGAAACGATACCAAAATATATAAATGGCTGGAGAGAT 2989  
Db 854 IleGlyGlnThrVal---GluAlaIleArgLeuAsnAlaArgLeuLeuGluSerAsn 871  
RESULT 13  
S37794  
aminopeptidase yscII (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein YKL157w; protein YKL61  
C;Species: Saccharomyces cerevisiae  
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: S37794; S37987; S44571; S19642  
R;Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the EMBL Data Library, September 1993  
A;Description: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci of yeast 10, 35-40, 1994  
A;Reference number: S37786  
A;Accession: S37794  
A;Molecule type: DNA  
A;Residues: 1-844 <VAN>  
A;Cross-references: UNIPROT:P32454; EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g4074  
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the Protein Sequence Database, March 1994  
A;Reference number: S37976  
A;Accession: S37987  
A;Molecule type: DNA  
A;Residues: 1-844 <VA2>  
A;Cross-references: EMBL:Z28157; NID:g486272; PIDN:CAA81999.1; PID:g486273; MIPS:YKL157w  
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
Yeast 10, 35-40, 1994  
A;Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci of yeast 10, 35-40, 1994  
A;Reference number: S44563  
A;Accession: S44571  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-844 <VA3>  
A;Cross-references: EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g407491  
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the EMBL Data Library, September 1993  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993

R;Garcia-Alvarez, N.; Cueva, R.; Suarez-Rendueles, P.  
Eur. J. Biochem. 202, 993-1002, 1991  
A;Title: Molecular cloning of soluble aminopeptidases from Saccharomyces cerevisiae. Seq  
A;Reference number: S19642; MUID:92111552; PMID:1765107  
A;Accession: S19642  
A;Molecule type: DNA  
A;Residues: 1-163, 'V', 165-441, 'E', 443-843, 'VNRDRDVVNKYLKNGYY', <GAR>  
A;Cross-references: EMBL:X63998; NID:g3367; PIDN:CAA45403.1; PID:g3368  
C;Genetics:  
A;Gene: SGD:APE2; LAP1  
A;Cross-references: SGD:S0001640; MIPS:YKL157w  
A;Map position: 11L  
C;Superfamily: membrane alanyl aminopeptidase  
C;Keywords: aminopeptidase; glycoprotein; metalloprotein; zinc  
P;250,622/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;305,309/Binding site: zinc (His) #status predicted  
F;306/Active site: Glu #status predicted

Alignment Scores:  
Pred. No.: 6,65e-68 Length: 844  
Score: 1116.00 Matches: 281  
Percent Similarity: 50.45% Conservative: 171  
Best Local Similarity: 31.36% Mismatches: 372  
Query Match: 18.88% Indels: 72  
DB: 2 Gaps: 24

US-10-039-073-2 (1-3366) x S37794 (1-844)

Qy 332 CCTTGGCAGAGTAAGCTCCACAGTGGTGCATTCCTCTCCATATGACCTCTTTGTC 391  
Db 6 ProAsnArgGluIle---LeuProAspAsnValValProLeuHisTyrAspLeuThrVal 24  
Qy 392 CACCCCAATCTCACCTCTCGGACTTTGTCATCTGAGAGATCGAAGTCTTGGTCAGC 451  
Db 25 GluProAspPheLysThrPheLysPheGluGlySerValLysIleGluLeuLysIleAsn 44  
Qy 452 AAT--GCTACCCAGTTTATCATCTTGCACAGCAAAAGATCTTGAAATCAGAAATGCCACC 508  
Db 45 AsnProAlaIleAspThrValThrLeuAsnThrValAspThrAspIleHisSerAlaLys 64  
Qy 509 CTTCACTCAGAGGAGATTCAGATACATGAAACAGGAAAGAACTGAAGTTTGTAGT 568  
Db 65 IleGlyAspValThrSerSer-----GluIleLeuSer 75  
Qy 569 TACCTGCTCATGAAACAAATTCACCTGCTGTTCCAGAGAAACTTACGCTCACCTGAAA 628  
Db 76 GluGluGluGlnValThrPheAlaPheProLysGlyThrMetSerSerPheLys 95  
Qy 629 TACTATGTGGCTATGGAC-----TTCCAAGCCAACTTAGGTGATGGCTTTGAAGGGTTT 682  
Db 96 GlyAsnAlaPheLeuAspIleLysPheThrGlyIleLeuAsnAspAsnMetAlaGlyPhe 115  
Qy 683 TATAAAGCACATACAGA---ACTCTGTGTGTAACAAAGAAATTCCTTCAGTAACAGAT 739  
Db 116 TyrArgAlaLysTyrGluAspLysLeuThrGlyGluThrLysTyrMetAlaThrThrGln 135  
Qy 740 TTTGAGCCCAACCCAGCAGCATGGCTTTCCCTGCTTTGTGATGAAACCGTTGTTCAAGCC 799  
Db 136 MetGluProThrAspAlaArgAlaPheProCysPheAspGluProAsnLeuLysAla 155  
Qy 800 AACTTTTCAATCAAGATACAGAGAGAGCAGCATATTGCATCTCCAACTCCCAAG 859  
Db 156 SerPheAlaIleThrLeuValSerAspProSerLeuThrHisLeuSerAsnMet---Asp 174  
Qy 860 GTTAAGCAATGAACTTGAGAGAGTCTTTTGGGAAGATCATTGGAACACTACTGTAA 919  
Db 175 ValLysAsnGluTyrValLysAspGlyLysValThrLeuPheAsnThrThrProLys 194  
Qy 920 ATGAGTACATCTCTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGCCTTCACT 979  
Db 195 MetSerThrTyrLeuValAlaPheAlaGluLeuLysTyrValGluSer---Lys 213  
Qy 980 TCATCAGGGGTCAAGGTGTCTCATCTATGCAATCCCAAGAAACGGAATCAACACATTAT 1039



A:Accession: S46750  
A:Molecule type: DNA  
A:Residues: 1-856 <DND>  
A:Cross-references: UNIPROT:P37898; EMBL:U00062; NID:g488162; PIDN:AAB68919.1; PID:g488162  
R:Caprioglio, D.R.; Padilla, C.; Werner-Washburne, M.  
J. Biol. Chem. 268, 14310-14315, 1993

A:Title: Isolation and characterization of AAP1. A gene encoding an alanine/arginine aminopeptidase  
A:Reference number: S48291; MUID:93300827; PMID:8100228

A:Accession: S48291  
A:Molecule type: DNA  
A:Residues: 107-549,570-645,'E',647-652 <CAP>  
A:Cross-references: EMBL:L12542

C:Genetics:  
A:Gene: SGD:AAP1  
A:Cross-references: SGD:S0001089; MIPS:YHR047c  
A:Map position: 88  
C:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase

Alignment Scores:  
Pred. No.: 1,42e-64 Length: 856  
Score: 1067.00 Matches: 282  
Percent Similarity: 48.46% Conservative: 159  
Best Local Similarity: 30.99% Mismatches: 381  
Query Match: 18.05% Indels: 88  
DB: 2 Gaps: 23

US-10-039-073-2 (1-3366) x S46750 (1-856)

QY 350 CTCCTCCAGTGGTGCATTCCTCTCCATATGACCTCTTTGTCACCCCAATCTCACCTCT 409  
Db 6 LeuProAenAenValThrProLeuHisTyrAspIleThrLeuGluProAenPheArgAla 25  
QY 410 CTGGACTTTGTCATCTGAGAACTCGAAGATCGAAGCTCTGTGTCAGC-----AATGCT 457  
Db 26 PheThrPheGluGlySerLeuLysIleAspLeuGlnIleAenAspHisSerIleAenSer 45  
QY 458 ACCCAGTTT-----ATCATCTTGCACAGCAAGATCTTGAATCACCAGATGCC 505  
Db 46 ValGlnIleAenTyrLeuGluIleAspPheHisSerAlaArgIleGluGlyValAsnAla 65  
QY 506 ACCCTTCAGTCAGAGGAATTCAGATACATGAAACCCAGGAAAGAACTGAAAGTTTG 565  
Db 66 IleGluValAenLysAenGln----- 74  
QY 566 AGTTACCTGCTCATGAACAATTCGACTGCTGCTGCTCA-----GAGAACTT 613  
Db 75 -----GlnLysAlaThrLeuValPheProAenGlyThrPheGluAenLeu 89  
QY 614 ACGCCTCACCTGAAATACTATGTGCTATGACTTCCAAAGCCAAAGTTAGGTGATGGCTT 673  
Db 90 GlyProSerAlaLysLeuGluIlele-----PheSerGlyIleLeuAenAspGlnMet 107  
QY 674 GAAGGGTTTATAAAGCACATACAGA---ACTCTTGGTGGTGAACAAGAAATTCCTTGCA 730  
Db 108 AlaGlyPheTyrArgAlaLysTyrThrAspLysValThrGlyGluThrLysTyrMetAla 127  
QY 731 GTAACAGATTTTGGCCACCCAGCAGCATGCTTCCCTGCTTTGATGACCGCTTG 790  
Db 128 ThrThrGlnMetGluAlaThrAspAlaArgArgAlaPheProCysPheAspGluProAen 147  
QY 791 TTCAAGCCCACTTTTCAATCAAGATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850  
Db 148 LeuLysAlaThrPheAlaValThrLeuValSerGluSerPheLeuThrHisLeuSerAen 167  
QY 851 ATGCCAAAGGTTAAGCAATTCGACTGAGAGAGGCTCTTTTGGAGAGATCACTTTGAAACT 910  
Db 168 Met---AepValA:gsAenGluThrIleLysGluGlyLysLysTyrThrThrPheAenThr 186  
QY 911 ACTGTAAAAATGAGTACATCTTGTAGCCCTACATAGTTGTGATTTCCACTCTCTGAGT 970  
Db 187 ThrProLysMetSerThrTyrLeuValAlaPheIleValAlaAspLeuA:gtTyrValGlu 206

QY 971 GGCTTCACCTTCATCAGGGGTCAAAGGTGCTCCATCTATGCTATCCCGACAGAAACCGAATCAA 1030  
Db 207 Ser---AsnAenPheArgIleProValArgValTyrSerThrProGlyAspGluLysPhe 225  
QY 1031 ACACATTATGCTTTGAGGATCCTGAGCTACTGTTATTTATGAAAAGTACTTTTGAT 1090  
Db 226 GlyGlnPheAlaAlaAenLeuAlaA:ArgThrLeuArgPhePheGluAspThrPheAen 245  
QY 1091 ATCTACTATCCACTCTCCAACTGGATTAATTTGCTATTCTCTGCTTTGACCTGGAGCC 1150  
Db 246 IleGluTyrProLeuProLysMetAepMetValAlaValHisGluPheSerAlaGlyAla 265  
QY 1151 ATGGAATAATGGGGCTTCATTATAGGAGACGCTCACTGCTTTTGACCCCAAGACC 1210  
Db 266 MetGluAenTrpGlyLeuValThrTyrArgValIleAspLeuLeuAspIleGluAen 285  
QY 1211 TCTTCTGCTTCCGATAAAGTGTGGTCCACAGAGTCATATCCAGAGCTGCAAA---TTTGAT 1270  
Db 286 SerSerLeuAspArgIleGlnArgValAlaGluValIleGlnHisGluLeuAlaHisGln 305  
QY 1271 TGGTTTGGCAACCTGCTCAATGGAATGGTGAATGATATTTGGCTTAAGGAGGGTTT 1330  
Db 306 TrpPheGlyAenLeuValThrMetAepTrpTrpGluGlyLeuTrpLeuAenGluGlyPhe 325  
QY 1331 GCAAAATACATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAAA---TTTGAT 1387  
Db 326 AlaThrTrpMetSerTrpTyrSerCysAenLysPheGlnProGluTrpLysValTrpGlu 345  
QY 1388 GACTATTTTGAATGTGTGTTTGAAGTAATTTACAAAGATTCATTGAATTCATCCCGC 1447  
Db 346 GlnTyrValThrAspAenLeuGlnArgAlaLeuAenLeuAspSerLeuArgSerHis 365  
QY 1448 CCTATCTCCAAACCCAGCGGAAACCCCGACTCAATACAGGAAATGTTTGATGAAGTTCC 1507  
Db 366 ProIleGluValProValAenAenAlaAspGluIleAenGlnIlePheAenAlaIleSer 385  
QY 1508 TATAACAAGGAGCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAAATTC 1567  
Db 386 TyrSerLysGlySerSerLeuLeuArgMetIleSerLysTrpLeuGlyGluThrPhe 405  
QY 1568 CAGAAAGGAATATTCAGTACTTTAAAGAGTTTCAGCTATAGAAATGCTAAGAATGATGAC 1627  
Db 406 IleLysGlyValSerGlnTyrLeuAenLysPheLysTyrGlyAenAlaLysThrGlyAsp 425  
QY 1628 TTCTGAGAGCTGCTCAATAGTTTGTAGAAAGTATTTACATCTGCTGTCGAGTTGT 1687  
Db 426 LeuTrpAspAlaLeu-----AlaAspAlaSerGlyLysAspValCys 439  
QY 1688 CATTCGGATCCCAAGATGACAAAGTAACATGCTCCCTCTTCTGGGGGAAAAATGCAGAGTC 1747  
Db 439 ----- 439  
QY 1748 AAAGAGATGATGACTACATGGACTCTCCAGAAAGGAATCCCTGCTGCTGTTTAAACAA 1807  
Db 440 ---SerValMetAenIleTrpThrLysArgValGlyPheProValLeuSerValLysGlu 458  
QY 1808 GACGGGTGTTCTCTCCAGCTGCAACAGGAGCGCTCTCTCCAG---GGGGTTTTCCAGAA 1864  
Db 459 HisLysAenLysIleThrLeuThrGlnHisArgTyrLeuSerThrGlyAspValLysGlu 478  
QY 1865 GACCTCGAATGGAGGGCCCTGCGAGGAGAGGTACCTGTGGCATATCCATTGACTACTCC 1924  
Db 479 GluGluAspThrThrIle-----TyrProIleLeuLeuAlaLeuLysAepSer 494  
QY 1925 ACAGATTCTTCTAATGTGATCCACAGACATCTTAAATCAAGACAGATACTCTGGAT 1984  
Db 495 ThrGlyIleAspAenThrLeu-----ValLeuAenGluLysSerAlaThrPheGlu 511  
QY 1985 CTACCTGAAAAGACAGTGTGGGTGAAATTTAATGTGCACTCAAAATGGTTACTACATCGTT 2044  
Db 512 Leu---LysAenGluGluPhePheLysIleAenGlyAspGlnSerGlyIlePheIleThr 530  
QY 2045 CACTATGAGGGTCATGGATGGGACCAACTCATTTACAGCTGAATCAGAAACCAACACTT 2104

Db	531	SerTyrSerAspGluArgTrpAlaLeuLeuSerLysGlnAlaAsn-----Leu	546
Qy	2105	CTCAGACTAAGGACAGAGTAGGTCTGATTCATCATGTCTTTCAGCTAGTTGGTCAGGG	2164
Db	547	LeuSerValGluAspArgValGlyLeuValAlaAspAlaLeuSerAlaSerGly	566
Qy	2165	AGACTGACCCTAGACAAAGCTCTTGACATGACTTACTACCTCCAAACATGAAACAGCAGC	2224
Db	567	TyrThrSerThrThrAsnPheLeuAsnLeuLeuSerAsnTrpLysAsnGluAspSerPhe	586
Qy	2225	-----CCGCACTCTCGAAGGCTCGAGTTCTTGGAAATCGTTTACCACATGATG	2275
Db	587	ValValTrpGluGlnIleIleAsnSerLeuSerAlaLeuLysSerThrTrpValPhe---	605
Qy	2276	GACAGAGGAATATTCTGATATCTCTGAAACCTCAAGGCTTACCTTCTTACGTATTTT	2335
Db	606	-----GluProGluAspIleLeuAsnAlaLeuAspLysPheThrLeuAspLeuVal	622
Qy	2336	AAGCCAGTGATTGACGCCAAGCTGGAGT-----GACAAGGCTCAGCTGGACAGG	2389
Db	623	LeuAsnLysLeuSerGluLeuGlyTrpAsnIleGlyGluAspAspSerPheAlaIleGln	642
Qy	2390	ATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGACCTCGAACCATGCTCTTGCATCCAG	2449
Db	643	ArgLeuLysValThrLeuPheSerAlaAlaCysThrSerGlyAsnGluLysMetGlnSer	662
Qy	2450	AAAGCTGCTGAACCTCTTCTCCAGTGGATCCAGTCCAGTGGAAATTTAAATATACCACA	2509
Db	663	IleAlaValGluMetPheGluGluIuTr--AlaAsnGlyAsnLysGlnAlaIleProAla	681
Qy	2510	GATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACACAGCAGCATGGAATTAC---	2566
Db	682	LeuPheLysAlaValValPheAsnThrValAlaArgLeuGlyGlyGluAsnAsnTyrGlu	701
Qy	2567	---CTTTTAGCAATATGAACTGCTCAATGTCAAAGTCTGCTGAACAAACAAATTCGTAT	2623
Db	702	LysIlePheAsnIleTyrGlnAsnProValSerSerGluGluLysIleIleAlaLeuArg	721
Qy	2624	GCTTTGTCAAGCAGCATCATCAGAAAAGTTACTGAAAGTTAAATTGAATAGGAATGAA	2683
Db	722	AlaLeuGlyArgPheGluAspLysGluLeuLeuGluArgThrLeuSerTyrLeuLeuAsp	741
Qy	2684	GGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTCTCATGCGAATGCCAGACGTCCA	2743
Db	742	GlyThrValLeu---AsnGlnAspPheTyrIleProMetGlnGlyIleArgValHisLys	760
Qy	2744	AAGGGCAGCAACTAGCATGGATTTTGTAAAGAAAAATTTGGACCCATCTTCTGAAAAAA	2803
Db	761	LysGlyIleGluArgLeuTrpAlaTrpMetGlnGluHisTrpAspGluIleAlaLysArg	780
Qy	2804	TTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCAACACAGCTCACTTTCT	2863
Db	781	LeuGlnProGlySerProValLeuGlyValLeuThrLeuGlyLeuThrAsnPheThr	800
Qy	2864	TCCAGGATATGTTGCAAGAGGTGAACACTATTTTTGAAATCTCTTGAGGCTCAGGATCA	2923
Db	801	SerPheGluAlaLeuGluLysIleSerAlaPheTyrSerArgLysValThrLysGlyPhe	820
Qy	2924	CATCTGGATATTTTCAAACGTCTTCTGAAACGATAACCAAAAAATAAAATGGCTGGAG	2983
Db	821	AspGlnThrLeuAlaGln---AlaLeuAspThrIleArgSerLysAlaGlnTrpValSer	839
Qy	2984	AAGAACTCTCCGACTCTGAGGACTTGGCTA	3013
Db	840	ArgAspArgGluIleValAlaThrTyrLeu	849

**RESULT 15**

T39789

155763  
aminopeptidase - fission yeast (*Schizosaccharomyces pombe*)

C:Species: schizosaccharomyces pombe

C,species: SCHIZOSACCHAROMYCES pombe  
C,Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 09-Jul-2004

C: Date: V3-DEC-1999  
C: Accession: T39789

R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21816  
A:Accession: T39789  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-882 <SE>  
A:Cross-references: UNIPROT:Q9USX1; EMBL:AL120233; SPDB:GN00067; SPDB:PIDN:CAB58971.1; GSPDB:GN00067; SPDB:PIDN:CAB58971.1; cosmid c.1921  
C:Genetics:  
A:Gene: SPDB:SPBC1921.05  
A:Map position: 2  
C:Superfamily: membrane alanyl aminopeptidase

**Alignment Scores:**

Pred. No.:	3,036-63	Length:	882
Score:	1047.50	Matches:	277
Percent Similarity:	47.67%	Conservative:	162
Best Local Similarity:	30.08%	Mismatches:	391
Query Match:	17.72%	Indels:	91
DB:	2	Gaps:	24

US-10-039-073-2 (1-3366) x T39789 (1-882)

[illegible]



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 26, 2005, 06:07:35 ; Search time 527.604 Seconds  
(without alignments)  
6533.911 Million cell updates/sec

Title: US-10-039-073-2  
Perfect score: 5912  
Sequence: 1 cccgcgtccgcgatgtt.....aaaaaaaaaaaaaaaaaaaa 3366

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO spoal\_p/US10039073/runat\_26092005\_070409\_21306/app.query.fasta\_1.6606  
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPT=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODES=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10039073 @CGN 1 1 1214 @runat\_26092005\_070409\_21306 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_03.\*  
1: uniprot\_eprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	85.5	960	Q9HBX2	Q9hb22 homo sapien
2	5047	85.4	960	Q725K1	Q725k1 homo sapien
3	4789.5	81.0	915	Q6179	Q6179 homo sapien
4	2768	46.8	532	Q8TD32	Q8td32 homo sapien
5	2516.5	42.6	929	ART1_HUMAN	Q9nz08 h adipocyte
6	2512.5	42.5	941	Q6UWY6	Q6uw66 homo sapien
7	2480	41.9	930	ART1_MOUSE	Q9eqh2 mus musculus
8	2430	41.1	930	ART1_RAT	Q9ij22 rattus norv
9	2034.5	34.4	1003	Q6PE23	Q6pe23 brachydanio
10	2027	34.3	1025	LCAP_RAT	P97629 r leucyl-cy
11	2022	34.2	1025	Q8C129	Q8c129 mus musculus
12	1999	33.8	1025	LCAP_HUMAN	Q9uiq6 homo sapien
13	1883	31.9	694	Q8C9W5	Q8c9w5 mus musculus
14	1853.5	31.4	997	Q6PCG5	Q6pcg5 xenopus lae
15	1690	28.6	350	Q8WVJ4	Q8wvj4 homo sapien
16	1564	26.5	549	Q8C4S7	Q8c4s7 mus musculus

17	1455.5	24.6	942	1	AMPE_PIG	Q95334 sus scrofa
18	1444	24.4	957	1	AMPE_HUMAN	Q07075 homo sapien
19	1391.5	23.5	1012	2	Q9VFW7	Q9vfw7 drosophila
20	1391	23.5	945	1	AMPE_RAT	P50123 rattus norv
21	1390.5	23.5	945	1	AMPE_MOUSE	P16406 mus musculus
22	1389.5	23.5	1036	2	Q86P55	Q86p55 drosophila
23	1373.5	23.2	994	2	Q86N05	Q86n05 drosophila
24	1371.5	23.2	991	2	Q7PQR3	Q7pqr3 anopheles g
25	1367	23.1	903	2	Q8INH5	Q8inh5 drosophila
26	1367	23.1	1025	2	Q8INH6	Q8inh6 drosophila
27	1361.5	23.0	988	2	Q9VFX0	Q9vfx0 drosophila
28	1347	22.8	885	2	Q8IHC5	Q8ihc5 drosophila
29	1344	22.7	942	2	Q9VFW9	Q9vfw9 drosophila
30	1343	22.7	885	2	Q9VFW8	Q9vfw8 drosophila
31	1329.5	22.5	691	2	Q8BZ14	Q8bz14 mus musculus
32	1329.5	22.5	862	2	Q8IGR1	Q8igr1 drosophila
33	1327	22.4	1025	1	THDE_RAT	Q10836 rattus norv
34	1322	22.4	1024	2	Q6UWJ4	Q6uwj4 homo sapien
35	1320	22.3	1024	1	THDE_HUMAN	Q9ukue homo sapien
36	1312	22.2	964	1	AMPN_RAT	P15684 rattus norv
37	1310	22.2	1025	1	THDE_MOUSE	Q8K093 mus musculus
38	1298	22.0	966	1	AMPN_FELCA	P79171 felis silve
39	1290.5	21.8	1007	2	Q9U0D1	Q9u0d1 aphysia cal
40	1280.5	21.7	866	2	Q9W0E4	Q9w0e4 drosophila
41	1280.5	21.7	1053	2	Q8IRH0	Q8irh0 drosophila
42	1280.5	21.7	1075	2	Q8IRH1	Q8irh1 drosophila
43	1275	21.6	997	2	Q7QAH5	Q7qah5 anopheles g
44	1274	21.5	965	1	AMPN_RABIT	P15541 oryctolagus
45	1272.5	21.5	866	2	Q9GPG3	Q9gpg3 drosophila

## ALIGNMENTS

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DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE AMINOPEPTIDASE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schomburg L.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191545; AAG28383.1; -;  
DR MEROPS; M01.024; -;  
DR GO; GO:0004177; F:aminopeptidase activity; IEA.  
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001930; Peptidease\_M1.  
DR InterPro; IPR006025; Peptidease\_M1.  
DR Pfam; PF01433; Peptidease\_M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
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SQ SEQUENCE 960 AA; 110461 MW; 261EFC06870D644E CRC64;

Alignment Scores:  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.45% Indels: 0  
DB: 2 Gaps: 0

US-10-039-073-2 (1-3366) x Q9HBX2 (1-960)

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QY 266 CCATCTAGTATTACTTCCACTGAGGATCCTGGGCTTTCCAGTAGCCACTAAATGGGGAA 325  
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaIleAsnGlyGlu 60  
QY 326 CGATTTCCTGGCAGGAGCTAAGGCTCCCAAGTGTGTCATCTCTCCATTATGACCTC 385  
Db 61 ArgPheProTTPGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
QY 386 TTTGTCCACCCCAATCTCACCCTCTCTGAGCTTTGTCATCTGAGAAGTCGAAGTCTTG 445  
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QY 1886 CAGGAGAGTACCTGTGGCATATCCCAATTCACCTACTCCACGAGTGTCTTCTAATGTGATC 1945  
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QY 2486 AGTGAAAAATTAATATATACCAACAGATGTTTTAAAGATTGTGTATCTCTGTGGTGCTCAG 2545
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Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTrpSerValGlyAlaGln 800
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RESULT 2
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ID Q725K1 PRELIMINARY; PRT; 960 AA.
AC Q725K1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase long form variant.
CN Name=1-rap;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12799365; DOI=10.1074/jbc.M305076200;
RA Tanlaka T., Hattori A., Maeda S., Nomura Y., Nakayama H.,
RA Mizutani S., Tsujimoto M.;
RT "Human leukocyte-derived arginine aminopeptidase: The third member of
RT the oxytocinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 278:32275-32283(2003).
DR EMBL; AB109031; BAC78818.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
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DR Pfam; PF01433; Peptidase_M1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 960 AA; 110447 MW; 27898FE2107E814E CRC64;
Alignment Scores:
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Score: 5047.00 Matches: 959
Percent Similarity: 99.90% Conservative: 0
Best Local Similarity: 99.90% Mismatches: 1
Query Match: 85.37% Indels: 0
DB: 2 Gaps: 0
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US-10-039-073-2 (1-3366) x Q725K1 (1-960)

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Db 21 GlyPheTrpCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
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QY 266 CCATCTAGTTATCACTTCACTGAGGATCTCTGGGCTTTCCAGTAGCCACTAAATGGGAA 325
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QY 326 CGATTTCTCTGGCAGGAGCTAAAGCTCTCCAGTGTGGTCTCTCTCCATTATGACCTC 385
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QY 446 GTACAGCAATCTCCAGTATTATCATCTTCACAGCAAGAGTCTTGAATCACCAGATGCC 505
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QY 506 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAAACAGGAAAGAACTGAAAGTTTG 565
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Db 281 GlyValIysValSerIleTyrAlaSerProAspLysArgAenGlnThrHisTyrAlaLeu 300  
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QY 1886 CAGAGAGGTACCTGTGGCATATCCCATTTGACTTCCAGAGTTCTTCTTAATGTGATC 1945  
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QY 1946 CACAGACACATTTCAAAATCAAGACAGATACTCTGGATCTACCTGAAAGACAGTTGG 2005  
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
QY 2006 GTGAAATTTAATGTGGACTCAAATGGTTACTACATCGTTTCACTATGAGGGTCAATGGATGG 2065  
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
QY 2066 GACCAACTCATACAGCTGAATCAGAACACACATCTTCTCAGACCTTAAGGACAGATA 2125  
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660

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QY 2186 CTTGACATGACTTACTACCTCCAAACATGAAACAAGCAGCCCCGACTTCTCGAAGGTCTG 2245  
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QY 2246 AGTTACTTGGAAATCGTTTACCATCATGATGGACAGAAGGAATATTTTCAGATATCTCGAA 2305  
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720  
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QY 2366 GACAAGGCTCAGTCTGGGACAGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2425  
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
QY 2426 CTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCC 2485  
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QY 2546 ACNACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTCTGAA 2605  
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QY 2606 CAAAAAATAATCTGTATGCTTTGTCAACGAGCAAGCATCAGAAAAGTTACTGAAAGTTA 2665  
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QY 2666 ATTGAATCTAGGAATGGAAGGAAGTTTCAAGACACAGAACTTGGCAGCTCTCTTCAT 2725  
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860  
QY 2726 GCATTGCCAGCGTCCAAAGGGCAGCAACTAGCATGGGATTTTCTAAGAGAAAAATTGG 2785  
Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
QY 2786 ACCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGCG 2845  
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900  
QY 2846 ACAACAGCTCACCTTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2905  
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QY 2906 CTTGAGGCTCAAGGATCACATCTGGATATTTTTCAAACTGTTCTGAAACGATAACAAA 2965  
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QY 2966 AATATAAATGCTGGAGAGATCTTCCGACTCTGAGACTTGGGCTTAATGTTAATCT 3025  
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ID Q6P179  
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE LRAP protein.  
GN Name-LRAP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,  
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC065240; AH65240.1; -;  
DR GO; GO:0004179; F:membrane ananyl aminopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
SQ SEQUENCE 915 AA; 105525 MW; 10075BE1C076377F CRC64;  
  
Alignment Scores:  
Pred. No.: 2,166-312 Length: 915  
Score: 4789.50 Matches: 915  
Percent Similarity: 95.31% Conservative: 0  
Best Local Similarity: 95.31% Mismatches: 0  
Query Match: 81.01% Indels: 45  
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Db 21 GlyPheTyrcysLeuThrAlaIleleuProGlnIleCysIleCysSerGlnPheSerVal 40  
  
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QY 386 TTGTGTCACCCCAATCTCACCTCTCTGGACTTTGTTGGCATCTGAGAAGATCGAAGTCTTG 445  
Db 81 PheValHisProAsnLeuThrSerLeuAsePheValAlaSerGluIleGluValleu 100  
  
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Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAseProGluIleThrAsnAla 120  
  
QY 506 ACCCTTCAGTCAGAGGAGATTCAAGATACATGAAACCCAGGAAGAACTGAAAGTTTGTG 565  
Db

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Db 141 SerTyrcysProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
QY 626 AAATCTATGTTGGCTATGGACTTCCNAGCCCAAGTAGGTAGTGGCTTTGNAAGGGTTTAT 685  
Db 161 LysTyrcysValAlaMetAsePheGlnAlaLysLeuGlyAseGlyPheGluGlyPheTyrc 180  
QY 686 AAAAGCACATACAGAACTCTTGGTGGTGAAACAAGAATCTTGCAGTAACAGATTTTGA 745  
Db 181 LysSerThrTyrcysThrLeuGlyGlyGluThrArgIleLeuAlaValThrAsePheGlu 200  
QY 746 CCAACCCAGGACGATGGCTTTCCCTTGGCTTTGATGAACCGTGTTCACAGCCCACTTT 805  
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAsePheGluProLeuPheLysAlaAsn 220  
QY 806 TCATCAAGATACCAAGAGAGAGAGGAGCATATTCACATATCCACATATCCCAAGGTTAAG 865  
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetPro----- 237  
QY 866 ACAATTGAACCTTGAAGGAGGTCTTTTGGAGAGTCACTTTGAAACTCACTGTAAAAATGAGT 925  
Db 237 ----- 237  
QY 926 ACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA 985  
Db 237 ----- 237  
QY 986 GGGGTCAAGGTGTCATCTATGCATCCCGACAGCAACCGAATCAACACATATTCCTTTG 1045  
Db 238 -----LysValSerIleTyrcysAlaSerProAsePheArgAseGlnThrHisTyrcAlaLeu 255  
QY 1046 CAGGCATCAGTGAAGTACTTGAATTTTATGAAAGTACTTTGTATATCTACTATCCACTC 1105  
Db 256 GlnAlaSerLeuLysLeuLysAsePheTyrcysLysTyrcPheAsePheIleTyrcProLeu 275  
QY 1106 TCCAACTGGATTTAAATGCTATTCTGACTTTTCACCTGGAGGCATCGAAAATTTGGGCG 1165  
Db 276 SerLysLeuAsePheLeuAlaIleProAsePheAlaProGlyAlaMetGluAseTrpGly 295  
QY 1166 CTCAATCATATAGGAGAGCTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGAT 1225  
Db 296 LeuIleThrTyrcysGluThrSerLeuLeuAsePheProLysTyrcSerSerAlaSerAse 315  
QY 1226 AAATGTTGGGTCAACAGAGTCATAGCCCATCAACTGGGCGCACCATGTTTGGCAACCTG 1285  
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QY 1286 GTCAAAATGGAATGGTGAATGATATTGCTTAAAGGAGGCTTTTGCAAAATACATCGAA 1345  
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QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGATGATATTTTGTGATG 1405  
Db 356 LeuIleAlaValAseAlaThrTyrcProGluLeuGlnPheAsePheTyrcPheLeuAseVal 375  
QY 1406 TGTTTTGAAGTAAATTCACAAAGATTCATTGAAATTCATCCCGCCCTATCTCCAAACACGCG 1465  
Db 376 CysPheGluValIleThrLysAsePheLeuAseSerSerArgProIleSerLysProAla 395  
QY 1466 GAAACCCCGACTCAATACAGGAAATGTTGATGAAGTTTCTTATTAACAAGGAGCTTGT 1525  
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QY 1526 ATTTTGAATATGCTCAGGATTTTCTGGGTGAGAGAAATTCAGAAAGGATTAATTCAG 1585  
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QY 1586 TACTTAAAGAGTTCACTATAGAAATGCTAAGAAATGATGATGTTGTGGAGCAGTCTGTCA 1645  
Db 436 TyrLeuLysLysPheSerTyrcArgAseAlaLysAseAsePheLeuTrpSerSerLeuSer 455

Qy	1646	AATAGTTGTTTGTAGAAAGTGATTTTACATCTCGTGGAGTTTGTCTATTCGGATCCCAAGATG	1705
Db	456	AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet	475
Qy	1706	ACAAAGTAACTGCTCGCTTTCTGGGGAAATAACGAGAGTCAAGAGATGATGACTACA	1765
Db	476	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	495
Qy	1766	TGGACTCTCCAGAAAGNAATCCCTCTGCTGGTGTAAACAAGACGGGTCTCACTCCGA	1825
Db	496	TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg	515
Qy	1826	CTGCAACAGGAGCCCTTCTCCAGGGGTTTCCAGGAAGACCTGAAATGAGGGCCCTG	1885
Db	516	LeuGlnGlnLysArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	535
Qy	1886	CAGGAGAGTACCTGTGGCATATCCCATTTGACCTACTCCACGAGTTCTTCAATGTGATC	1945
Db	536	GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle	555
Qy	1946	CACAGACACATCTCAAAATCAACACAGATACTCTGGATCTACCTGAAAGACCAAGTGG	2005
Db	556	HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp	575
Qy	2006	GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAATGGATGG	2065
Db	576	VallysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp	595
Qy	2066	GACCAACTCATATCACAGCTGAATCAGAACACACATCTTCCAGACTTAAGGACAGATA	2125
Db	596	AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal	615
Qy	2126	GGTCTGATTCATGATGTGTTTCAGCTAGTGGTCAGGGAGACTGACCTAGACAAAGCT	2185
Db	616	GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla	635
Qy	2186	CTTGACATGACTTACTACTCTCAACATCAACAGCAGCCCGCACTTCTCGAAGGTCTG	2245
Db	636	LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu	655
Qy	2246	AGTTACTGGAAATCGTTTTACCACATGATGACAGAGGAATATTTTCAATATCTCTGAA	2305
Db	656	SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspLysGlu	675
Qy	2306	AACCTCAAGCGTTACCTTCTCAGTATTTTAAGCCAGTGTATGACAGGCAAGCTGGAGT	2365
Db	676	AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer	695
Qy	2366	GACAAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCTGTGAC	2425
Db	696	AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp	715
Qy	2426	CTGAACCATGCTCTTGATCCAGAAAGCTGCTGAATCTTCTCTCCAGTGGATGCCATCC	2485
Db	716	LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer	735
Qy	2486	AGTGGAAATTAATATATACCAACAGATGTTTAAAGATTGTGATTTCTGTGGGTGCTCAG	2545
Db	736	SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln	755
Qy	2546	ACAAACAGCAGGATGGAATTTACTTTTGTAGCAATATGAACTGTCAATGTCAAGTGTGAA	2605
Db	756	ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu	775
Qy	2606	CAAAACAAAATCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAGATTACTGAATTGA	2665
Db	776	GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu	795
Qy	2666	ATTCAACTAGGAATGGAGGAAGGTTATCAAGACACAGACTTGGCAGCTCTCTTCAT	2725
Db	796	IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis	815

Qy	2726	GCATGTCACAGAGCTCCAAAGGGGCGACAACTAGCATGGGATTTTGTAAAGAGAAAATTGG	2785
Db	816	AlaIleAlaArgArgProLysGlyGlnLeuAlaTrpAspPheValArgGluAsnTrp	835
Qy	2786	ACCATCTTCTGAAAAAATTTGACTGGGGCTCATATGACATAAGGATGATCACTCTGGC	2845
Db	836	ThrHisLeuLeuLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly	855
Qy	2846	ACACAGCTCACCTTCTTCCRAAGGATAAGTTCACAGAGTGAAACTATTTTGAATCT	2905
Db	856	ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer	875
Qy	2906	CTTGAGGCTCAAGGATCACATCTCGATATTTTCAAACTGTTCTGGAACGATAACCAAA	2965
Db	876	LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys	895
Qy	2966	AATATAAATGGCTGGAGAGAAGATCTTCCGACTCTGAGGACTTGGCTAATGGTTAATCT	3025
Db	896	AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr	915
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AC	Q8TD32;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Leukocyte-derived arginine aminopeptidase short form.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=213741137; PubMed=11481040;		
RA	Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;		
RT	"Genomic organization of the human adipocyte-derived leucine		
RT	aminopeptidase gene and its relationship to the placental leucine		
RT	aminopeptidase/oxycotinase gene.";		
RL	J. Biochem. 130:235-241(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Tanioka T., Hattori A., Masuda S., Nomura Y., Nakayama H.,		
RA	Mizutani S., Tsujimoto M.;		
RT	"Human leukocyte-derived arginine aminopeptidase: The third member of		
RT	the oxycotinase subfamily of aminopeptidases.";		
RL	J. Biol. Chem. 0:0-0(2003).		
DR	EMBL; AY028805; AAK37776.1; -.		
DR	MEROPS; M01.024; -.		
DR	GO; GO:0004177; F:aminopeptidase activity; IEA.		
DR	GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001930; Peptidase.M1.		
DR	InterPro; IPR006025; Pept.M.zn.BS.		
DR	Pfam; PF01433; Peptidase.M1; 1.		
DR	PRINTS; PR00756; ALADIP7ASE.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	Aminopeptidase.		
SQ	SEQUENCE 532 AA; 60937 MW; DA0F4F00AD9E0D71 CRC64;		
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QY 266 CCATCTAGTTATCACTTCACTGAGGATCTCTGGGGCTTCCAGTAGCCACTAATGGGAA 325  
DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
QY 326 CCATTTCTTGCAGGAGTAAGGCTCCCGAGTGGTCAATTCCTCTCCATTCACCTC 385  
DB 61 ArgPheProTrpGlnGluLeuArgLeuProSerValIleProLeuHisTyrAspLeu 80  
QY 386 TTTGTCCACCCCAATCTCACTCTCTGGAATTTGTCATCTGAGAAGATCGAAGCTTG 445  
DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
QY 446 GTCAGCAATGTCACCCAGTTTATCATCTTGCACACCAAGATCTTGAATACAGATGCC 505  
DB 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
QY 506 ACCCTTCAGTCAGAGAAATCAAGATACATGAACACAGGAAAGAACTGAAAGTTTG 565  
DB 121 ThrLeuGlnSerGluLysSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
QY 566 AGTTACCTGCTCATGAACAAATTCACCTGCTGTTCCAGAGAACTTACGCTCACCTG 625  
DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
QY 626 AATATCTATGCTGCTATGCACTTCCAGCCAGTTAGGTGATGGCTTTGAAGGTTTTAT 685  
DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
QY 686 AAAAGCACATACAGAACTCTTGCTGGTGAACAGAAATCTTGCAGTAACAGATTTGAG 745  
DB 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200  
QY 746 CAACCCAGCGCATGCTTCCCTTCTGTTGATGAACCGTGTGTTCAAGCCCACTTT 805  
DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
QY 806 TCAATCAAGATACGAAGAGAGAGCAGGATATTCACACTATCCAACTCCCAAGGTTAAG 865  
DB 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
QY 866 ACAATTGAACTTGAAGGAGGCTTTTGAAGATCACTTTGAACACTGTAATAATAGT 925  
DB 241 ThrIleGluLeuGluGlyLysLeuLeuGluAspHisPheGluThrThrValLysMetSer 260  
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DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
QY 986 GGGGTCAAGGTGTCATCTATGCATCCCGAGCAACCGAATCAACACATATGCTTTG 1045  
DB 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
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DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
QY 1166 CTCATTACATATAGGAGACGTCACTGCTTTTGTAGCCCAAGACCTCTTCGTTCCGAT 1225  
DB 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
QY 1226 AAACGTGGTCCACAGAGTCATAGCCCATGAACCTGGCGCACCGAGTGGTTGGCAACCTG 1285  
DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380

QY 1286 GTCACAAATGGAATGCTGAATGATATTTGGCTTAAGGAGGCTTTTGCAAAATACATGAA 1345  
DB 381 ValThrMetGluTyrTrpAsnAspIleTrpLeuAsnGluGlyPheAlaLysTyrMetGlu 400  
QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTGAATGTG 1405  
DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420  
QY 1406 TGTTTTGAAGTAATTTACAAAAGATTTCATTTGAATTCATCCCGCCCTATCTCCAAACCA 1465  
DB 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
QY 1466 GAAACCCCGACTCAAAATACAGGAAATGTTTGATGAAGTTTCTTATACAAAGGAGCTTGT 1525  
DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
QY 1526 ATTTTGAATATGCTCAAGGATTTTCTGGTGAGAGAAATTCAGAAAGGAATTAATTCAG 1585  
DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln 480  
QY 1586 TACTTAAAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGATGCTTGTGGAGCAGTCTGTC 1645  
DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer 500  
QY 1646 AATAGTTGTTAGAAAGTATTTACATCTCGTGGAGTTTGTCAATTCGATCCCAAGATG 1705  
DB 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520  
QY 1706 ACAAAGTAACATGCTC 1720  
DB 521 ThrSerAsnMetVal 525  
RESULT 5  
ART1\_HUMAN STANDARD; PRT: 929 AA.  
AC Q9NZ08; OS0278; Q8NEL4; Q8TAD0; Q9UHF8; Q9UKY2;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-LAP) (ARNS-1) (aminopeptidase PILS) (Purumycin-insensitive leucyl-specific aminopeptidase) (PILS-AP) (Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator).  
DE Name=ARTS1; Synonyms=APPILS, KIAA0525;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=White adipose tissue;  
RX MEDLINE=99238715; PubMed=10220586;  
RA Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;  
RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly related to placental leucine aminopeptidase/oxytocinase.";  
RL J. Biochem. 125:931-938(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Leukocyte;  
RX MEDLINE=2137413; PubMed=11481040;  
RA Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;  
RT "Genomic organization of the human adipocyte-derived leucine aminopeptidase gene and its relationship to the placental leucine aminopeptidase/oxytocinase gene.";  
RL J. Biochem. 130:235-241(2001).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC Schomburg L.;  
RT "Molecular characterization of human aminopeptidase PILS.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Cui X., Alsaaty S., Lawrence M., Combs C.A., Rouhani F.N.,

RA Levine S.J.;  
 RT "Identification of an aminopeptidase regulator of type I tumor  
 RT necrosis factor receptor shedding";  
 RL Submitted (JAN-2000) to the ENBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND REVISION TO 718.  
 RA Nagase T., Iihikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RL Submitted (MAY-2002) to the ENBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 62-929 FROM N.A. (ISOFORM 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Iihikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro";  
 RL DNA Res. 5:31-39(1998).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Testis;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fancie J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE OF 25-37, AND CHARACTERIZATION.  
 RX MEDLINE=20512052; PubMed=11056387;  
 RA Hattori A., Kitatani K., Matsumoto H., Miyazawa S., Rogi T.,  
 RA Tsuruoka N., Mizutani S., Natori Y., Tsujimoto M.;  
 RT "Characterization of recombinant human adipocyte-derived leucine  
 RT aminopeptidase expressed in Chinese hamster ovary cells.";  
 RL J. Biochem. 128:755-762(2000).  
 CC -1- FUNCTION: May play a role in the inactivation of peptide hormones.  
 CC May be involved in the regulation of blood pressure through the  
 CC inactivation of angiotensin II and/or the generation of bradykinin  
 CC in the kidney.  
 CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-  
 CC Xbb-, in which Xaa is preferably Leu, but may be other amino acids  
 CC including Met, Cys and Phe.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9NZ08-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9NZ08-2; Sequence=VSP\_005450;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous.  
 CC -1- PTM: N-glycosylated.  
 CC -1- SIMILARITY: Belongs to the peptidase M1 family.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF106037; AAF07395.1; ALT\_INIT.  
 DR EMBL; AY028806; AAK37777.1; ALT\_INIT.  
 DR EMBL; AY028807; AAK37778.1; ALT\_INIT.  
 DR EMBL; AF183569; AAF20384.1; ALT\_INIT.  
 DR EMBL; AF222340; AAF34664.1; ALT\_INIT.  
 DR EMBL; AB011097; BRA25451.2; ALT\_INIT.  
 DR EMBL; BC030775; AAH30775.1; ALT\_INIT.  
 DR IntAct; Q9NZ08; -;  
 DR MEROPS; M01\_018; -;  
 DR H-InvDB; HIX0005052; -;  
 DR MIM; 606832; -;  
 DR GO; GO:0005829; C:Cytosol; NAS.  
 DR GO; GO:0005783; C:endoplasmic reticulum; NAS.  
 DR GO; GO:0005576; C:extracellular; IDA.  
 DR GO; GO:0016021; C:integral to membrane; NAS.  
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IPI.  
 DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.  
 DR GO; GO:0004239; F:methionyl aminopeptidase activity; NAS.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IPI.  
 DR GO; GO:0008270; F:zinc ion binding; NAS.  
 DR GO; GO:0045444; P:adipocyte differentiation; NAS.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via...; NAS.  
 DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; IDA.  
 DR GO; GO:0050714; P:positive regulation of protein secretion; IDA.  
 DR GO; GO:0008217; P:regulation of blood pressure; NAS.  
 DR GO; GO:0045088; P:regulation of innate immune response; NAS.  
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 DR InterPro; IPR001930; Peptidase\_M1.  
 DR Pfam; PF01433; Peptidase\_M1; 1.  
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 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR Alternative splicing; Aminopeptidase; Direct protein sequencing;  
 KW Glycoprotein; Hydrolase; Metalloprotease; Polymorphism; Protease;  
 KW Signal; Zinc.  
 FT SIGNAL 1 24 Adipocyte-derived leucine aminopeptidase.  
 FT CHAIN 25 929 Zinc (catalytic) (By similarity).  
 FT METAL 341 341 By similarity.  
 FT ACT\_SITE 342 342 Zinc (catalytic) (By similarity).  
 FT METAL 345 345 Zinc (catalytic) (By similarity).  
 FT METAL 464 464 Zinc (catalytic) (By similarity).  
 FT ACT\_SITE 426 426 Proton donor (Potential).  
 FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 402 402 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 748 748 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 889 889 N-linked (GlcNAc...) (Potential).  
 FT VARSPLIC 928 929 RM -> HDPEADATG (in isoform 2).  
 FT VARIANT 115 115 /FTId=VSP\_005450.  
 FT VARIANT 115 115 R -> P (in dBSNP:26653).  
 FT VARIANT 264 264 /FTId=VAR\_012779.  
 FT VARIANT 264 264 I -> M (in dBSNP:26618).  
 FT VARIANT 334 334 /FTId=VAR\_012780.  
 FT VARIANT 334 334 G -> D (in dBSNP:27895).  
 FT VARIANT 337 337 /FTId=VAR\_012781.  
 FT VARIANT 337 337 M -> V (in dBSNP:2287987).  
 FT VARIANT 516 516 /FTId=VAR\_012782.  
 FT VARIANT 516 516 K -> R (in dBSNP:27434).  
 FT VARIANT 718 718 /FTId=VAR\_012783.  
 FT VARIANT 718 718 Q -> E (in dBSNP:27044).  
 FT CONFLICT 502 502 /FTId=VAR\_012784.  
 FT CONFLICT 563 563 G -> R (in Ref. 3).  
 FT CONFLICT 713 713 D -> N (in Ref. 2, 5 and 6).  
 FT CONFLICT 713 713 R -> Q (in Ref. 2, 5 and 6).  
 SQ SEQUENCE 929 AA; 105846 MW; 75C6AD58D0D70D51 CRC64;

Alignment Scores: 4.86e-160 Length: 929  
 Pred. No.:



Db 666 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 685  
Qy 2306 AACCTCAAGCTTACCTTCTTCACTATTATTAAGCCAGTATTGACAGCAAGCTGGAGT 2365  
Db 686 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuLeuLeuThrTrpThr 705  
Qy 2366 GACAAGGCTCAGTCTGGGACAGGATGCTCGCTCGCTCTCTTTGAAGCTGGCTGTGAC 2425  
Db 706 AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuAlaCysVal 725  
Qy 2426 CTGAACCATGCTCTTCATCCAGAAAGCTCTGCACTCTCTCCAGTGGATGCAATCC 2485  
Db 726 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 745  
Qy 2486 AGTGAAATTAATATATACCAACAGATGTTTAAAGATTGTGATTCTGTGGGTGCTCAG 2545  
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Qy 2546 ACAACAGCAGGATGGAATTAACCTTTTGAAGCAATATGAACCTGTCAATGTCAAGTGTGAA 2605  
Db 766 SerThrGluGlyTyrAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 785  
Qy 2606 CAAAACAAAATTCGTATGCTTTGTCAACGACGACATCATGAGAAAGTTACTGAAGTTA 2665  
Db 786 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 805  
Qy 2666 ATTGAATAGGAATGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2725  
Db 806 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 825  
Qy 2726 GCGATTGCCAGCTCCAAAGGGCAGCAACTACGATGGGATTTTGTGAAGAAATTTGG 2785  
Db 826 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 845  
Qy 2786 ACCCATCTTCGAAAAATTTGACTTGGCTCATATGACATAAGGATGATCATCTCGGC 2845  
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Qy 2846 ACAACAGCTCACTTTCTTCAAGGATAAGTTGCAAGGTTGAAGTAACTATTTTGAATCT 2905  
Db 866 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 885  
Qy 2906 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAACGATCAACAA 2965  
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
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GN ORFNames=UNQ584;  
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Curdell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liso D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Wagts A.,  
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
effort to identify novel human secreted and transmembrane proteins: a  
bioinformatics assessment.";  
RL Genome Res. 13:2285-2270(2003).  
DR EMBL; AY358590; AAQ88953.1; -.  
DR GO; GO:0004179; P:proteolysis and peptidolysis; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001930; Peptidase M1.  
DR InterPro; IPR006025; Pept\_Mn\_Zn\_BS.  
DR Pfam; PF01433; Peptidase M1; I.  
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DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.  
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Best Local Similarity: 50.96% Mismatches: 268  
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Qy 272 AGTTATCATCTCACTCAGGATCCTGGGCTTCCAGTAGTCCACTAATGGGACGATTT 331  
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47  
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Qy 392 CACCCCAATCTCACTCTCTGGACTTTTGTGCACTCTGAGAAGATCGAAGTCTTGGTCAGC 451  
Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrLysValGluIleThrAlaSer 87  
Qy 452 AATGCTACCGATTATCATCTTTCACAGCAAGATCTTGAATACAGAAATGCGACCTT 511  
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Qy 632 TATGTGGCTATGGACTTCCAGCCAAAGTAGTGATGGCTTGAAGGGTTTATAAAGC 691  
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Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
446 AsnMetLeuArgGluTyrSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465
QY 1592 AAGAAGTTTCAGTATAGAAATCTAAGAAATGATGACTTGTGGAGCAGTCTGTCAATAGT 1651
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485
QY 1652 TGTTTAGAAAGTATTTTACATCTCGT-----GGAGTTTGTTCATTCGGATCCCAAGATG 1705
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
QY 1706 ACNAGTAACATGCTCGCTTCTCGGGGAAAATGACAGAGTCAAGAGATGATGACTACA 1765
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
504 SerSerSerSerHisThrPheGlnGluGlyValAspValLysThrMetMetAsnThr 523
QY 1766 TGAGCTCCAGAAAGGAATCCCTGCTGGTGTAAACAAGACGGGTGTCTACTCCGA 1825
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543
QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCAGGAAGACCCCTGAATGGAGGGCCCTG 1885
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
544 MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 557
QY 1886 CAGGAGAGGTACTCTGGCATATCCCATGACTACTCCAGAGTCTTCTTAATGCTGATC 1945
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
558 AspThrGlyTyrTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal 577
QY 1946 CACAGACATTTCTAAATCAAAAGACAGATCTCTGGATCTACCTGAAAGAACCACTGGTGG 2005
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
578 HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp 597
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QY 2006 GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAATGGATGG 2065
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
598 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617
QY 2066 GACCAACTCATTTACACAGCTGAATCAGAAACACACACTTCTCAGACCTTAAGCAGCAGAGTA 2125
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
QY 2126 GGTCTGATTCATGATGTGTTTCAGCTAGTGGTCCAGAGAGCTGACCCCTAGACAAAGCT 2185
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
638 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657
QY 2186 CTTGACATGACTTACTACTCAACATCAACACAGCAGCCCGCAGCTTCTCGAAGGTCTG 2245
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677
QY 2246 AGTTACTTGGAAATCGTTTACCATGATGACAGAGGAATATTTACAGATATCTCTGAA 2305
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678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
QY 2306 AACCTCAAGCGTTTACCTTCTTTCAGTATTTTAAAGCCAGTGTGACAGCAAGCTGGAGT 2365
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717
QY 2366 GACAAGGCGCTCAGTCTGGGACAGGATGCTCGCTCGCTCTCTTGAAGCTGCCCTGTGAC 2425
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
718 AspGluGlySerValSerGluGlnMetLeuArgSerGluLeuLeuLeuAlaCysVal 737
QY 2426 CTGAACCATGCTCTGTCATCCAGAAAGCTCTGAACTCTTCTCCAGCTGATGGAATCC 2485
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
QY 2486 AGTGGAAAAATTAATATACCAACAGATGTTTAAAGAATTTGTGTATTTCTGGTGGTCTCAG 2545
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
QY 2546 ACAACAGCAGATGGAATTACCTTTTAGAGCAATATGAAGTCTCAATGCTCAAGTCTGAA 2605
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
QY 2606 CAAACAAAAATTCGTATGCTTCTCAACGAGCAAGCATCAGAAAGCTTACTGAAGTTA 2665
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
QY 2666 ATTGAACCTAGGAATGGAAGGAAGTTTATCAAGACACAGAACTTGGCAGCTCTCTCTCAT 2725
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY 2726 GCGATTGCCAGACGCTCCAAAGGGCAGCACTACATGGGATTTTGTAAAGAGAAATTTGG 2785
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
QY 2786 ACCCATCTCTGAAAAAATTTGACTTGGCTCATATGACATAAGCATCATCTCTCGC 2845
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
QY 2846 ACAACAGCTCACTTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2905
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
QY 2906 CTTGAGGCTCAGGATCAGATCAGATCTGATATTTTCAACTGTTCTGGAAACCAATACCAA 2965
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
QY 2966 AATATAAATGGCTGGAGAGAATCTTCCGACTCTGAGGACTTCGGCTA 3013
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

RESULT 7
ART1_MOUSE
ID -ART1_MOUSE STANDARD; PRT; 930 AA.
AC Q9EQH2; Q9EQH3;
DT 28-FEB-2003 (Rel. 41, Created)
```

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Adipocyte-derived leucine aminopeptidase precursor (RC 3.4.11.-) (A-  
 DE LAP) (ARTS-1) (Aminopeptidase PIS) (Puromycin-insensitive leucyl-  
 DE specific aminopeptidase) (PIS-AP) (VEGF induced aminopeptidase).  
 GN Name=Arts1; Synonym=Apples;  
 OS Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hattori A., Kitatani K., Matsumoto H., Mizutani S., Tsujimoto M.;  
 RT "Molecular cloning of murine adipocyte-derived leucine aminopeptidase  
 RT and its expression in adipocyte cell line, 3T3-L1 cells";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21961541; PubMed=11964289; DOI=10.1182/blood.V99.9.3241;  
 RA Miyashita H., Yamazaki T., Akada T., Niizeki O., Ogawa M.,  
 RA Nishikawa S., Sato Y.;  
 RT "A mouse orthologue of puromycin-insensitive leucyl-specific  
 RT aminopeptidase is expressed in endothelial cells and plays an  
 RT important role in angiogenesis.";  
 RL Blood 99:3241-3249(2002).  
 CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.  
 CC May be involved in the regulation of blood pressure through the  
 CC inactivation of angiotensin II and/or the generation of bradykinin  
 CC in the kidney (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-  
 CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.  
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- SIMILARITY: Belongs to the peptidase M1 family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF227511; AAG44260.1; -;  
 DR EMBL; AB047552; BAB11982.1; -;  
 DR MEROPS; M01.018; -;  
 DR MGD; MGI:1933403; Arts1.  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0005783; C:endoplasmic reticulum; ISS.  
 DR GO; GO:0005576; C:extracellular; ISS.  
 DR GO; GO:0016021; C:integral to membrane; ISS.  
 DR GO; GO:0005138; F:interleukin-6 receptor binding; ISS.  
 DR GO; GO:0004178; F:leucyl aminopeptidase activity; ISS.  
 DR GO; GO:0004239; F:methionyl aminopeptidase activity; ISS.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; ISS.  
 DR GO; GO:0008270; F:zinc ion binding; ISS.  
 DR GO; GO:0045444; P:adipocyte differentiation; ISS.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; ISS.  
 DR GO; GO:0005059; P:membrane protein ectodomain proteolysis; ISS.  
 DR GO; GO:0050714; P:positive regulation of protein secretion; ISS.  
 DR GO; GO:0008217; P:regulation of blood pressure; ISS.  
 DR GO; GO:0045088; P:regulation of innate immune response; ISS.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR001930; Peptidase\_M1.  
 DR InterPro; IPR003163; Yeast DNA bind.  
 DR Pfam; PF01433; Peptidase\_M1; 1.  
 DR PRINTS; PR00756; ALADIPTASE.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Aminopeptidase; Glycotoxin; Hydrolase; Metalloprotease; Protease;  
 KW Signal; Zinc.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 930 Adipocyte-derived leucine aminopeptidase.

FT METAL	342	342	Zinc (catalytic) (By similarity).
FT ACT SITE	343	343	By similarity.
FT METAL	346	346	Zinc (catalytic) (By similarity).
FT METAL	465	465	Zinc (catalytic) (By similarity).
FT ACT_SITE	427	427	Proton donor (Potential).
FT CARBOHYD	59	59	N-linked (GLNAC. .) (Potential).
FT CARBOHYD	143	143	N-linked (GLNAC. .) (Potential).
FT CARBOHYD	403	403	N-linked (GLNAC. .) (Potential).
FT CARBOHYD	540	540	N-linked (GLNAC. .) (Potential).
FT CARBOHYD	655	655	N-linked (GLNAC. .) (Potential).
FT CARBOHYD	749	749	N-linked (GLNAC. .) (Potential).
FT CARBOHYD	890	890	N-linked (GLNAC. .) (Potential).
FT CONFLICT	540	541	NA -> KG (in Ref. 2).
SQ SEQUENCE	930 AA; 106598 MW; 17430DB5EAD7668 CRC64;		

  

Alignment Scores:			
Pred. No.:	1.36e-157	Length:	930
Score:	2480.00	Matches:	462
Percent Similarity:	69.73%	Conservative:	167
Best Local Similarity:	51.22%	Mismatches:	263
Query Match:	41.95%	Indels:	10
DB:	1	Gaps:	4

  

US-10-039-073-2 (1-3366) x ART1_MOUSE (1-930)			
QY 311	GCACCTAATGGGAAACGATTTCCTTGGCAGGAGCTAAGCTCCAGTGTGGTTCATTCCT	370	
DB 30	AlaserasnGlyaspSerPheProTpaAsnAsnMetArgLeuProGluTyrMetThrPro	49	
QY 371	CTCCATTATGACCTCTTTGTCACCCCAATCTCACCTCTCTGACCTTTGTTGTCATCTGAG	430	
DB 50	IleHisTyrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPheTyrGlyLysThr	69	
QY 431	AGATCGAGCTCTGGTCAGCAATGCTACCCAGTTCATCTTCATCTGCAACCAAGATCTT	490	
DB 70	GluValGluIleLeuAlaSerArgProThrSerThrIleIleMetHisSerHisLeu	89	
QY 491	GAATCAGCAATGCCACCTTCAGTCAGAGGAAAGATCAAGATACATACCAAGCAACCAAGAA	550	
DB 90	GlnIleSerIysAlaThrLeuArg-----ArgGlyAlaGlyGluMetLeuSerGluGlu	107	
QY 551	GAATGAAAGTTTGTAGTTACCTGCTCATGAAACAAATTGCATCTGCTGTTGCCAGAGAA	610	
DB 108	ProLeuLysValLeuGluTyrProAlaHisGluGlnValAlaLeuLeuAlaGlnPro	127	
QY 611	CTTACGCTCACCTGAAATACTATGCGCTATGCGCTTCCAGCTTCCAGCAAGTTAGGTGATGC	670	
DB 128	LeuLeuAlaGlySerLeuTyrThrValIleAspTyrAlaAlaAsnLeuSerGluSer	147	
QY 671	TTTGAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGTGAAACAAAGAAATCTTTGCA	730	
DB 148	PheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGlyGluMetArgIleLeuAla	167	
QY 731	GTAAACAGATTTTGAGCAACCCAGGACCGCATGGCTTCCTCTGCTTTGTATGAACCGTTG	790	
DB 168	AlaThrGlnPheGluProThrAlaAlaArgMetAlaPheProCysPheAspGluProAla	187	
QY 791	TTCAAAGCCAACTTTCAATCAAGATACAGAGAGAGAGAGAGGATATTCACCTATCCAAAC	850	
DB 188	LeuLysAlaSerPheSerIleLysIleLysArgAspProArgHisLeuAlaIleSerAsn	207	
QY 851	ATGCCAAAGGTTAAGCAATTTGAATTTGAAGAGGCTTTTGGAAAGATCACTTTTGAACCT	910	
DB 208	MetProLeuValLysSerValAsnValAlaGluGlyLeuIleGluAspHisPheAspIle	227	
QY 911	ACTGTAAAATAGATCATACCTTTGAGCCGTACATAGTTTGTGATTTCCACTCTCTGAGT	970	
DB 228	ThrValLysMetSerThrTyrLeuValAlaPheIleIleSerAspPheLysSerValSer	247	
QY 971	GGCTTTCATCTCATCAGGGTCAAGGTGTCCTATCTATGCTATCCCGACAGCAACCGAATCAA	1030	
DB 248	LysMetThrLysSerGlyValLysValSerValTyrAlaValProAspLysIleAsnGln	267	



GN Name=Arts1; Synonyms=Appils;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBTaxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC STRAIN=Sprague-Dawley; TISSUE=Pineal gland;  
RX MEDLINE=20285344; PubMed=10824104;  
RA Schomburg L., Kollmus H., Friedrichsen S., Bauer K.;  
RT "Molecular characterization of a puromycin-insensitive leucyl-specific  
RL Eur. J. Biochem. 267:3198-3207(2000).  
CC -!- FUNCTION: May play a role in the inactivation of peptide hormones.  
CC May be involved in the regulation of blood pressure through the  
CC inactivation of angiotensin II and/or the generation of bradykinin  
CC in the kidney (By similarity).  
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-  
CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.  
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9J22-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9J22-2; Sequence=VSP\_005451, VSP\_005452;  
CC -!- TISSUE SPECIFICITY: Ubiquitous.  
CC -!- SIMILARITY: Belongs to the peptidase M1 family.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL; AF148323; AAF73106.1; -;  
DR EMBL; AF148324; AAF73107.1; -;  
DR MEROPS; M01.018; -;  
DR GO; GO:0005829; C:cytosol; ISS.  
DR GO; GO:0005783; C:endoplasmic reticulum; ISS.  
DR GO; GO:0005576; C:extracellular; ISS.  
DR GO; GO:0016021; C:integral to membrane; ISS.  
DR GO; GO:0005138; F:interleukin-6 receptor binding; ISS.  
DR GO; GO:0004178; F:leucyl aminopeptidase activity; ISS.  
DR GO; GO:0004239; F:methionyl aminopeptidase activity; ISS.  
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; ISS.  
DR GO; GO:0008270; F:zinc ion binding; ISS.  
DR GO; GO:0045444; P:adipocyte differentiation; ISS.  
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; ISS.  
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.  
DR GO; GO:0050714; P:positive regulation of protein secretion; ISS.  
DR GO; GO:0008217; P:regulation of blood pressure; ISS.  
DR GO; GO:0045088; P:regulation of innate immune response; ISS.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR001930; Peptidase\_M1.  
DR Pfam; PF01433; Peptidase\_M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Alternative splicing; Aminopeptidase; Glycoprotein; Hydrolase;  
KW Metalloprotease; Protease; Signal; Zinc.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 930 Adipocyte-derived leucine aminopeptidase.  
FT METAL 342 342 Zinc (catalytic) (By similarity).  
FT ACT SITE 343 343 By similarity.  
FT METAL 346 346 Zinc (catalytic) (By similarity).  
FT METAL 465 465 Zinc (catalytic) (By similarity).  
FT ACT\_SITE 427 427 Proton donor (potential).  
FT CARBOHYD 59 59 N-linked (GlcNAc . .) (potential).  
FT 143 143 N-linked (GlcNAc . .) (potential).

FT CARBOHYD 403 403 N-linked (GlcNAc . .) (potential).  
FT CARBOHYD 655 655 N-linked (GlcNAc . .) (potential).  
FT CARBOHYD 749 749 N-linked (GlcNAc . .) (potential).  
FT CARBOHYD 890 890 N-linked (GlcNAc . .) (potential).  
FT VARSPLIC 883 884 FF -> CM (in isoform 2).  
FT /FTID=VSP\_005451.  
FT VARSPLIC 885 930 Missing (in isoform 2).  
FT /FTID=VSP\_005452.  
SQ SEQUENCE 930 AA; 106418 MW; 92BE7173CBD0BE7F CRC64;  
Alignment Scores:  
Pred. No.: 3,05e-154 Length: 930  
Score: 2430.00 Matches: 456  
Percent Similarity: 68.90% Conservative: 171  
Best Local Similarity: 50.11% Mismatches: 265  
Query Match: 41.10% Indels: 18  
DB: 1 Gaps: 6  
US-10-039-073-2 (1-3366) x ART1\_RAT (1-930)  
QY 299 GCTTCCCTCCAGTACCTAATGGGAACGATTTCTTGGCAGGAGCTAAGGCTCCCCAGT 358  
DB 26 AlaserProlysalaserAenGlyAlaserPheProTrpAsnAenMetArgLeuProGlu 45  
QY 359 GTGGTCATTCCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCCTCTCTGGACTTT 418  
DB 46 TyrIleThrProIleHisTyrAspLeuMetIleHisAlaAenLeuSerThrLeuThrPhe 65  
QY 419 GTTGCATCTGAGAAGATCGAAGCTTGGTCAGCAAGTCTACCCAGTATTATCATCTTGCAC 478  
DB 66 TrpGlyThrGluValGluIleThrValSerGlnProThrSerThrIleMetHis 85  
QY 479 AGCAAGATCTTCAATACCAATCCACCTCCAGCTTTCAG-----TCAGAGGAAGATTCAAGA 532  
DB 86 SerHisGlnLeuGlnIleSerLysAlaThrLeuArgGlyAlaGlu----- 102  
QY 533 TACATGAACACAGAAAGAAAGTGAAGTTTGAAGTTTACCTCTCATGAACAAATGCA 592  
DB 103 ---MetLeuProGluGluProLeuLysLeuMetGluTyrSerAlaHisGluInValAla 121  
QY 593 CTGCTGGTCCAGAGAACTTACGCTCCTCACCTCAATATCTATGCTATGCTATGCTTCCAA 652  
DB 122 LeuLeuThrAlaGlnProLeuLeuAlaGlySerValTyrThrValIleIleThrTyrAla 141  
QY 653 GCCAAGTTAGTGATGCTTTGAAGGGTTTATAAAGACACATACAGAACTCTTGGTGGT 712  
DB 142 AlaAsnLeuSerGluAsnPheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGly 161  
QY 713 GAACAAGAAATCTTGAGTAAACAGATTTTGAAGCAACCCAGCAGCATGGCTTTCCCT 772  
DB 162 GluArgGlyLeuAlaAlaThrGlnPheGluProThrAlaAlaArgMetAlaPhePro 181  
QY 773 TGCTTTGATGAACCGTTGTTCAAGCCAACTTTTCAATCAAGATACCAAGAGAGAGAGAG 832  
DB 182 CysPheAspGluProAlaLeuLysAlaSerPheSerIleLysIleLysArgAspProArg 201  
QY 833 CATATTGCACTATCCCAACATGCGCAAGTTTGAAGCAACTTGAAGAGGGTCTTTTG 892  
DB 202 HisLeuAlaIleSerAsnMetProLeuValLysSerValThrValAlaGluGlyLeuIle 221  
QY 893 GAAGATCACTTTGAAACTACTGTAAATAATGAGTACATACCTTGTAGCCTCATAGTTTGT 952  
DB 222 GluAspHisPheAspIleThrValLysMetSerThrTyrLeuValAlaPheIleIleSer 241  
QY 953 GATTTCCACTCTCTGAGTGCCTTCACTTTCATCATGGGTCAAGGTCCATCTATGATCC 1012  
DB 242 AspPheLysSerValSerLysMetThrLysSerGlyValLysValSerValTyrAlaVal 261  
QY 1013 CCAGACAAACGGATCAACACATATTATGCTTTGAGGCACTCATCTGAAGCTACTTGTATTT 1072  
DB 262 ProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAlaAlaValThrLeuLeuGluPhe 281  
QY 1073 TATGAAAAGTACTTTGATGATCTACTATCTACTCTCCAACTGGATTTAATGCTATTCCT 1132





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QY 1456 CAACACCGCGGAAACCCGACTCAATACATACAGAAATGTTGATGAAGTTTCTCTATAACAA 1515
DB 511 rThrPheValSerThrProGluGlnValGluMetPheAspSerValSerTyrGluLy 531
QY 1516 GGGAGCTTGTATTTTGAATATGCTCAAGGATTTCTGGGTGAGGAGAAATCCAGAAAGG 1575
DB 531 sGlyAlaSerIleLeuLeuMetLeuAsnAlaThrLeuArgAspGlyGluPheHisLeuG 551
QY 1576 AATAATTCAGTACTTAAAGAGTTTCAGCTATAGAAATGCTAAGATGATGTTGTGGAG 1635
DB 551 yValIleGluTyrLeuGlnAsnTyrAsnLeuSerAsnThrGluSerLysAspLeuTyrAs 571
QY 1636 CAGTCTGTCAAAATAGTTGTTAGAAAGTCATTTACATCTGGTGAGTTTGTCTCCGA 1695
DB 571 nSerLeuSerGlnValSerLysGlnSer----- 580
QY 1696 TCCCAAGATGACAAGTAAACATGCTCGCCTTCTTGGGGGAAATGCAGAGGTCAAGAGAT 1755
DB 581 -----LeuAsnValSerGluWe 586
QY 1756 GATGACTACATGGAATCTCCAGAAAGGAATCCCTCTGCTGGTGGTTAAACAGCGGTG 1815
DB 586 tMetAsnThrTrpThrValHisLeuGlyPheProLeuValThrValLysArgAsnGlyPr 606
QY 1816 TTCACTCCGACTGCACAGGAGCGTTCCTCCAGGGGGTTCAGGAGACCCCTGAATG 1875
DB 606 oGlnValThrLeuSerGlnGluHisPheLeuAsnAla-----G 620
QY 1876 GAGGCGCTCGCAGGAGAGTACCTGTGCATATCCATTGACCTACTCCAGGATTCCTC 1935
DB 620 uAsnGlyThrAspAspSerLeuTrpHisIleProLeuThrTyrValAsnAspSerCy 640
QY 1936 TAATGTGATCCACAGA-----CACATTCCTAAATCAAAACAGACAGATACTCT 1980
DB 640 sSerValLeuArgSerCysLysGlnValPheHis---LeuLysAspLysGluAlaThrLe 659
QY 1981 GGATCTACTGMAAGACAGCTGGTGGTGAATTTAATGTGGACTCAAAATGTTACTACAT 2040
DB 659 uGlnLeuProGluGlnValLysTrpLeuLysPheAsnPheArgSerAspGlyPheTyrIl 679
QY 2041 CGTTCACATGAGGCTCATGATGGACCACTCATACACAGCTGMAATCAGAACACACAC 2100
DB 679 eValHisTyrAspGluGlnGlyTrpSerAspLeuIleSerAlaLeuLysValAspValAs 699
QY 2101 ACTTCTCAGACCTAAGCAGACAGTAGTCTGATTCATGATGTTTTCAGTGTGTTGGTC 2160
DB 699 nValLeuProSerGluAspLysAlaAlaLeuIleAsnAsnIlePheAlaLeuSerArgLe 719
QY 2161 AGGAGACTGACCCTAGCAAAAGCTCTTGACATGACTTACTACCTCCAAACATGAAACAG 2220
DB 719 uGlyLysValSerPheArgGlnValLeuAsnLeuMetAspTyrIleArgAsnGluThrGl 739
QY 2221 CAGCCCCGCACTCTCGAAGGCTGAGTTACTTGAATCGTTTACCACATGATGGACAG 2280
DB 739 urhAlaProLeuThrGluAlaLeuSerGlnLeuGlyGlnIleTyrArgLeuLeuAspLys 759
QY 2281 AAGGAATATTTTCAGATATCTCTGAAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAGCC 2340
DB 759 sArgSerAspLeuAsnLeuAlaSerSerMetThrThrTyrIleGluSerHisPheGlySe 779
QY 2341 ACTGATTCAGAGCGMAAGCTGGATGACAGAGGCTCAGTCTGGGACAGGATGCTCCGCTC 2400
DB 779 rLeuMetGluSerGlnSerTrpGluValGluThrSerValSerLysMetThrLeuArgSe 799
QY 2401 GGCTCTCTTGAAGCTGGCTGTGACCTCAACCATGCTCTCTTGCATCCAGAAAGCTGCTGA 2460
DB 799 rAlaLeuLeuGluThrAlaCysAlaLeuAsnArgProAsnCysThrThrGlnAlaArgAr 819
QY 2461 ACTCTCTCCAGCTGGATGGAATCCAGTGGAAAAATTAATATACCAACAGATGTTTAA 2520
DB 819 gLeuPheAspGlnTrpLeuAlaSerAsnLysThrLeuGlnIleProSerAspLeuMetAr 839
QY 2521 GATTGTGTATCTGTGGGTGCTCAGACCAACAGCAGGATGGAATACCTTTTAGAGCAATA 2580

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DB 839 gThrValPheLysValAlaAlaLysThrAspGluGlyTrpSerLysLeuLeuGlySerTy 859
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DB 859 rLysHisSerIleTyrAspThrGluLysArgLysMetLeuGluAlaLeuAlaSerThrGl 879
QY 2641 GCATCAGAAAAGTTACTGAAGTTAATGAAGTAACTAGGAAGTGAAGAAAGGTTTCAAGAC 2700
DB 879 nAspValArgLysIleIleTrpValLeuGlnLysSerLeuAspGlySerGluIleGlnAs 899
QY 2701 ACAGAACTTGGCAGCTCTCTTCATGCGATTCGAGAGCTCCAAAGGGGACCACTAGC 2760
DB 899 nGlnGluPheProLeuValIleHisThrValCysArgAspPheAlaGlyTyrLeuTyrAl 919
QY 2761 ATGGGATTTTGAAGAAAATTCGACCCATCTCTGAAAAAATTTGACTTGGGCTCAT 2820
DB 919 aTrpAspPheMetLysGluAsnTrpGluLysIleThrGlnLysPheProIleGlySerPh 939
QY 2821 TGACATGAAGATGATCATCTCTCGCACACACAGCTCCTTTTCTCCAAAGGATAAGTTGCA 2880
DB 939 eAlaIleGlnSerIleIleThrSerThrThrSerGlnPheSerThrLysThrHisLeuAl 959
QY 2881 AGAGTCAAACTATTTTGAATCTCTGAGGCTCAAGGATCACATCTGGATATTTTCA 2940
DB 959 aGluValGlnAsnPheSerSerLeuGlyAlaLysGlySerGlnMetArgIleValGl 979
QY 2941 AACTGTTCTGAAACGATAACCAAAATATATAAATGCTGAGAGAAATCTTCGAGCTCT 3000
DB 979 nGluAlaIleGluThrIleLysHisAsnMetArgTrpMetGluLysAsnLeuAsnThrLe 999
QY 3001 GAGGACTTGGCTA 3013
DB 999 uGlnSerTrpLeu 1003

RESULT 10
LCAP_RAT
ID LCAP_RAT STANDARD; PRT; 1025 AA.
AC P97629; Q11009;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)
DE (Oxytocinase) (Otrase) (Insulin-regulated membrane aminopeptidase)
DE (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine
DE aminopeptidase) (P-LAP) (Vesicle protein of 165 kDa) (Vp165) (GP160).
GN Name=Lpsep; Synonyms=Irap, Otrase;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RA MEDLINE=96007507; PubMed=7559527; DOI=10.1074/jbc.270.40.23612;
RA Kessler S.R., Scott H.M., Mastick C.C., Abersold R., Lienhard G.E.;
RT "Cloning and characterization of a novel insulin-regulated membrane
RT aminopeptidase from Glut4 vesicles.";
RL J. Biol. Chem. 270:23612-23618(1995).
RN (2)
SEQUENCE OF 168-176; 387-399; 731-740 AND 893-905.
RX MEDLINE=94164972; PubMed=8119954;
RA Mastick C.C., Abersold R., Lienhard G.E.;
RT "Characterization of a major protein in GLUT4 vesicles. Concentration
RT in the vesicles and insulin-stimulated translocation to the plasma
RT membrane.";
RL J. Biol. Chem. 269:6089-6092(1994).
CC -1- FUNCTION: Release of an N-terminal amino acid, cleave before
CC cysteine, leucine as well as other amino acids. Degrades peptide
CC hormones such as oxytocin, vasopressin and angiotensin III, and
CC plays a role in maintaining homeostasis during pregnancy. May be
CC involved in the inactivation of neuronal peptides in the brain.
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may

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be the angiotensin IV receptor in the brain (By similarity).  
-1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys[-Xaa, in which the half-cystine residue is involved in a disulfide loop, notably in oxytocin and vasopressin].  
-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
-1- SUBUNIT: Homodimer. Binds tankyrases 1 and 2 (By similarity).  
-1- SUBCELLULAR LOCATION: Type II membrane protein. Localized mainly in intracellular vesicles together with GLUT4. Relocalizes to the plasma membrane in response to insulin. The dileucine internalization motif and/or the interaction with tankyrases may be involved in intracellular sequestration.  
-1- TISSUE SPECIFICITY: Highly expressed in heart, brain, spleen, lung, kidney and white adipose tissue. Detected at lower levels in skeletal muscle and liver.  
-1- PTM: N-glycosylated.  
-1- SIMILARITY: Belongs to the peptidase M1 family.

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EMBL; U76997; AAB19066.1; -;  
EMBL; U32990; AAB38021.1; -;  
PIR; I55441; I55441.  
DR MEROPS; M01.011; -;  
DR InterPro; IPR001930; Peptidase\_M1.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR Pfam; PF01433; Peptidase\_M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Aminopeptidase; Direct protein sequencing; Glycoprotein; Hydrolase;  
KW Metal-binding; Metalloprotease; Protease; Signal-anchor;  
KW Transmembrane; Zinc.  
FT DOMAIN 1 109 Cytoplasmic (Potential).  
FT TRANSNEM 110 131 Signal-anchor for type II membrane protein (Potential).  
FT ACT\_SITE 132 1025 Extracellular (Potential).  
FT SITE 53 54 Dileucine internalization motif (Potential).  
FT SITE 76 77 Dileucine internalization motif (Potential).  
FT SITE 96 101 Tankyrase binding (By similarity).  
FT METAL 464 464 Zinc (catalytic) (By similarity).  
FT ACT\_SITE 465 465 By similarity.  
FT METAL 468 468 Zinc (catalytic) (By similarity).  
FT METAL 487 487 Zinc (catalytic) (By similarity).  
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).  
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FT CARBOHYD 525 525 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 664 664 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 682 682 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 695 695 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 758 758 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 834 834 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 850 850 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 989 989 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 909 916 LMKSLDQ -> YGTTQRAW (in Ref. 1; AAB38021).  
FT CONFLICT 916 1025 Missing (in Ref. 1; AAB38021).  
SQ SEQUENCE 1025 AA; 117201 MW; 8AD3BA3A446FB5EF CRC64;

, Alignment Scores:

Pred. No.:	3.2e-127	Length:	1025
Score:	2027.00	Matches:	402
Percent Similarity:	61.81%	Conservative:	158
Best Local Similarity:	44.37%	Mismatches:	310
Query Match:	34.29%	Indels:	36
DB:	1	Gaps:	5
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QY	305	CMAGTAGCCACTAATCGGGAACGATTCTTCCTGGCAGAGCAAGCTAGGCTCCCACTGGTGGTC	364
DB	153	ProilleAlaThrAsnGlyLysValPheProTpaAlaGlnIleArgLeuProThrAlaIle	172
QY	365	ATTCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTTGCA	424
DB	173	IleProGlnArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly	192
QY	425	TCGTGAGAGATCGAAGCTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTTGCACAGCAA	484
DB	193	SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr	212
QY	485	GATCTTGAATACGAATGCCACCTTCAGTCAGAGAGAGATCAAGATACATGAAACCA	544
DB	213	GlyHisAsnIleSerSerValThrPheMetSerAlaValSerSerGln	228
QY	545	GGAAAGAACTGAAGCTTTTGGAGTTACCTGCTCATGAACAAATTCACCTGCTGGTTCCA	604
DB	229	GluLysGlnValGluIleLeuGluTyrProTyrHisGluGlnIleAlaValAlaPro	248
QY	605	GAGAACTTACCGCTCACCTGAAATACTATGTGGCTATGGACTTCCAAGCCAAAGTTAGGT	664
DB	249	GluSerLeuLeuThrGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer	268
QY	665	GATGGCTTGAAGGGTTTATATAAGACATACAGAACTCTTGGTGGTGAACAGAAAT	724
DB	269	AsnSerTyrTyrGlyPheTyrGlyIleThrTyrThrAspLysSerAsnGluLysAsn	288
QY	725	CTTGCACTAAGATTTTGGAGCCCAACCCAGGCGCATGCTTCCCTTCCTTCTTGTATGAA	784
DB	289	PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu	308
QY	785	CGTTGTTCCAAAGCCAACTTTTCAATCAAGATACAGAGAGAGAGAGAGCATATATGCACTA	844
DB	309	ProAlaPheLysAlaThrPheIleIleLysIleThrArgAspGluHisThrAlaLeu	328
QY	845	TCCAACATGCCAAAGCTTAAAGCAATGAACCTTGAAGAGGCTTTTGGAGAGATCACTTT	904
DB	329	SerAsnMetProLysLysSerSerValProThrGluGluGlyLeuIleGlnAspGluPhe	348
QY	905	GAACCTACTGTAAATAAGTAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCT	964
DB	349	SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetArgAsn	368
QY	965	CTGAGTGGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCTATGATCCCAAGCAACCG	1024
DB	369	LeuSerGln---AspValAsnGlyThrLeuValSerValTyrAlaValProGluLysIle	387
QY	1025	AATCAACACATATGCTTTTGGAGGCATCAGTGAAGCTACTTATGATTTTGAAGATAC	1084
DB	388	AspGlnValTyrHisAlaLeuAspThrThrValLysLeuGluPheTyrGlnAsnTyr	407
QY	1085	TTTGATATCTACTATCCTCTCTCAACCTGGATTTTAAATTTGCTATTCTGCTTTGCACCT	1144
DB	408	PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla	427
QY	1145	GGAGCCATGGAATTTGGGCGCTCATTATACATATAGGAGACGCTACTGCTTTTGACCCC	1204
DB	428	GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspAsn	447
QY	1205	AAGACCTCTTCTCTCCGATAAAGTGTGGGTACACAGAGTCATAGCCCATGACTGGCG	1264
DB	448	AlaThrSerSerValAlaAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla	467

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QY 1265 CACCAAGTGGTTGGCAACTGGTCAATGGAATGGTGAATGATATTTGGCTTAAGGAG 1324
Db 468 HieGlnTrpPheGlyAsnLeuValThrMetGlnTrpTrpAsnAspLeuTrpLeuAsnGlu 487
QY 1325 GGTTTTGGCAAAATACATGGAACCTTATCGCTGTGTAATGCTACATATCCAGAGCTGCAATTT 1384
Db 498 GlyPheAlaThrPheMetGluTyrrPheSerValGluLysIlePheLysGluLeuAsnSer 507
QY 1385 GATGACTATTTTGAATGTGTGTTTGAAGTAATTACAAAAGATTCATTAATTCATCC 1444
Db 508 TyrGluAaspPheLeuAspAlaArgPheLysThrMetArgLysAaspSerLeuAsnSerSer 527
QY 1445 CGCCCTATCTCAAAACCGGGAACCCGAGCTCAAAATACAGGAATATGTTGATGAAGTT 1504
Db 528 HisProIleSerSerValGlnSerSerGluGlnIleGluGluMetPheAaspSerLeu 547
QY 1505 TCCTATAACAAGGGAGCTGTGATTTTGAATATGCTCAAGGATTTTCTCGGTGAGGAGAA 1564
Db 548 SerTyrrPheLysGlyAlaSerLeuLeuMetLysSerTyrrLeuSerGluAaspVal 567
QY 1565 TTCCAGAAGGAATTAATTCAGTACTTAAGAAGATTTCAGCTATAGAAATGCTAAGAATGAT 1624
Db 568 PheGlnHisAlaIleLeuTyrrLeuHisAsnHisSerTyrrAlaAlaIleGlnSerAasp 587
QY 1625 GACTTGTGAGCAGCTCTGCTCAAAATAGTTGTTTAGAAAGTATTTTACATCTGGTGGAGTT 1684
Db 588 AspLeuTrpAaspSerPheAsnGlu----- 595
QY 1685 TGTCAATTCGGATCCCAAGATGACAAGTAACATGCTCGCTTCTCGGGGGAATAATGCACAG 1744
Db 596 -----ValThrGlyLysThrLeuAasp 602
QY 1745 GTCAAGAGATGATGACTACATGACTCTCCAGAAAGGAATCCCTCTGCTGTGTTTAAA 1804
Db 603 ValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
QY 1805 CAAGACGGGTGTCTACTCGACTGCAACAGAGCGCTTCTCCACGGGGGTTTTCCAGGAA 1864
Db 623 ArgLysGlyThrGluLeuLeuGlnGlnGluArgPhePheProSerMet----- 639
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Db 640 GlnProGluIleGlnAaspSerAaspThrSerHisLeuTrpHisIleProIleSerTyrrVal 659
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Db 660 ThrAaspGlyArgAsnTyrrSerGluTyrrArgSerValSerLeuLeuAaspLysLysSerAasp 679
QY 1976 ACTCTGGATCTACCTGAAAGACCAAGTTGGGTGAAATTAATGTGGACTCAAAATGGTTAC 2035
Db 680 ValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGlyTyrr 699
QY 2036 TACATCGTTCACTATGAGGGTCATCGATGGGACCAACTCATTACACAGCTGAATCAGAAC 2095
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QY 2096 CACACACTTCTCAGACCTTAAGACACAGATGAGTCTGATTCATGTGTTTCAGCTAGTT 2155
Db 720 ProTyrrValLeuSerAspLysAaspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
QY 2156 GGTGAGGAGACTGACCTGACCAAGCTCTTGACATGACTTACTACTCAACATGAA 2215
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QY 2876 TTGCAAGAGGTGAACATTTTGAATCTCTTGAGGCTCAAGGATCATCTCGATATT 2935
Db 980 LeuSerGluValGlnGluPhePheGluAsnGlnSerGluAlaThrLeuGlnLeuArgCys 999
QY 2936 TTTCAAACTGTTCTGGAACGATAACCAAAAAATATAAAATGGCTGGAGAAAGATCTTCCG 2995
Db 1000 ValGlnGluAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeuLys 1019
QY 2996 ACTCTGAGGACTTGGCTA 3013
Db 1020 ThrLeuThrLeuTrpLeu 1025
RESULT 11
Q8C129 PRELIMINARY; PRT; 1025 AA.
AC Q8C129;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:473249018 product:INSULIN-REGULATED MEMBRANE
DE AMINOPEPTIDASE IRAP homolog.
GN Name=Lnap;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
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CC [3] SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).  
CC MEDLINE=20223264; PubMed=10759854;  
CC Raamussen T.E., Pedraza-Diaz S., Hardre R., Laustsen P.G.,  
CC Carrion A.G., Kristensen T.;  
CC "Structure of the human oxytocinase/insulin-regulated aminopeptidase  
CC gene and localization to chromosome 5q21.";  
CC Eur. J. Biochem. 267:2297-2306(2000).  
CC [4]  
CC SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
CC MEDLINE=21286092; PubMed=11389728;  
CC Matsunoto H., Nagaoka T., Hattori A., Rogi T., Tsuruoka N.,  
CC Mizutani S., Tsujimoto M.;  
CC "Expression of placental leucine aminopeptidase/oxytocinase in  
CC neuronal cells and its action on neuronal peptides.";  
CC Eur. J. Biochem. 268:3259-3266(2001).  
CC [5]  
CC CHARACTERIZATION.  
CC MEDLINE=92117646; PubMed=1731608;  
CC Tsujimoto M., Mizutani S., Adachi H., Kimura M., Nakazato H.,  
CC Tomoda Y.;  
CC "Identification of human placental leucine aminopeptidase as  
CC oxytocinase.";  
CC Arch. Biochem. Biophys. 292:388-392(1992).  
CC [6]  
CC FUNCTION.  
CC MEDLINE=21623680; PubMed=11707427; DOI=10.1074/jbc.C100512200;  
CC Albiston A.L., McDowell S.G., Macsacos D., Sim P., Clune E.,  
CC Mustafa T., Lee J., Mendelsohn F.A., Simpson R.J., Connolly L.M.,  
CC Chai S.Y.;  
CC "Evidence that the angiotensin IV (AT(4)) receptor is the enzyme  
CC insulin-regulated aminopeptidase.";  
CC J. Biol. Chem. 276:48623-48626(2001).  
CC -I- FUNCTION: Release of an N-terminal amino acid, cleave before  
CC cysteine, leucine as well as other amino acids. Degrades peptide  
CC hormones such as oxytocin, vasopressin and angiotensin III, and  
CC plays a role in maintaining homeostasis during pregnancy. May be  
CC involved in the inactivation of neuronal peptides in the brain.  
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may  
CC be the angiotensin IV receptor in the brain.  
CC -I- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-  
CC Xaa, in which the half-cystine residue is involved in a disulfide  
CC loop, notably in oxytocin and vasopressin.  
CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -I- SUBUNIT: Homodimer. Binds tankyrases 1 and 2.  
CC -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted.  
CC During pregnancy serum levels are low in the first trimester, rise  
CC progressively during the second and third trimester and decrease  
CC rapidly after parturition. In brain only the membrane-bound form  
CC is found. The protein resides in intracellular vesicles together  
CC with GLUT4 and can then translocate to the cell surface in  
CC response to insulin and/or oxytocin. Localization may be  
CC determined by dileucine internalization motifs, and/or by  
CC interaction with tankyrases.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Experimental confirmation may be lacking for some  
CC isoforms;  
CC Name=1;  
CC IsoId=Q9UIQ6-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9UIQ6-2; Sequence=VSP\_005448;  
CC Name=3;  
CC IsoId=Q9UIQ6-3; Sequence=VSP\_005449;  
CC -I- TISSUE SPECIFICITY: Highly expressed in placenta, heart, kidney  
CC and small intestine. Detected at lower levels in neuronal cells in  
CC the brain, in skeletal muscle, spleen, liver, testes and colon.  
CC -I- PTM: The pregnancy serum form is derived from the membrane-bound  
CC form by proteolytic processing.  
CC -I- PTM: N-glycosylated.  
CC -I- SIMILARITY: Belongs to the peptidase M1 family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; D50810; BAA09436.1; ALT\_INIT.  
CC EMBL; U62768; AAB66672.1; -  
CC EMBL; U62769; AAB66673.1; -  
CC EMBL; AJ131023; CAB61646.1; JOINED.  
CC EMBL; AJ131025; CAB61646.1; JOINED.  
CC EMBL; AJ131026; CAB61646.1; JOINED.  
CC EMBL; AJ131027; CAB61646.1; JOINED.  
CC EMBL; AJ131028; CAB61646.1; JOINED.  
CC EMBL; AJ131029; CAB61646.1; JOINED.  
CC EMBL; AJ131030; CAB61646.1; JOINED.  
CC EMBL; AJ131031; CAB61646.1; JOINED.  
CC EMBL; AJ131032; CAB61646.1; JOINED.  
CC EMBL; AJ131033; CAB61646.1; JOINED.  
CC EMBL; AJ131034; CAB61646.1; JOINED.  
CC EMBL; AJ131035; CAB61646.1; JOINED.  
CC EMBL; AJ131036; CAB61646.1; JOINED.  
CC EMBL; AJ131037; CAB61646.1; JOINED.  
CC EMBL; AJ131038; CAB61646.1; JOINED.  
CC EMBL; AJ131039; CAB61646.1; JOINED.  
CC EMBL; AJ131025; CAB94753.1; -  
CC EMBL; AJ131026; CAB94753.1; JOINED.  
CC EMBL; AJ131027; CAB94753.1; JOINED.  
CC EMBL; AJ131028; CAB94753.1; JOINED.  
CC EMBL; AJ131029; CAB94753.1; JOINED.  
CC EMBL; AJ131030; CAB94753.1; JOINED.  
CC EMBL; AJ131031; CAB94753.1; JOINED.  
CC EMBL; AJ131032; CAB94753.1; JOINED.  
CC EMBL; AJ131033; CAB94753.1; JOINED.  
CC EMBL; AJ131034; CAB94753.1; JOINED.  
CC EMBL; AJ131035; CAB94753.1; JOINED.  
CC EMBL; AJ131036; CAB94753.1; JOINED.  
CC EMBL; AJ131037; CAB94753.1; JOINED.  
CC EMBL; AJ131038; CAB94753.1; JOINED.  
CC EMBL; AJ131039; CAB94753.1; JOINED.  
CC PIR; A59383; A59383.  
CC MEROPS; M01.011; -  
CC Genew; HGNC:6656; LNRP.  
CC MTM; 151300; -  
CC InterPro; IPR001930; Peptidase\_M1.  
CC InterPro; IPR006025; Pept\_M\_Zn\_BS.  
CC Pfam; PF01433; Peptidase\_M1; 1.  
CC PRINTS; PR00756; ALADIPTASE.  
CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
CC Alternative splicing; Aminopeptidase; Direct protein sequencing;  
CC Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Polymorphism;  
CC Protease; Signal-anchor; Transmembrane; Zinc.  
CC DOMAIN 1 110 Cytoplasmic (Potential).  
CC TRANSMEM 111 131 Signal-anchor for type II membrane  
CC protein (Potential).  
CC DOMAIN 132 1025 Extracellular (Potential).  
CC SITE 53 54 Dileucine internalization motif  
CC SITE 76 77 (Potential).  
CC SITE 76 77 Dileucine internalization motif  
CC (Potential).  
CC SITE 96 101 Tankyrase binding.  
CC SITE 154 155 Cleavage (in pregnancy serum form).  
CC METAL 464 464 Zinc (catalytic) (By similarity).  
CC ACT\_SITE 465 465 By similarity.  
CC METAL 468 468 Zinc (catalytic) (By similarity).  
CC METAL 487 487 Zinc (catalytic) (By similarity).  
CC CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 448 448 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 525 525 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 598 598 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 664 664 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 682 682 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 760 760 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 834 834 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 850 850 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 999 999 N-linked (GlcNAc...) (Potential)
FT VARSPLIC 1 14 Missing (in isoform 2).
FT VARSPLIC 1 19 /FTID=VSP_005448.
FT VARSPLIC 1 19 Missing (in isoform 3).
FT VARSPLIC 1 19 /FTID=VSP_005449.
FT VARIANT 763 763 A -> T (in dbSNP:2303138).
FT VARIANT 763 763 /FTID=VAR_012812.
FT CONFLICT 66 66 V -> D (in Ref. 2).
FT CONFLICT 386 386 N -> K (in Ref. 1).
FT CONFLICT 892 892 K -> Q (in Ref. 1).
FT CONFLICT 944 944 F -> L (in Ref. 1).
SQ SEQUENCE 1025 AA; 117318 MW; 0A2763F9CE62753A CRC64;

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## Alignment Scores:

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Pred. No.: 2,41e-125 Length: 1025
Score: 1999.00 Matches: 400
Percent Similarity: 61.81% Conservative: 160
Best Local Similarity: 44.15% Mismatches: 310
Query Match: 33.81% Indels: 36
DB: 1 Gaps: 6

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US-10-039-073-2 (1-3366) x LCAP\_HUMAN (1-1025)

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QY 305 CAGTAGCCACTAAATGGGAGCAATTCCTCGCAGGAGTAAAGCTCCCGAGTGTGTC 364
DB 153 PropheAlaThrAsnGlyLeuPheProIleAlaGlnIleArgLeuProThrAlaVal 172
QY 365 ATTCCTCTCCATATGACCTCTTTGCCACCCCAATCTCACCTCTCTGGAGTTGTGCA 424
DB 173 ValProLeuArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
QY 425 TCTGAGAGATCGAAGTCTTGTCAGCAATGTCACCCAGTTATCATCTTCGACAGCAAA 484
DB 193 SerValThrIleSerValGlnAlaLeuGlnValThrTrpAsnIleIleLeuHisSerThr 212
QY 485 GATCTTGAATCACCAGATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAACCA 544
DB 213 GlyHisAsnIleSerArgValThrPheMetSerAlaValSerSerGln----- 228
QY 545 GGAAGAAGAACTGAAAGTTTGTAGTTACCTGCTCATGAACAAATGCTGCTGTTCCA 604
DB 229 GluLysGlnAlaGluLeuGluTyrAlaTyrHisGlyGlnIleAlaIleValAlaPro 248
QY 605 GAGAACTTACGCTCCTCAGTGAATACATATGTGGCTATGAGCTTCCAGCCCAAGTTAGT 664
DB 249 GluAlaLeuLeuAlaGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer 268
QY 665 GATGCTTTGAGGGTTTATATAAAGCACATACAGAACTCTTGGTGGTGAACAGAAATT 724
DB 269 SerSerTyrTyrGlyPheTyrGlyPheSerTyrThrAspGluSerAsnGluLysTyr 288
QY 725 CTTGCAGTAACAGATTTTGTAGCCCAACCCAGGACGATGGCTTTCCCTTGTCTGTGATGAA 784
DB 289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
QY 785 CGGTGTTTCAAGCCCACTTTTCAATCAGATACGAGAGAGAGAGAGAGATATGCACTA 844
DB 309 ProAlaPheLeuAlaThrPheIleIleIleIleIleIleIleIleIleIleIleIleIle 328
QY 845 TCCAACTGCCCAAGGTTTAAGACAATTTGAACCTTGAAGGAGGTCTTTTGAAGATCACTTT 904
DB 329 SerAsnMetProLysSerSerValValLeuAspGlyLeuValGlnAspGluPhe 348

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QY 905 GAAACTACTGTAAATAAGTAGTACATACCTTGTAGCTTACATAGTTTGTGATTTCCACTCT 964
DB 349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetLysAsn 368
QY 965 CTGAGTGGCTTCACTTATCATCAGGGGTCAAGGTGCTCATCTATGATCCCGACAGAAACGG 1024
DB 369 LeuSerGln----AspValAsnGlyThrLeuValSerIleTyrAlaValProGluAsnIle 387
1025 AATCAAAACACATTAATGCTTTTCAGGCATCACTGAAGCTACTTGTATTTTATGAAAGTAC 1084
DB 388 GlyGlnValHisTyrAlaLeuGluThrThrValLysLeuLeuGluPhePheGlnAsnTyr 407
1085 TTTGATATCTACTATCACTCTCCAACTGATTAATTAATGCTATTCCTGACTTTCACCT 1144
DB 408 PheGluIleGlnTyrProLeuLysLeuAspLeuValAlaIleProAspPheGluAla 427
1145 GGAGCCATGGAAATTTGGGGCTCATATACATATAGGAGAGCTGACTCTTTTTCACCCC 1204
DB 428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspSer 447
1205 AAGACCTCTTCTGCTTCGATATAAAGTGTGGGTCCACAGAGTCATAGCCCATCACTGGCG 1264
DB 448 AsnThrSerSerMetAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
1265 CACCAGTGGTTTGGCAACCTGTCACAAATGGAATGGTGAATGATATTTGGCTTAAGAG 1324
DB 468 HisGlnTrpPheGlyAsnLeuValThrMetLysTrpTrpAsnAspLeuTrpLeuAsnGlu 487
1325 GGTTTTCCAAATACATGGAATTCCTGCTTAATGCTATCATATCCAGAGTCGAATTT 1384
DB 488 GlyPheAlaThrPheMetGluTyrPheSerLeuGluLysIlePheLysGluLeuSerSer 507
1385 GATGACTATTTTGAATGTGTGTTTGAAGTAATACAAAAGATTTCATTAATTCATCC 1444
DB 508 TyrGluAspPheLeuAspAlaArgPheLysThrMetLysLysAspSerLeuAsnSerSer 527
1445 CGCCTATCTCCAAACAGCGGAAACCCCGACTCAATATACAGGAAATTTTGTATGAAGTT 1504
DB 528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547
1505 TCCTATAACAGGAGCTTGTATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAA 1564
DB 548 SerTyrPheLysGlySerSerLeuLeuMetLeuLysThrTyrLeuSerGluAspVal 567
1565 TTCCAGAAAGAAATAATTTCAGTACTTAAAGAAAGTTTCAGTATAGAAATGCTAAGAAATGAT 1624
DB 568 PheGlnHisAlaValValLeuTyrLeuHisAsnHisSerTyrAlaSerIleGlnSerAsp 587
1625 GACTTGTGGAGCAGCTGTGTCAAATAGTGTGTTTGAAGAGTATTTTACATCTGGTGGAGTT 1684
DB 588 AspLeuTrpAspSerPheAsn----- 594
1685 TGTCAATTCGGATCCCAAGATGACAAGTAACATGCTCGCTTCTTCTGGGGGAAAAATGCACAG 1744
DB 595 -----GluValThrAsnGlnThrLeu-----Asp 602
1745 GTCAAGAGAGATGACTACATGCACTCTCCAGAAAGAAATCCCTGCTGCTGGTGTAAA 1804
DB 603 ValLysArgMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
1805 CAAGACGGGTGTTTCACTCCGACTCAACAGAGAGCGCTTCTCCAGGGGGTTCACAGAA 1864
DB 623 LysLysGlyLysGluLeuPheIleGlnGlnIleArgPhePheLeuAsnMet----- 639
1865 GACCTCAATGGAGGGCCCTGCAGGAGAGGTACTGTGGCATATCCCATGACCTACTCC 1924
DB 640 LysProGluIleGlnProSerAspThrSerTyrLeuTrpHisIleProLeuSerTyrVal 659
1925 ACAGATTTCTTCAATGTGATCCACAGACAC-----ATTCTTAAATCAAGACAGAT 1975
DB 660 ThrGluGlyArgAsnTyrSerLysTyrGlnSerValSerLeuLeuAspLysLysSerGly 679
1976 ACTCTGGATCTACCTGAAAAGACCAGTTGGGTGAAATTTTAAATGTGGACTCAATGGTTAC 2035

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RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AK040350; BAC30569.1; --

DR MGD; MGI:1933403; Art61.

DR GO; GO:0005737; C:cytoplasm; IDA.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.

DR GO; GO:0004239; F:methionyl aminopeptidase activity; IDA.

DR GO; GO:0004576; F:positive regulation of angiogenesis; IMP.

DR InterPro; IPR001930; Peptidase M1.

DR Pfam; PF01433; Peptidase M1; 1.

DR PRINTS; PR00756; ALADIPASE.

DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.

KW Aminopeptidase; Receptor.

FT NON TER 1

SQ SEQUENCE 694 AA; 80186 MW; B1EA3680BBC608B CRC64;

Alignment Scores:

Pred. No.: 1,318-117 Length: 694  
Score: 1883.00 Matches: 348  
Percent Similarity: 69.55% Conservative: 134  
Best Local Similarity: 50.22% Mismatches: 203  
Query Match: 31.85% Indels: 8  
DB: 2 Gaps: 3

US-10-039-073-2 (1-3366) x Q8C9W5 (1-694)

QY 938 GCCTACATAGTTTGTGATTTTCACCTCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGTG 997

DB 1 AlaPheIleIleSerAaspPheIysSerValSerIysMetThrIysSerGlyValIysVal 20

QY 998 TCCATCTATGATCCCGACAGAAACCGGAATCAAAACACATATATGCTTTGCGAGCATCACTG 1057

DB 21 SerValTyrAlaValProAaspIysIleAenGlnAlaAaspTyrAlaLeuAaspAlaAlaVal 40

QY 1058 AAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCTCCACTCTCCAACTGAT 1117

DB 41 ThrLeuLeuGluPheTyrGluAaspTyrPheAenIleProTyrProLeuProIysGlnAasp 60

QY 1118 TTAATGTGATTTCTGACTTTGACCTGGAGCGATCGAAATTTGGGGCTTCATTACATAT 1177

DB 61 LeuAlaAlaIleProAaspPheGlnSerGlyAlaMetGluAenTrpGlyLeuThrTyr 80

QY 1178 AGGAGAGCGTCACTGCTTTTGAACCCCAAGACCTCTTCTGCTTCGATAAACTGTGGTGC 1237

DB 81 ArgGluSerSerLeuTyrAaspIysGluIysSerSerAlaSerSerIysLeuGlyIle 100

QY 1238 ACCAGAGTCATAGCCCATGAACTGGCGCACCGAGTGGTTGGCAACTGGTGCATAGGAA 1297

DB 101 ThrMetIleValSerHieGluLeuAlaHieGlnTrpPheGlyAenLeuValThrMetGlu 120

QY 1298 TGGTGGAAATGATATTGGCTTAAGGAGGGTTTGCAAAATACATCGAACTTATCGCTGT 1357

DB 121 TrpTrpAenAaspLeuTrpLeuAenGluGlyPheAlaIysPheMetGluPheValSerVal 140

QY 1358 AATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTTGAAGTA 1417

DB 141 ThrValThrHieProGluLeuIysValGluAaspTyrPhePheGlyIysCysPheAenAla 160

QY 1418 ATTACAAAAGATTCATTGAAATTCATCCCGCTATCTCCAAACACGCGGAACCCCGACT 1477

DB 161 MetGluValAaspAlaLeuAenSerSerHieProValSerThrProValGluAenProAla 180

QY 1478 CAAATACAGGAATGTTGATGAAGTTTCCCTATAACAGGGAGCTTGTGATTTTGAATATG 1537

DB 181 GlnIleArgGluMetPheAaspValSerTyrGluIysGlyIysAlaCysIleLeuAenMet 200

QY 1538 CTCAGGATTTTCTCGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTAAAGAG 1597

DB 201 LeuArgAaspTyrLeuSerAlaAaspThrPheIysArgGlyIleValGlnTyrLeuGlnIys 220

QY 1598 TTCAGCTATAGAAATGCTAAGATCATGACTTGTGGACGAGTCTCTCAATAGTTGT--- 1654

DB 1598

DB 221 TyrSerTyrIysAenThrIysAenGluAaspLeuTrpAenSerMetMetHieIleCysPro 240

QY 1655 TTAGAAAGTGAATTTTACATCTGTTGGAGTTTGTTCATTTCCGATCCCAAGATCAAGATTAAC 1714

DB 241 ThrAaspGlyThrGlnThrMetAaspGlyPheCys---SerArgSerGlnHieSerSerSer 259

QY 1715 ATGCTCCGCTTCTGGGGGAAAATGCAGAGGTCAAGAGATGATGACTACATGAGTCTTC 1774

DB 260 ThrSerHieTrpArgGlnGluValAaspValIysThrMetMetAenThrTrpThrLeu 279

QY 1775 CAGAAAGGAATCCCGCTGCTGCTGTTTAAACAAGACGGGTCTTCACTCCGATCCCAACAG 1834

DB 280 GlnIysGlyPheProLeuIleThrIleThrValSerGlyArgAenValHieMetIysGln 299

QY 1835 GAGCGTTCCTCCAGGGGTTTCCAGAAAGACCCCTGAATGGAGGGCCCTCAGAGAGAGG 1894

DB 300 GluHieTyrMetIysGly-----SerGluArgPheProGluThrGly 313

QY 1895 TACCTGTGGCATATCCCATGACCTACTCCACGAGTCTTCTTAATGTGATCCACAGACAC 1954

DB 314 TyrLeuTrpHieValProLeuThrPheIleThrSerIysSerAaspSerValIleArgPhe 333

QY 1955 ATTCTAAATCAAGACACAGACTCTGATCTACTCTGAAAGACACAGTTGGTGAATTT 2014

DB 334 LeuLeuIysThrIysThrAaspValLeuLeuProGluAlaValGlnTrpIleIysPhe 353

QY 2015 AATGTGACTCAATGTTACTACATCTGTTACTATGAGGTCTATGAGTGGAGCAACTC 2074

DB 354 AenValGlyMetAenGlyTyrTyrIleValHieTyrAlaAaspAaspGlyTrpAlaSerLeu 373

QY 2075 ATTACACAGCTGATCAGAACACACACTTCTCAGACCTAAGGACAGTAGTCTGATT 2134

DB 374 SerGlyLeuLeuIysGlyAlaHieThrThrIleSerSerAenAaspArgAlaSerLeuIle 393

QY 2135 CATCATGTGTTTACGTAGTTGGTCAGGGAGACTGACCTTAGACAAAGCTCTTCACATG 2194

DB 394 AenAenAlaPheGlnLeuValSerIleGluIysLeuSerIleGluIysAlaLeuAaspLeu 413

QY 2195 ACTTACTACCTCCAAATGAAACAGCAGCGCCCGACCTTCTCGAAGGTCTGAGTTACTTG 2254

DB 414 ThrLeuTyrLeuIysAenGluThrGluIleMetProIlePheGlnAlaLeuAenGluLeu 433

QY 2255 GAATCGTTTACCACATGATGACAGAGAAAGATATTTTCAGATATCTCTGAAAACCTCAAG 2314

DB 434 IleProMetTyrIysLeuMetGluIysArgAaspMetIleGluValGluThrGlnPheIys 453

QY 2315 CGTTTACCTTCTCAGTATTTTAAGCCAGTGAATTCACAGGCAAGCTGGAGTGACAAAGGC 2374

DB 454 AspPheLeuLeuIysLeuLeuIysAaspLeuIleAaspIysGlnThrTrpThrAaspGluIy 473

QY 2375 TCAGTCTGGGACAGGATGCTCCGCTCTCTTGAAGCTGGCTGTGACCTGAACCAT 2434

DB 474 SerValSerGluArgMetLeuArgSerGlnLeuLeuLeuLeuAlaCysValArgAenTyr 493

QY 2435 GCTCCTTGATCCAGAAAGCTGCTGAATCTTCTCCAGTGGATGGATCCAGTGGAAAA 2494

DB 494 GlnProCysValGlnArgAlaGluArgTyrPheArgGluTrpIysSerSerAenGlyAen 513

QY 2495 TTAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACCAACAGCA 2554

DB 514 MetSerIleProIleAaspValThrLeuAlaValPheAlaValGlyAlaGlnAenThrGlu 533

QY 2555 GGATGGAATTAACCTTTTAGAGCAATATGAATGTCAATGTCAAGTGTGTAACAAACAAA 2614

DB 534 GlyTrpAaspPheLeuTyrSerIysTyrGlnSerSerLeuSerSerThrGluIysSerGln 553

QY 2615 ATTCTGTATGCTTTCACAGCAACATCAGAAAAGTTACTGAAGTTAATTAAGTAACTA 2674

DB 554 IleGluPheSerLeuCysThrSerIysAaspProGluIysLeuGlnTrpLeuLeuAaspGln 573

QY 2675 GGAATGCAAGAAAGTTATCAACACACAGAACTTGGCAGCTCTCTTCATGCGATGCC 2734

DB 574 SerPheIysGlyGluIleIleIysThrGlnGluPheProHieIleLeuLeuIleGly 593

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QY 2735 AGACGTCACAAAGGGCGAGCAACTAGCATGGGATTTTCTAAGAGAAAAATTCGACCCATCTT 2794
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 594 ArgAsnProValGlyTyrProLeuAlaTrpLysPheLeuArgGluAsnTrpAsnLysLeu 613
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2795 CTGAAAAAATTTGACTGGGCTCATATGACATAGGATGATCATCTCTGGCACACAGCT 2854
: : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 614 ValGlnLysPheGluLeuGlySerSerSerileAlaHisMetValMetGlyThrThrAsp 633
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2855 CACTTTTCTCCAGGATAAGTTCGAAGAGTGGAACATATTTTGAATCTCTTGAGGCT 2914
||||| : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 634 GlnPheSerThrArgAlaArgLeuGluValLysGlyPhePheSerSerLeuLysGlu 653
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2915 CAAGCATCACATCTGGATATTTTCAAACTGTTCTGGAAAGGATAACCAAAATATATAAA 2974
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 654 AsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGluAsnIleArg 673
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2975 TGGCTGGAGAGAATCTCCGACTCTGAGGACTTGGCTA 3013
||| : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 674 TrpMetAspLysAsnPheAspLysIleArgLeuTrpLeu 686
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
Q6PCG5 PRELIMINARY; PRT; 997 AA.
ID AC Q6PCG5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MG69084 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Splice;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSU=Splice;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSU=Splice;
RX Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC059334; AAHS9334.1; -;
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DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase.M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase.M1; 1.
DR PRINTS; PR00756; ALADIPPTASE.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 997 AA; 113619 MW; 460E0EC8B95D2A14 CRC64;

Alignment Scores:
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Score: 1853.50 Matches: 394
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Best Local Similarity: 39.76% Mismatches: 316
Query Match: 31.35% Indels: 105
DB: 2 Gaps: 19

US-10-039-073-2 (1-3366) x Q6PCG5 (1-997)
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QY 185 -----CNAATGTTTAAATTCACAGAGATTTTACTGCTTAAACAGGCATC 229
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Db 98 ArgAspGlyLeuCysProValSerSerProArgThrValIleValCysValValVal 117
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QY 230 TTGCCCAATATGCAATTTGTTCTCAGTCTCAGTGCCCTAGTATATCACTTACCTGAG 289
: : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 IleIleAlaValSerLeuValThrValValValValValValValValValValVal 137
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 290 GAT-----CCTGGGGCTTCCAGTAGCAGCTAATGGGAA 325
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Db 138 GluGlyCysHisGluLysLysAlaMetGluLeuValValValValValValValVal 157
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QY 326 CGATTTCTTGGCAGGAGCTTAAGCTCCCGAGTGGTGCTCATCTCTCCATTTATGACCTC 385
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Db 158 ValPheProTrpAlaIleSerArgLeuProAsnSerIleLysProIleHisTyrIleLeu 177
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QY 386 TTGTGTCACCCCAATCTCACTCTCGAGCTTTGTTGTCATCTCGAAGATCGAAGTCTTG 445
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Db 178 ThrLeuHisProAsnMetThrThrMetSerPheThrGlyThrValGlnIleAsnLeuAsn 197
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QY 446 GTCAGCAATGCTACCCAGTTTATCATCTGCACAGCAAGATCTTGAAATCAGCAATGCC 505
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Db 198 IleThalaArgSerLysAsnIleValLeuHisSerSerAspLeuArgIleThrLysAla 217
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QY 506 ACCCTTCAGTCAGAGGAATTCAGATATACGAAACCAGGA-----AAGAAGCTG 556
||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 AsnVal-----LeuValProGlyGlyThrThrMetAspAla 229
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QY 557 AAGTTTGTGATTACCTGCTCATGACAAATTCGCTGCTGCTCCAGAGAACTTACG 616
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Db 230 GluValLeuGluTyrProArgPheGluGluIleAlaIleSerProGluSerLeu--- 248
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QY 617 CTTCACTGAAATACTATATGCTGCTGAGCTTCCAGCCCAAGTTAGGTGATGGCTTTGAA 676
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Db 249 ProLysGlyAsnCysLeuLeuThrIleGluTyrThrSerAsnPheSerSerTyrTyr 268
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QY 677 GGGTTTTATAAAGCATACATACAGAACTCTTTGGTGGTGAACAAGAAATCTTCGCGTAACA 736
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Db 269 GlyPheTyrLysIleAspTyrMetAspLysGlySerLys---ArgSerLeuAlaIleThr 287
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QY 737 GATTTTGGCCCAACCCAGGCATCGCTTCCCTTGTCTTGTATGAAACCGTTGTTCAAA 796
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Db 288 GlnPheGluProThrAlaAlaArgLysAlaPheProCysPheAspGluProAlaPheLys 307
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QY 797 GCCAACTTTTCAATCAAG---ATACGAAGAGAGAGCAGGCGCATATTGCACTATCAACATG 853
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Db 308 SerThrPheGlnIleAsnIleIleArgLysAspGluSerMetIleSerLeuSerAsnMet 327
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QY 854 CCAAAGTTAAGACAATTTGAATTTGAAGGAGGTCTTTTGGAAAGATCACTTTGAAACTACT 913
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Db 328 ProLysAlaLysThrSerThrThrAsnAspGlyLeuLeuLeuAspGluPheSerThrSer 347  
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Db 348 ValLysMetSerThrTyrLeuValAlaPheIleValGlyAspIleLysAsnThrArg 367  
Qy 974 TTCACCTTCATCAGGGGTCAAGGTGCTCATCTATGCATCCCGACAGAACGGAAATCAACA 1033  
Db 368 GluThrAsnAspThrLeu---ValSerValTyrThrValProGluLysThrAspGlnVal 386  
Qy 1034 CATTATGCTTTCAGGACCTCACTGAAGCTACTTGTATTTTATGAAAGTACTTTCATATC 1093  
Db 387 LysTyrAlaLeuAspSerAlaValLysLeuLeuAspPheTyrSerAsnTyrTyrGlyIle 406  
Qy 1094 TACTATCCACTCTCCAACTCGATTAATGTCTATTCCTGACTTTGACCTCGAGCCATG 1153  
Db 407 LysTyrProLysLeuLysLeuAspLeuValAlaIleProAspPheGlnAlaAlaMet 426  
Qy 1154 GAAATTTGGGGCTCATATACATATAGGAGAGCTGCTACTGCTTTTGGACCCAGACTCT 1213  
Db 427 GluAsnTrpGlyLeuIleThrPheArgGluThrSerLeuLeuTyrAsnGluAspSerSer 446  
Qy 1214 TCTGCTTCCGATAAATCTGGGTACACAGAGTCATAGCCCATGAACTGGCGCACCAGTGG 1273  
Db 447 SerIleLysAspLysGlnThrIleAlaIleAlaIleGluLeuThrIleGlnTrp 466  
Qy 1274 TTTGGCAACTGGTCAATGAAATGGTGAATGATATTTGGCTTAAAGAGGGTTTGCAT 1333  
Db 467 PheGlyAsnLeuValThrMetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAla 486  
Qy 1334 AAATACATGAACTTATCCTCTTAATGCTACATATCCAGAGCTGCAATTTGATCACTAT 1393  
Db 487 ThrTyrMetGluTyrPheSerValSerSerLeuPheProGluLeuAsnSerGluAsnSer 506  
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Db 507 PheLeuLysMetArgPheMetAlaLeuLysLysAspSerLeuAsnAlaSerHisProIle 526  
Qy 1454 TCCAAACGACGGGAACCCGACTCAATACAGGAAATGTTTGAATGAAATTCCTATAAC 1513  
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Qy 1514 AAGGAGCTGTATTTGNAATGCTCAAGGATTTCTGGGTGAGGAGAAATTCAGAAA 1573  
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Qy 1574 GGAATAATTCAGTACTTAAAGAAAGTTCAGCTATAGAAATGCTAAGAAATGACTGTGG 1633  
Db 567 SerIleArgSerTyrLeuGlnSerHisGlnTyrGlySerThrThrSerAspSerLeuTrp 586  
Qy 1634 AGCAGCTGTCAATAGTTGTTTGAAGAGTGATTTTACATCTGGTGGAGTTTGTCAATTCG 1693  
Db 587 AspSerLeuAsn----- 590  
Qy 1694 GATCCCAAGATCACAAGTAAACATGCTCGCTTTCTGGGGGAAAATGACAGAGTCAAGAG 1753  
Db 591 -----ValValThrLysGluAsnProAsnValLysAsn 601  
Qy 1754 ATGATGACTACATGGACTCTCCAGAAAGGAATCCCGCTGCTGGTGTAAACAGACGGG 1813  
Db 602 MetMetLysThrTrpThrGlnLysAlaGlyTyrProLeuValThrAlaLeuArgLysGly 621  
Qy 1814 TGTTCACCTCCGACTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCCCTGAA 1873  
Db 622 GluGluIleThrValArgGlnGluArgPheLeuArgSerThr-----LysProAsp 638  
Qy 1874 TGGAGGGCCCTCGAGAGGTACTGCTGGGCATATCCCATTCACCTCCTCACAGTTCT 1933  
Db 639 ---HisAlaThrAsnAlaSerThrValTrpHisIleProLeuThrTyrValThrLysLys 657  
Qy 1934 TCTAATGTGATCCACAGA-----CACATTCTAAATCAAGACAGATACT 1978  
Db 658 CysAsnGlyValAspProAspCysAspLysValTyrLeuLeuLysAlaProThrGlyThr 677

Qy 1979 CTGATCTACCTACCTGAAAAGACACGATTTGGTGAATTTTAATGTGGACTCAAAATGGTTACTAC 2038  
Db 678 IleAsnValSerSerGluPheProTrpValLysPheAsnValAsnMetThrGlyTyrTyr 697  
Qy 2039 ATCGTTCACTATGAGGGTCATGGATGGGACCAACTCATTACACAGCTGAATCAGAACACAC 2098  
Db 698 IleValAspTyrGlyAlaAspGlyTrpAspAlaLeuIleGluIleUHIleArgAspHis 717  
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Db 738 ValGlyLysValProLeuAlaLysAlaPheLysLeuLeuGlyTyrLeuValAsnGluThr 757  
Qy 2219 AGCAGCCCGCAGCTTCTCGAAGGCTGAGTTACTTGGAACTCGTTTACCAC----- 2269  
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Qy 2270 ATGATGGACAGAGGAATATTTTCAGATATCTCTGAAAACCTCAAGCGTTACTCTTCAG 2329  
Db 775 IleLeuLeuLysArgGlyLeuAspAspLeuSerAspLysLeuMetGluArgGlyLeuAsp 794  
Qy 2330 TATTTTAAAGCAGTGATTCAGGCAAGCTGGAGTGACAAAGGCTCAGTCTGGGACAGG 2389  
Db 795 LeuLeuAsnAsnThrLeuIleLysGlnThrTrpLysAspGluGlyThrLeuAlaGluArg 814  
Qy 2390 ATGCTCCGCTCGGCTCTTCAAGCTGGCTGTCACCTGACCTGAACCATGCTCTTCGATCCAG 2449  
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Qy 2450 AAAGCTGCTGAACCTCTTCTCCAGTGGATGAAATCCAGTGGAAAATTAATATATACCAACA 2509  
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Qy 2570 TTAGAGCAATGAACTGTCATGCTCAAGTCTCAACAAACAAATTTCTGTATGCTTTG 2629  
Db 873 ArgArgArgTyrAspSerSerIleTyrGluSerGluLysSerLysIleLeuGluAlaLeu 892  
Qy 2630 TCAACGAGCAAGCACTCAGGAAAAGTTACTGAAGTTAATTAAGTACAGGAATGGAAGAAAG 2689  
Db 893 AlaSerThrAspAsnAlaLysAspLeuGlnGlyLeuMetGlnGluSerLeuAlaGlyGly 912  
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Db 913 SerIleArgSerGlnGluLeuProAsnValIleSerPheIleCysArgArgSerProGly 932  
Qy 2750 CAGCAACTAGCATGGGATTTTGAAGAAAATTTGGACCCCATCTCTGAAAATAATTTGAC 2809  
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Qy 2810 TTGGGCTCATATGACATAAGGATCATCTCTGGCACACAGCTCACTTT-----TCT 2863  
Db 952 -----LeuHisPhePheAsnSer 957  
Qy 2864 TCCAAGGATAGTTGCAAGAGGTGAAACTATTTTTTGAATCTCTTTGAGGCTCAAGGATCA 2923  
Db 958 ThrLysGluLysSerArgGluValTrpTyrValLysGluAla----- 971  
Qy 2924 CATCTGGATATTTTCAAACTGTTCTGAAAACGATTAACAAAATAATATAAATGCTCGAG 2983  
Db 972 -----LeuGluThrIleLysLeuAsnIleLysTrpMetLys 983  
Qy 2984 AAGAACTCTCCGACTCTGAGGACTTTGGCTAATG 3016  
Db 984 AsnAsnLeuAspSerLeuLysThrTrpLeuLeu 994

## RESULT 15

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ID Q8WVJ4 PRELIMINARY; PRT; 350 AA.
AC Q8WVJ4;2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DR 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LRAP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017927; AAH17927.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR PRINTS; PR00756; ALADIPTASE.
SQ SEQUENCE 350 AA; 40060 MW; 5234F40276A81253 CRC64;

Alignment Scores:
Pred. No.: 9.67e-105 Length: 350
Score: 1690.00 Matches: 322
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.08% Mismatches: 1
Query Match: 28.59% Indels: 0
DB: 2 Gaps: 0

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Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
Qy 206 GGATTTTACTGCTTAAACAGCCATCTGCCCCAATATGCAATTTGTTCTCAGTTCTCAGTG 265
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
Qy 266 CCATCTAGTTATCACTCACTGAGGATCCTGGGCTTTTCCAGTAGCCACTAATGGGGAA 325
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
Qy 326 CGATTTCTGGCAGGAGCTAAAGCTCCCGAGTGTGGTCAATTCCTCCCAATTAAGACCTC 385
Db 61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
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Qy 386 TTTGTCCACCCCAATCTCACCTCTCTGGAAGCTTTGTTGCAATCTGAGAGATCGAAGTCTTG 445
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Qy 446 GTCCAGCAATGCTACCCAGTTTATCATCTTTCACAGCAAAAGATCTTGAATACAGAAATGCC 505
Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
Qy 506 ACCCTTCAGTCAGGAGAAATTCAAGATACATGAAACCCAGGAAAAGAACTGAAAGTTTGTG 565
Db 121 ThrLeuGlnSerGluGluAspSerLysTyrMetLysProGlyLysGluLeuLysValLeu 140
Qy 566 AGTTACCTCGCTCATCAACAAATTCGCTGCTGTTCCAGAGAAACTTACGCTCCACTG 625
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Qy 626 AATATCTATGTGGCTATGGACTTCCAAAGCCAAAGTTAGGTGATGGCTTTGAAGGTTTAT 685
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
Qy 686 AAAGACATACAGAACTCTTGTGTGTGTAACAGAAATCTTCAGTAACAGATTTTGAG 745
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Qy 866 ACATTTGAATTCGAAGAGGCTTTTGGAGAGATCACTTTGAAACTACTGTAAAAATGAGT 925
Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
Qy 926 ACATACCTTTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA 985
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Qy 986 GGGGTCAAGGTGTCCATCTATGATGCCAGACAAAACGGAATCAACACACATTATGCTTTG 1045
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
Qy 1046 CAGGCATCACTGAGGACTCTGATTTTATGAAAGTACTTTGATATCTATCTACTATCCACTC 1105
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
Qy 1106 TCCAAAATCGGATTTA 1120
Db 321 SerLysLeuGlyMet 325

Search completed: September 26, 2005, 07:43:04
Job time : 634.604 secs
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PT target for diagnosis and treatment in aminopeptidase-related disorders  
PT and for identifying modulators of therapeutic use.

PS Claim 9; Fig 1; 92pp; English.

XX The invention relates to a novel human aminopeptidase, designated  
XX aminopeptidase 17867 (AAB60299) and to cDNA encoding aminopeptidase 17867  
CC (AAB27148). Human aminopeptidase 17867 contains a neutral zinc  
CC metalloproteinase zinc-binding region signature motif at residues 367-376,  
CC and an M1 aminopeptidase signature motif at residues 334-338. The  
CC invention also relates to host cells comprising human aminopeptidase  
CC 17867 DNA, the preparation of the protein, an antibody which binds to the  
CC protein, methods of detection of the protein, methods of modulating  
CC activity of the protein, and methods of identifying modulators of protein  
CC activity. Aminopeptidase 17867 proteins and nucleic acids are useful as  
CC targets for diagnosis and treatment in aminopeptidase-related diseases.  
CC Such diseases include a wide variety of lung disorders (e.g., pulmonary  
CC embolism, pulmonary hypertension, emphysema, bronchial asthma) and colon  
CC disorders (e.g., diarrhoea, dysentery, Crohn's disease, ulcerative  
CC colitis). In particular, they may be used in the diagnosis and treatment  
CC of breast and colon carcinoma, lung carcinoma (especially squamous cell  
CC carcinoma), and insulin-related disorders such as diabetes. The  
CC aminopeptidase 17867 proteins are also useful in drug screening methods  
CC to identify modulators of activity, and for raising antibodies for use in  
CC diagnosis and treatment. The present sequence represents human  
CC aminopeptidase 17867

XX Sequence 960 AA;

#### Alignment Scores:

Pred. No.:	0	Length:	960
Score:	5052.00	Matches:	960
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.45%	Indels:	0
DB:	4	Gaps:	0

US-10-039-073-2 (1-3366) x AAB60299 (1-960)

QY	146	ATGTTCCGATCTTCTGCAATGGTTAATTCACAGAAACCAATGTTAACTTCACAGA	205
DB	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
QY	206	GGATTTTACTGCTTAACAGCCATCTGCCCAATATATGCAATGCTTCTCAGTCTCAGTG	265
DB	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
QY	266	CCATCTAGTTATCACTTCACTGAGGATCCTGGGCTTTCCAGTAGCCACTTAATGGGGAA	325
DB	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	326	CGATTTCTCTCGCAGGAGCTAAGCTCCCAAGTGGTTCATCTCTCCATTATGACCTC	385
DB	61	ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu	80
QY	386	TTTGTCACCCCAATCTCACCTCTGAGCTTTGTCATCTCGAAGATCGAAGTCTTG	445
DB	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	446	CTCAGCAATGTAACCAAGTTTATCATCTTCACAGCAAAAGATCTTGAATCACAATGCC	505
DB	101	ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
QY	506	ACCTTCAGTCAGGAGGATTCAGATACATGAACCAAGCAAGAAAGTCTGCAAGTTTG	565
DB	121	ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140
QY	566	AGTTACCTGCTCATGAACAAATGCACTGCTGGTTCAGAGAACTTACCCCTCAGCTG	625
DB	141	SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160
QY	626	AAATACTATGTGGCTATGCACTTCAAGCCCAAGTTAGTGTGATGGCTTTGAAGGTTTAT	685

DB	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	686	AAAAGCACAATACAGAACTCTTGGTGGTGAACAAGAAATCTTGCAGTAACAGATTTTGAG	745
DB	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	746	CCAAACCCAGGACGACGATGGCTTCCCTTGTCTTGTGATGAACCGTTGTTCAAGGCCAACTTT	805
DB	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220
QY	806	TCAATCAAGATACAAAGAGAGACGACATATTCACACTATCCAAACATGCCAAAGGTTAAG	865
DB	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
QY	866	ACAATTCGAATTCAGGAGGCTCTTTGGAGATACACTTTGAAACTACTGTAAAAATCAGT	925
DB	241	ThrIleGluLeuGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260
QY	926	ACATACCTTGTAGCTACATAGTTTGTGATTTCACACTCTCTGAGTGGCTTCACTTCATCA	985
DB	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	986	GGGGTCAAGGTGTCCATCTATGCATCCCAACAAACGGAAATCAACACATATGCTTTG	1045
DB	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	1046	CAGGCATCACTGAGCTACTTGTGATTTTATGAAAGTACTTTTATATCTACTACTCCACTC	1105
DB	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
QY	1106	TCCAAACTCGATTAATTTGCTATCTCTGACCTTTCACCTCGAGCCATGGAATTTGGGC	1165
DB	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
QY	1166	CTCATCATATATAGGAGAGCTCACTGCTTTTGTGACCCCAAGACCTCTTCTGCTCCGAT	1225
DB	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
QY	1226	AAACTGGGTCCACAGGTCATAGCCCATGAACTGGCGCACCGAGTGGTTGGCAACTG	1285
DB	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
QY	1286	GTCAACAATGAATGGTGGATGATTTTGGCTTAAAGAGAGGTTTTCAAAATACATCGAA	1345
DB	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
QY	1346	CTTATCGCTGTTAATGCTACATATCCAGAGCTCCAAATTTGATGACTATTTTGAATGTG	1405
DB	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
QY	1406	TGTTTTGAAGTAATTAACAAGATTCATTAATTCATCCCGCCTATCTCCAAACCAAGCG	1465
DB	421	CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla	440
QY	1466	GAAACCCCGACTCAAAATACAGGAAATGTTTGTGATGAAGTTCCTATACCAAGGAGCTTG	1525
DB	441	GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
QY	1526	ATTTTGAATATGCTCAAGGATTTTTCGGGTGAGAGAAATTCAGAAAGGAATAATTCAG	1585
DB	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleIleGln	480
QY	1586	TACTTAAAGAGTTCAGCTATAGAAATGCTAAGAATGACTTGTGGAGCAGTCTCTCA	1645
DB	481	TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer	500
QY	1646	AATAGTTGTTAGAAAGTGAATTTTACATCTGTTGGTGGAGTTCATTCGGAATCCCAAGATG	1705
DB	501	AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet	520
QY	1706	ACAAGTAACTGCTCGCTTCTGGGGGAAATTCAGAGAGTCAAGAGATGATGACTACA	1765
DB	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	540

QY 1766 TGGACTCTCCAGAAAGGAATCCCTGCTGGTGGTTAAACAAGACGGGTGTTCACTCCGA 1825  
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560  
QY 1826 CTGCAACAGAGCGCTTCCTCCAGGGGGTTTTCCAGGAGACCCCTGATGGAGGCCCTG 1885  
Db 561 LeuGlnGlnLysGlyPheLeuGlnGlyValPheGlnGlnLysProGlnLysTrpArgAlaLeu 580  
QY 1886 CAGGAGAGGTACTCTGTGGCATATCCCATTTGACCTACTCCACAGATTTCTTAAATGTGATC 1945  
Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600  
QY 1946 CACAGACATTTCTAAATCAAGACAGATATCTGTGATCTACCTGAAAGACCAAGTTGG 2005  
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGlnLysThrSerTrp 620  
QY 2006 GTGAAATTAATGTGAGCTCAATGGTTACTACATCGTTCACTATGAGGGTCAATGATGG 2065  
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGlnGlyHisGlyTrp 640  
QY 2066 GACCACTCATTTACAGCTGAATCAGAACACACACACTTCTCAGACCTAAGGACAGATG 2125  
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
QY 2126 GGTCTGATTCATGATGTGTTTCAGCTAGTTGTGTGAGGAGACTGACCTTAGACAAAGCT 2185  
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
QY 2186 CTTGATCATGCTACTACTCTCAACATGAAACAGACAGCCCGCTCTTCCAGAGTCTG 2245  
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGlnThrSerSerProAlaLeuLeuGlnGlyLeu 700  
QY 2246 AGTTACTTGGAAATCGTTTACCATGATGAGGAGGAATATTTCAATATCTCTGAA 2305  
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720  
QY 2306 AACCTCAAGCGTTACTCTTCAGTATTTTAAAGCCAGTGATTCAGACGAAAGCTGGAGT 2365  
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
QY 2366 GACAGGGCTAGTCTGGACAGGATGCTCCGCTGGCTCTTGAAGCTGGCTGTGAC 2425  
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
QY 2426 CTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCCAGTGGATGGAATCC 2485  
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
QY 2486 AGTGAATAATTAATATACCAACAGATGTTTAAAGATTGCTATTTCTGTGGTCTCAG 2545  
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800  
QY 2546 ACAACAGCAGGATGAAATACCTTTTAGACCAATATGAATGCTCAATGTCAAGTCTGAA 2605  
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820  
QY 2606 CAAACAAATTTCTGTATCTGTTGTCACAGCAAGCATCAGAAAAAGTTACTGAAGTTA 2665  
Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGlnLysLeuLeuLysLeu 840  
QY 2666 ATTGAACATAGGAATGGAAGGATTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2725  
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis 860  
QY 2726 GCGATTGCCAGCTCCAAAGGGGCGAGCACTAGCATGGATTTTGTAAAGACAAATGG 2785  
Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
QY 2786 ACCCATCTTCTGAAAAATTTGACCTTGGGCTCATATGACATAAGATGATCATCTCTGCG 2845  
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900

QY 2846 ACAACAGCTCACTTTCTTCCAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2905  
Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920  
QY 2906 CTTGAGGCTCAAGATCACATCTGATATTTTCAAACCTGTTCTGGAACGATAACCAAA 2965  
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940  
QY 2966 AATATAAATCGCTCGGAGAAAGAACTTCTCCGACTCTGAGGACTTGGCTAATGGTTAATCT 3025  
Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960  
RESULT 2  
AAE04879  
ID AAE04879 standard; protein; 960 AA.  
XX  
AC AAE04879;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human protease protein-6 (PRTS-6).  
XX  
KW Human; protease protein-6; PRTS-6; cytostatic; hypotensive; gene therapy;  
KW gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;  
KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;  
KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;  
KW acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;  
KW developmental disorder; epithelial disorder; eczema; dementia; nontropic;  
KW neurological disorder; reproductive disorder; infertility; teratogenesis;  
KW immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;  
KW anaemia; antitumour; antiviral; antibacterial.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..35  
FT Protein /label= Signal\_peptide  
FT Binding-site /note= "Mature human PRTS-6"  
FT Binding-site 367..377  
FT Binding-site /label= Zinc\_binding\_region  
FT Binding-site 367..376  
FT Binding-site /label= Zinc\_binding\_region  
XX  
PN WO200146443-A2.  
XX  
PD 28-JUN-2001.  
XX  
PF 19-DEC-2000; 2000WO-US034811.  
XX  
PR 23-DEC-1999; 99US-0172055P.  
PR 21-JAN-2000; 2000US-0177334P.  
PR 28-JAN-2000; 2000US-0178884P.  
PR 02-FEB-2000; 2000US-0179903P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;  
PI Yue H, Nguyen DB, Tang YT, Yao MG, Lal P;  
XX  
DR WPI; 2001-418080/44.  
DR N-PSDB; AAD09543.  
XX  
PT Novel human protease proteins (PRTS) useful for diagnosing, treating,  
PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,  
PT cell proliferative disorders associated with abnormal expression of PRTS.  
XX  
PS Claim 1; Page 110-112; 129pp; English.  
XX  
CC The present sequence is human protease protein (PRTS-6). Human PRTS and  
CC its nucleic acid molecule are useful for the diagnosis, treatment and  
CC prevention of disorders associated with increased or decreased expression  
CC of PRTS. Examples of such disorders include, gastrointestinal disorder

CC such as anorexia, dysphagia; cardiovascular disorder such as  
 CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as  
 CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative  
 CC disorder such as acinic keratosis, cirrhosis; developmental disorder  
 CC such as epilepsy, anaemia; epithelial disorder such as allergic contact  
 CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,  
 CC dementia and reproductive disorder such as infertility and teratogenesis.  
 CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or  
 CC transgenic animals (mice or rats) to model human disease. PRTS DNA is  
 CC also in use for gene therapy. PRTS and its immunogenic fragments are  
 CC useful for screening libraries of compounds in several drug screening  
 CC assays. PRTS is useful for analysing the proteome of a tissue or cell  
 CC type

XX Sequence 960 AA;

Alignment Scores:  
 Pred. No.: 0 Length: 960  
 Score: 5052.00 Matches: 960  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 85.45% Indels: 0  
 DB: 4 Gaps: 0

US-10-039-073-2 (1-3366) x AAE04879 (1-960)

QY 146 ATGTTCCATTCTCTGCAATGTTAAATTCACACAGAAACCAATGTTTAAACATTCACAGA 205  
 DB 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20  
 QY 206 GGATTTTACTGCTTAACAGCCATCTTGCCCAATATGCAATTTGTTCTCAGTCTCAGTG 265  
 DB 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
 QY 266 CCATCTAGTTATCACTTCACAGAGCTCTGGGCTTCCAGTAGCCATTAATGGGGAA 325  
 DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
 QY 326 CGATTTCTCGCAGGAGTAAGCTCCCAAGTGTGGTCATCTCTCCATTATGACCTC 385  
 DB 61 ArgPheProThrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
 QY 386 TTGTGCCACCCCAATCTCACCTCTCTGGACTTTGTGTGCATCTGAGAGATCGAAGTCTTG 445  
 DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
 QY 446 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACCAATGCC 505  
 DB 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
 QY 506 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAATGAACCCAGGAAAGAACTGAAAGTTTGT 565  
 DB 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
 QY 566 AGTTACCTGCTCATGAACAAATTCGACTGCTGGTTCCAGAGAAACTTACGCCCTCACCTG 625  
 DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
 QY 626 AAATCTATGTGGCTATGGACTTCCAGCCCAAGTAGTAGTGGCTTGAAGGTTTAT 685  
 DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
 QY 686 AAAAGACATACAGAACTCTTGGTGGTGAACAAGAAATCTTTCAGTAACAGATTTTGTAG 745  
 DB 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200  
 QY 746 CCAACCCAGGACCGATGGCTTTCCCTTGTCTTTCATGAACCGTTGTTTCAAAGCCAACTTT 805  
 DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
 QY 806 TCATCAAGATACCAAGAGAGAGCAGGCATATTCGACTATCCACATGCCCAAGCTTAAG 865  
 DB 221 SerIleLysIleArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240

QY 866 ACAATTGAACCTTGAAAGAGGCTCTTTTGGAAAGATCACCTTTGAAACTACTGTAAAAATCAGT 925  
 DB 241 ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260  
 QY 926 ACATACCTCTAGCCTACATAGATTTTGTGATTTTCCACTCTCTGAGTGGCTTTCACATTCATCA 985  
 DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
 QY 986 GGGGTCAAGGTGTCCATCTATGATCCCCAGACAAACGGGAATCAAAACACATTAATGCTTTG 1045  
 DB 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
 QY 1046 CAGGCATCACTGAAGCTACTTGTATTTTATGAAAGTACTTTTGATATCTACTATCTCACTC 1105  
 DB 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
 QY 1106 TCCAAACTGGATTTAAATGCTATTCTCTGACTTTTGCACCTCGAGCCATGGAATAATTTGGGC 1165  
 DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
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 DB 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
 QY 1226 AAACTGTGGTCCACAGAGTCATAGCCCATGAACTGGCGCACAGTGGTTTGGCAACCTG 1285  
 DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
 QY 1286 GTCAAAATGGAATGGTGAATGATATTTGGCTTTAAGAGGGTTTGCAAAATACATGGAA 1345  
 DB 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400  
 QY 1346 CTTATCGCTGTTAATGCTACATATCCAGACTCGAATTTGATGACATATTTTGGTGAATGTG 1405  
 DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspTyrPheLeuAsnVal 420  
 QY 1406 TGTTTTGAAGTAATTAACAAAGATTCATTGAAATTCATCCCGCCCTATCTCCAAACACAGCG 1465  
 DB 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
 QY 1466 GAAACCCCGACTCAATACAGGAAATGTTTGTGATGAAGTTTCTTATACAAAGGGAGCTTGT 1525  
 DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
 QY 1526 ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATAATTCAG 1585  
 DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480  
 QY 1586 TACTTAAAGAAAGTTTCAGCTATAGAAATGCTAAGAATGATGACTTGTGGAGCAGTCTGTCA 1645  
 DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500  
 QY 1646 AATAGTTGTTTAGAAAGTATTTTATCTGTGTGGAGTTTGTTCATTCGGATCCCAAGATG 1705  
 DB 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520  
 QY 1706 ACAAGTAACATGCTCCCTTCTGGGGGAAATTCAGAGGTCAGAGGTCAGAGATGATGACTACA 1765  
 DB 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540  
 QY 1766 TGGACTCTCCAGAAAGAAATCCCTCTGCTGTGTGGTGTGTTTAAACAAAGACGGGTTCACCTCGA 1825  
 DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560  
 QY 1826 CTCGAACAGAGGCTTCTCTCCAGGGGGTTTTCAGAGAACCCCTGATAGAGGGCCCTG 1885  
 DB 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580  
 QY 1886 CAGGAGAGGTACCTGTGGCATATCCCACTTGCACCTACTCCACAGGTTCTTCTTAATGTATC 1945  
 DB 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600

QY 1946 CACAGACATCTTAAATCAAGACAGATACCTCGGATCTACCTGAAAGACCAAGTGG 2005  
Db |||||  
QY 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
Db |||||  
QY 2006 GTGAATTTAATGTGACATCAATGTTACTACATCGTTCTACTATGAGGTCATGATGG 2065  
Db |||||  
QY 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
Db |||||  
QY 2066 GACCAACTATTACACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAAGACAGATG 2125  
Db |||||  
QY 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
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QY 2126 GCTCTGATTCATGATGTTTTCAGCTAGTGTGTGAGGAGACTGACCTAGACAAAGCT 2185  
Db |||||  
QY 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
Db |||||  
QY 2186 CTTGACATGACTTACTTACCTCAACATGAACAGCAGCCCGCACTTCTCCAAAGTCTG 2245  
Db |||||  
QY 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProLysLeuGluGlyLeu 700  
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QY 2246 AGTTACTTGGAAATCGTTTACCACATGATGAGCAGAGGAATATTTCAGATATCTCGAA 2305  
Db |||||  
QY 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720  
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QY 2306 AACCTCAAGCGTTACTCTTTCAGTATTTTAAGCCAGTGTGACAGGCAAGCTGGAGT 2365  
Db |||||  
QY 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
Db |||||  
QY 2366 GACAAAGGCTCAGTCTGGACAGGATGCTCGGCTCTCTCAAGCTGGCCGTGAC 2425  
Db |||||  
QY 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
Db |||||  
QY 2426 CTGAACCATGCTCTTTCATCAGAAAGCTGTGTAACCTCTTCTCCAGTGAATGCAATCC 2485  
Db |||||  
QY 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
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QY 2486 AGTGAATAATTAATATACCAACAGATGTTTAAAGATGTGTATCTGTGGGTCTCAG 2545  
Db |||||  
QY 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800  
Db |||||  
QY 2546 ACAACAGCAGGATGAATTTACCTTTTACAGCAATATGAACCTCAATGTCAAGTCTCAA 2605  
Db |||||  
QY 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGlnTyrGluLeuSerMetSerSerAlaGlu 820  
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QY 2606 CAAACAAAATCTGTATGCTTTGTCAACGACGACATCAGAAAAGTTACTGAAGTTA 2665  
Db |||||  
QY 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu 840  
Db |||||  
QY 2666 ATTGAACCTAGGAATGAAGGAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2725  
Db |||||  
QY 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis 860  
Db |||||  
QY 2726 GCGATTGCCAGCTCCAAAGGGGCGACACTAGCATGGATTTTGTAAAGAAAATGG 2785  
Db |||||  
QY 861 AlaIleAlaArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
Db |||||  
QY 2786 ACCCATCTTCTCAAAAATTTTCACTTGGCTCATATGACATGAAGATGATCATCTCTGGC 2845  
Db |||||  
QY 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900  
Db |||||  
QY 2846 ACAACAGCTCACTTTTCTTCCAGGATAGTTGCAAGGGTGAACACTATTTTTTGAATCT 2905  
Db |||||  
QY 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920  
Db |||||  
QY 2906 CTTGAGGCTCAGGATCAGATCTGATATTTTCAAACTGTCTCGAAACCATACCAA 2965  
Db |||||  
QY 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940  
Db |||||  
QY 2966 AATATAAATGCTGAGAGGAATCTTCCGACTCTCAGGACTTGGCTGAATGTTAATACT 3025  
Db |||||  
QY 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960  
Db |||||

ABP69122  
ID ABP69122 standard; protein; 960 AA.  
XX  
AC ABP69122;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1169.  
XX  
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
KW arthritis; cytostatic; immunomodulator; neurotic; dermatological;  
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
KW antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN WO200270539-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US005095.  
XX  
PR 05-MAR-2001; 2001US-00799451.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
PI Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
DR WPI: 2002-759812/82.  
DR N-PSDB; ABZ11339.  
XX  
PT New polynucleotides comprising sequences assembled from expressed  
PT sequence tags (SSTs), useful for treating cell-proliferative,  
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
PT or coagulation disorders.  
XX  
PS Claim 9; SEQ ID NO 1169; 1012pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated polynucleotide (I) comprising a  
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-  
CC ABZ12066) or their mature protein coding portion, active domain coding  
CC protein or complementary sequences. The polynucleotides are useful for  
CC identifying expressed genes or for physical mapping of human genome. The  
CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight  
CC markers, as a food supplement, for generating antibodies, in medical  
CC imaging, screening and diagnostic assays and for treating cell-  
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
CC arthritis, etc. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 960 AA;  
  
Alignment Scores:  
Pred. No.: 0 Length: 960  
Score: 5048.00 Matches: 959  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.90% Mismatches: 0  
Query Match: 85.39% Indels: 0  
DB: 5 Gaps: 0  
  
US-10-039-073-2 (1-3366) x ABP69122 (1-960)

QY 146 ATGTTCCATTCTTCTGCAATGGTTAAATTCACACAGAAAAACCAATGTTTAAACATTCACAGA 205  
Db |||||  
1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20  
QY 206 GGATTTTACTGCTTAAACAGCCATCTTGCGCCCAAAATATGCATTTGTTCTCAGTTCTCAGTG 265  
Db |||||  
21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
QY 266 CCATCTAGTTATCACTTCACTGAGGATCCTGGGGCTTTCCAGTAGCCACCTAAATGGGGAA 325  
Db |||||  
41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaIleAsnGlyGlu 60  
QY 326 CGATTTCTTGGCAGGAGCTAAGGCTCCCGAGTGGTGTCATTCCTCTCCATTAATGACCTC 385  
Db |||||  
61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
QY 386 TTTGTCCACCCCAATCTCACCTCTCTGACCTTGTGTCATCTGAGAAGATCGAAGTCTTG 445  
Db |||||  
81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
QY 446 GTCAGCAATGTACCAGTCTTATCATCTTGACAGCAAAAGATCTTGAATCACCAATGCC 505  
Db |||||  
101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
QY 506 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAAACAGGAAAAGAACTGAAGTTTG 565  
Db |||||  
121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
QY 566 AGTTACCTGCTCATGAACAAATTGCACCTGCTGGTTCAGAGAAACTTTACCCCTCACCTG 625  
Db |||||  
141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
QY 626 AAATACTATGTGGCTATGCACTTCCAGCCCAAGTTAGGTGATGGCTTTGAAGGGTTTTAT 685  
Db |||||  
161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
QY 686 AAAAGCACATACAGAACTCTTGGTGGTGAACAAGAAATCTTGCAGTAACAGATTTTGAG 745  
Db |||||  
181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200  
QY 746 CCAACCCAGGACCGATGGCTTCCCTTGGCTTTGATGNAACCGTTGTTCAAGCCCACTTT 805  
Db |||||  
201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
QY 806 TCAATCAAGATACGAAGAGAGACGAGCATATTGCACCTATCAACATGCCAAAGGTTAAG 865  
Db |||||  
221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
QY 866 ACAATTGAACCTGAAGGAGGTCTTTTGAAGATCACTTTGAAACTACTGTAAAAATGAGT 925  
Db |||||  
241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260  
QY 926 ACATACCTTTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA 985  
Db |||||  
261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
QY 986 GGGGTCAAGGTGTCATCTATGTCATCCCGACAGCAAAACGGAATCAAAACATTAATGCTTTG 1045  
Db |||||  
281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
QY 1046 CAGGCATCACTGAAGCTACTTGAATTTTATGAAAGTACTTTTGATATCTACTATCCACTC 1105  
Db |||||  
301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
QY 1106 TCCAAACTGGATTAAATTGCTATTCTTCGACTTTGCACTGAGCCATGGAGCCATGGAAAATTGGGC 1165  
Db |||||  
321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
QY 1166 CTCATTACATATAGGAGACGCTCACTGCTTTTGCACCCCAAGACCTCTTCTGCTTCGAT 1225  
Db |||||  
341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
QY 1226 AAACGTGGGTCAACAGAGTCATAGCCCATGAACTGGCGCACCAAGTGGTTTGGCAACCTG 1285

Db |||||  
361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
QY 1286 GTCACATGGAATGGTGGAAATGATATTGGCTTAAGGAGGGTTTTGCAAAATACATCGAA 1345  
Db |||||  
381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400  
QY 1346 CTTATCCCTGTTAATGTCATACATATCAGAGCTGCAATTTTGATGACTATTTTTCGAATGTG 1405  
Db |||||  
401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspPhePheLeuAsnVal 420  
QY 1406 TGTTTGAAGTAATTACAAAAGATTCAATGAATTCAATCCCGCCCTATCTCAAACACAGCG 1465  
Db |||||  
421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
QY 1466 GAAACCCCGACTCAATACACAGGAAATGTTTGTGATGAAGTTTCCCTATACAAAGGAGCTTGT 1525  
Db |||||  
441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
QY 1526 ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGAGAAAATTCAGAAAAGGAATAAATTCAG 1585  
Db |||||  
461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480  
QY 1586 TACTTAAAGAGTTCACTATAGAAATGCTAAGAATGATGACTTGTGGAGCAGTCTGTCA 1645  
Db |||||  
481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer 500  
QY 1646 AATAGTTGTTTACAAAAGTGAATTTTACATCTGTTGGAGTTTGTTCATTCGGATCCCAAGATG 1705  
Db |||||  
501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520  
QY 1706 ACAAGTAAACATGCTCGCCTTTCTGGGGGAAAATTCAGAGAGTCAAGAGATGATGACTACA 1765  
Db |||||  
521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540  
QY 1766 TGGACTCTCCAGAAAGAAATCCCTCTGCTGGTGGTTAAACAAGACGGGTGTTCACTCCGA 1825  
Db |||||  
541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560  
QY 1826 CTCACACAGGAGCGCTTCTCCAGGGGGTTTCCAGGAAGACCTGTAATGAGGGCCCTG 1885  
Db |||||  
561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluLysThrSerTrp 580  
QY 1886 CAGGAGAGGTACCTGTGGCATATCCCAATGACCTACTCCACGAGTCTTCTTAATGTATC 1945  
Db |||||  
581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600  
QY 1946 CACAGACACATCTCTAAATCAAAAGACAGATACTCTGGATCTACTGAAAAGACCAAGTTGG 2005  
Db |||||  
601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
QY 2006 GTGAAATTTAATGTGGACTCAAATGGTTTACTACATCTTCCACTATGAGGGTTCATGGATGG 2065  
Db |||||  
621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
QY 2066 GACCAACTCAATTACACAGCTGAAATCAGAACACACACTTCTCAGACCTTAAGGACAGAGTA 2125  
Db |||||  
641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
QY 2126 GGTCTGATTCATGATGTGTTTCAGCTAGTTGGTGCAGGGAGACGTGACCCCTAGACAAAGCT 2185  
Db |||||  
661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
QY 2186 CTTTGACATGACTTACTACCTCCCAACATGAAACAGCAGCCCGCACCTTCTCGAAGGTCTG 2245  
Db |||||  
681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700  
QY 2246 AGTTACTTGGAACTCGTTTACCACATGATGACAGAGGAATATTTTCAGATATCTCTGAA 2305  
Db |||||  
701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720  
QY 2306 AACCTCAAGGTTACCTTCTTCTAGTATTTTAAAGCCAGTGATTGACAGGCAAGCTGAGT 2365  
Db |||||

Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
QY 2366 GACAGGGCTCAGTCGGACAGGATGCTCCGCTCTCTTGAAGCTGGCTGTGAC 2425  
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
QY 2426 CTGAACCATGCTCTTGGATCCAGAAAGTGTGAACTCTTCCAGTGGATGAATCC 2485  
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
QY 2486 AGTGGAAAATAAATATACCAACAGATGTTTTAAAGATTGTCTATTCTGTGGTCTCAG 2545  
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTrpSerValGlyAlaGln 800  
QY 2546 ACAACAGCAGGATGGAATTTACCTTTTAGACCAATATGAACCTGCAATGTCAAGTCTGAA 2605  
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGlnTyrGluLeuSerMetSerSerAlaGlu 820  
QY 2606 CAAACAAAATCTGTATGCTTTGTCAACGACCAAGCATCAGGAAAAAGTTACTGAAGTTA 2665  
Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu 840  
QY 2666 ATTGAACCTAGGAATGGAAGAAAGTTATCAAGACACAGAACTTGCAGCTCTCTTCAT 2725  
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860  
QY 2726 GCGATTGCGCAGCTGCAAGGGGAGCAACTAGCATGGGATTTTGTAAAGAGAAATGG 2785  
Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
QY 2786 ACCCATCTCTGAAAAATTTGACTTGGCTGATATGATGATGATGATGATGATGATGATGAT 2845  
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900  
QY 2846 ACAACAGCTCAGTTTCTTCCAGGATAGTTGCAAGAGGTGAAGTAACTATTTTGAATCT 2905  
Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920  
QY 2906 CTTGAGGCTCAAGGATCAGATCTGGATATTTTCAAACTGTTCTGGAAACGATACCAAA 2965  
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940  
QY 2966 AATATAAATGCTGAGAGAAATCTTCGACTCTGAGACTGAGACTGAGCTTAATTAATCT 3025  
Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960  
RESULT 4  
ID ABP63022 standard; protein; 785 AA.  
XX  
AC ABP63022;  
XX  
DT 14-OCT-2002 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 459.  
XX  
KW Human; vulnery; dermatological; neuroprotective; nootropic; cancer;  
KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;  
KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;  
KW burn; central nervous system disorder; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; immune disorder;  
KW autoimmune disorder; multiple sclerosis; diabetes; allergy.  
XX  
OS Homo sapiens.  
XX  
PN WO200218424-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 31-AUG-2001; 2001WO-US027093.  
XX  
PR 01-SEP-2000; 2000US-00654935.  
XX

(HYSE-) HYSEQ INC.  
Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
Zhao Qa, Wang D, Liu C, Drmanac RT, Wehrman T;  
WPI, 2002-583321/62.  
N-PSDB; ABQ93501.  
New polynucleotide and polypeptides, useful for treatment and diagnosis  
of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral  
sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple  
sclerosis, diabetes and allergies.  
Claim 20; SEQ ID NO 459; 284pp + Sequence Listing; English.  
The invention relates to an isolated polynucleotide (I) comprising one of  
245 sequences (ABQ93288-ABQ93532). Treating a condition comprising  
administering to a mammalian subject a composition comprising the protein  
(II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).  
(I), (II) and (III) are useful for gene therapy of diseases and (II) can be used for  
therapeutic treatment. Diseases that may be treated include wound healing  
and tissue repair, burns, central nervous system disorders (e.g.  
Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral  
sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple  
sclerosis, diabetes and allergies. Note: The sequence data for this  
patent did not form part of the printed specification, but was obtained  
in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 785 AA;  
SQ  
Alignment Scores:  
Pred. No.: 0 Length: 785  
Score: 4141.00 Matches: 782  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 2  
Query Match: 70.04% Indels: 0  
DB: 5 Gaps: 0  
US-10-039-073-2 (1-3366) x ABP63022 (1-785)  
QY 146 ATGTTCCATTCTTCTGCAATGGTTAATTCACAGAAAACCAATGTTTAACTTCACAGA 205  
Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20  
QY 206 GGATTTTACTGCTTAACAGCCATCTGCCCAATATGCTTCTCTCTCTCTCTCTCTCTCTCT 265  
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
QY 266 CCATCTAGTTATCACTTCACTGAGGATCTCTGGGCTTTCCAGTAGCCACTTAATGGGAA 325  
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
QY 326 CGATTTCTTGGCAGGAGCTTAAGCTCCCGAGTGTGTCATCTCTCCATATGACCTC 385  
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
QY 386 TTTGTCACCCCATCTCAGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 445  
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
QY 446 GTACGAATGCTACCCAGTTTATCATCTTGCACAGCAAAAGATCTTGAATCAGCAATGCC 505  
Db 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
QY 506 ACCCTTCAGTCAGGAGGATTCAGATACATGAACACAGAGAAAGAAAGTGTGTTG 565  
Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
QY 566 AGTTACCTCTCATGAACAAATTCAGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 625  
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160

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Qy 626 AAATACTATGTGGCTATGGAATTCACAGCCCAAGTTAGTGATGGCTTTGAAGGGCTTTTAT 685
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
Qy 686 AAAAGCACAATCAGAACTCTTGGTGGTGAACAAGAATCTTGGAGTAACAAGATTTTGAG 745
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
Qy 746 CCACCCAGGCACCATGGCTTCCCTTGGCTTTCATGNAACCGTTTTCAAAGCCCAACTTT 805
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
Qy 806 TCAATCAAGATACGAAGAGAGAGCAGGCATATTGCACATATCAACATGCGCCAAAGGTTAAG 865
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
Qy 866 ACAATTGAACCTGAAGAGGCTCTTTTGAAGATCACCTTTGAAACTACTGTAAAATAGT 925
Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
Qy 926 ACATACCTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACATCATCA 985
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
Qy 986 GGGGTCAAGGTGTCCATCTATGCATCCCGACACAAACGGAATCAAAACACATTATGCTTTG 1045
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
Qy 1046 CAGGCATCACTGAAGCTACTGATTTTATGAAAGTACTTTGTATATCTACTATCCACTC 1105
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
Qy 1106 TCCAACTGGGATTAATTGCTATTCCTGACTTCACCTGAGCGCATCGAAAATTGGGGC 1165
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
Qy 1166 CTCATTACATATAGGAGACGCTACTGCTTTTTCACCCCAAGAGCTCTCTCTGCTTCGGAT 1225
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
Qy 1226 AAATGTGGGTCAACAGAGTCATAGCCCATGAACCTGCGGACCAAGTGTTTGGCAACTG 1285
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
Qy 1286 GTCACAAATGGAATGCTGAATGATATTTGGCTTAAGAGGGCTTTGCAAAATACATCGAA 1345
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400
Qy 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTTCGAATGTG 1405
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
Qy 1406 TGTTTTGAAGTAATTAACAAAGATTCATTGAATTCATCCCGCCCTATCTCCCAACACGCG 1465
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
Qy 1466 GAAACCCCGACTCAAAATACAGAAATGTTTCATGAAGTTTCCTTAACAGGGAGCTTGT 1525
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
Qy 1526 ATTTTGAATATGCTCAAGGATTTTCTGGTGAGGAGAAATTCAGAAAGGAATTAATTCAG 1585
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln 480
Qy 1586 TACTTAAAGAAGTTCAGCTATAGAAATCTGAAGATGATGACTTGTGAGCAGTCTGTCA 1645
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaAsnAsnAspAspLeuTrpSerSerLeuSer 500
Qy 1646 AATAGTCTTTAGAAAGTGATTTTACATCTCGTGGAGTTTCTCATTCGGATCCCAAGATG 1705
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520
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Qy 1706 ACAAGTAACATGCTCGCTTTTCTGGGGAAAAATCGAGGTCRAAGAGATGATGACTACA 1765
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540
Qy 1766 TGGACTCTCCAGAAAAGAAATCCCCCTGCTGCTGGTGGTTAAACAAGACGGGTGTTCTCCGA 1825
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560
Qy 1826 CTSCAACAGGAGCGCTTCCCTCCAGGGGTTTTCAGGAAGACCCCTGAATCGAGGCCCTG 1885
Db 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
Qy 1886 CAGGAGAGTACCTGTGGCATATCCCATTGACCTACTCCACGAGTCTTCTTAATGTGATC 1945
Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600
Qy 1946 CACAGACACATTTCAAAATCAAAAGACAGATACCTCTGATCTACTGAAAGACAGTTGG 2005
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
Qy 2006 GTCAAAATTAATGTGGACTCAAAATGGTTACTACATCGTTCCACTATGAGGGTTCATGATGG 2065
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KW Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; inflammation.
XX
OS Homo sapiens.
XX
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XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
PI

XX WPI; 2001-476161/51.  
DR N-PSDB; ABA06560.  
XX Isolated nucleic acid molecule encoding an inflammation-associated  
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PT condition.  
XX  
PS Claim 11; SEQ ID NO 646; 859pp + Sequence Listing; English.  
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CC The present invention provides human cDNAs, proteins and related genomic  
CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence  
CC is a protein of the invention  
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PR	01-SEP-2000;	2000US-0229344P.		PR	17-NOV-2000;	2000US-0249214P.



Db	381	SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisIleTyrGluGlyHis	400
Qy	2060	GGATGGGACCAACTCATTTACACAGCTGAATCAGAACCAACACACATCTCTCAGACCTCAAGGAC	2119
Db	401	GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuAspGProLysAsp	420
Qy	2120	AGATGAGTCTGATTCATGATGTGTTCACGTAGTGTGGTCAGGGAGACGTGACCCCTAGAC	2179
Db	421	ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	440
Qy	2180	AAAGCTCTTGACATGACTTACTACCTCCACATGAAACAGACGCCCGGCATCTCTCGAA	2239
Db	441	LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	460
Qy	2240	GGTCTGAGTTACTTTGGAAATCGTTTTACCACATGATGCACAGAAGCAATATTTTCAGATATC	2299
Db	461	GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle	480
Qy	2300	TCTGAAACCTCAAGCGTTACCTTCTTCAGTATTTTAAGCCAGTGTGACAGCAAAAGC	2359
Db	481	SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer	500
Qy	2360	TGGAGTGACAAGGGCTCAGTCTGGGACAGGATGCTCGCTCGGCTCTCTTGAAGCTGGCC	2419
Db	501	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	520
Qy	2420	TGTCACCTGAACCATGCTCCTTGTCATCCAGAAAGCTGCTGAACCTCTCTCCAGTGGATG	2479
Db	521	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	540
Qy	2480	GAATCCAGTGGAAATTAATATATACCAACAGATGTTTTAAAGATGTGTGTATCTGTGGGT	2539
Db	541	GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly	560
Qy	2540	GCTCAGACAACAGCAGGATGAATTACCTTTTAGAGCAATATGAACCTGTCAATGTCAAGT	2599
Db	561	AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer	580
Qy	2600	GCTCAACCAACAAATCTGTATGCTTTGTCAACGAGCAGCATCAGGAAAAGTTACTG	2659
Db	581	AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	600
Qy	2660	AAGTAAATGAACTAGGAATGGAAAGAAAGTTATCAAGACACAGAACTTTGGCAGCTCTC	2719
Db	601	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeu	620
Qy	2720	CTTCATGCGATGTCAGACGTCCTCAAGGGGCGACCACTAGCATGGGATTTGTGAAGAA	2779
Db	621	LeuHisAlaIleAlaArgGProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	640
Qy	2780	AATTTGGACCCATCTCTGAAAAAATTTGACTTGGGCTCATATGCATTAAGATGATCATC	2839
Db	641	AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle	660
Qy	2840	TCTGGCACAAACAGCTCACTTTCTTCAAGGATAAGTTGCAAGAGTGAAACTATTTTTT	2899
Db	661	SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnLysLeuPhePhe	680
Qy	2900	GAATCTCTTGAGGCTCAAGGATCATCTCGATATTTTTTCAAACTGTTCTGGAAACGATA	2959
Db	681	GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle	700
Qy	2960	ACGAAAAATATAAATGGCTGGAGAGAATCTTCCGACTCTGAGGACTTGGCTTAATGGTT	3019
Db	701	ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu*****	720
Qy	3020	AATACT 3025	
Db	721	***Thr 722	

RESULT 8  
ABB10511

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PR 14-SEP-2000; 2000US-0233064P.  
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PR 08-NOV-2000; 2000US-0246609P.  
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PR 17-NOV-2000; 2000US-0249207P.  
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PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 03-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-476161/51.  
DR N-PSDB; ABA06733.  
XX  
XX Isolated nucleic acid molecule encoding an inflammation-associated  
PT polypeptide is used in preventing, treating or ameliorating a medical  
PT condition.  
XX  
XX Claim 11; SEQ ID NO 819; 859pp + Sequence Listing; English.  
PS  
XX The present invention provides human cDNAs, proteins and related genomic  
CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence  
CC is a protein of the invention  
XX  
SQ Sequence 722 AA;  
  
Alignment Scores:  
Pred. No.: 0 Length: 722  
Score: 3770.00 Matches: 717  
Percent Similarity: 99.31% Conservative: 0  
Best Local Similarity: 99.31% Mismatches: 5  
Query Match: 63.77% Indels: 0  
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Qy 860 GTTAAGACAACTTGAAGGAGGTCTTTTGAAGATCACCTTTGAACTACTGTAAAA 919  
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Qy 920 ATGAGTACATACCTTGTAGCCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCACT 979  
Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40  
  
Qy 980 TCATCAGGGTCAAGGTGTCCTATGCATCCCGACAAACGGAATCAACACATTAT 1039  
Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisLysr 60  
  
Qy 1040 GCTTTGCAGGCATCACTGAAGCTACTTGATTTTATGAAAGTACTTTGATATCTACTAT 1099  
Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80  
  
Qy 1100 CCACTCTCCAAACTGGATTAAATTGCTATTCTGACTTTTCGACTGGAGCCATGGAAAAAT 1159  
Db 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100  
  
Qy 1160 TGGGGCTCATATACATAGGGAGAGCTCACTGCTCTTTTGGCCCCAGACCTCTTCTGCT 1219  
Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120  
  
Qy 1220 TCCGATAAACTGTGGGTCCACAGAGTCATAGCCCATGAACTGGCGACCACTGTTTGGC 1279  
Db 121 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140  
  
Qy 1280 AACCTGTCACATGGAGTGGTGGATGATATTGGCTTAAGAGGGTTTGGAAAATAC 1339  
Db 1280 AACCTGTCACATGGAGTGGTGGATGATATTGGCTTAAGAGGGTTTGGAAAATAC 1339

Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160  
QY 1340 ATGGAACTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTTTG 1399  
Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180  
QY 1400 AATGCTGTTTTGAAGTAATACAAAGATTCATTGAATTCATCCGGCCCTATCTCCAAA 1459  
Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200  
QY 1460 CCAGCGGAAACCCGACTCAAAATACAGGAAATGTTTGAATGAAGTTTCTTATAACAAGGA 1519  
Db 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220  
QY 1520 GCTTGATTTTCAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATCCAGAAAGGAATA 1579  
Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGlyPhe\*\*LysGlyIle 240  
QY 1580 ATTCACTACTTAAAGATTTCAGCTATAGAAATGCTAAGATGATGACTTGTGGAGCAGT 1639  
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QY 1640 CTGTCAAAATAGTTGTTTGAAGATGATTTTACATCTGGTGGAGTTTGTTCATTCGGATCCC 1699  
Db 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspPro 280  
QY 1700 AAGATGACAAAGTAACATGCTCCCTTTCTGGGGGAAATGCAAGAGTCAAAAGAGATGATG 1759  
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QY 1760 ACTACATGACTCTCAGAAAGAAATCCCTGCTGGTGGTTAAACAAGACGGGTGTTC 1819  
Db 301 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSer 320  
QY 1820 CTCCTGCTCAACAGAGCGCTTCTCCAGGGGTTTTCCAGAGAGCCCTGAATGGAGG 1879  
Db 321 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340  
QY 1880 GCCCTGCAAGGAGGTACCTGTGGCATATCCCATTTGACCTATCCACGAGTTCTTCTAAT 1939  
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QY 1940 GTGATCCACAGACATTTCTAAATCAAGACAGATACCTCTGGATCTACCTGAAAGACC 1999  
Db 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380  
QY 2000 AGTTCGGTGAAATTTAATGTGACTCAAAATGTTACTACATCGTTCACTATGAGGGTCAT 2059  
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QY 2060 GGATGGGACCAACTCATTACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAGGAC 2119  
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Db 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 460  
QY 2240 GGTCTGAGTTACTTGAATCGTTTTTACCACATGATGGAGCAAGGAATATTTTCAGATATC 2299  
Db 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle 480  
QY 2300 TCTGAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAAGCCAGTGAATGACAGGCAAGC 2359  
Db 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500  
QY 2360 TGGAGTGCAAGGGCTCAGCTGGGACAGGATGCTCCGCTCGCTCTCTGAAGCTGGCC 2419  
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QY 2420 TGTCACTGAACCAATGCTCTTGGCATCCAGAAAGCTGCTGAACCTTCTCCAGTGGATG 2479  
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540  
QY 2480 GAATCCAGTGAAATTAATAATATACCAACAGATCTTTTAAAGATTGCTATTCTGTGGGT 2539  
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QY 2600 GCTCAACAAACAAATTTCTGATCTTGTTCACGAGCAAGCATCAGAAAAAGTTACTG 2659  
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QY 2720 CTTTCATCGATTGTCAGACGCTCCAAAGGGGAGCAACTAGCATGGGATTTTGTAAAGAA 2779  
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QY 2780 AATTGGACCCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATC 2839  
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660  
QY 2840 TCTGGCCACAGCAGCTCACTTTCTCCAGGATTAAGTTGCAAGAGGTGAACCTATTTT 2899  
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QY 2900 GAATCTCTTGAGGCTCAAGGATCACATCTGATATTTTCAAACTGTTCTCGAAACGATA 2959  
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QY 2960 ACCAAAAATATAAATCGCTGGAGAGAATCTTCCGACTCTGAGGACTTGCTAATGTT 3019  
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu\*\*\*\*\* 720  
QY 3020 AATACT 3025  
Db 721 \*\*\*Thr 722  
RESULT 9  
ABP67098  
ID ABP67098 standard; protein; 722 AA.  
XX AC ABP67098;  
XX 09-DEC-2002 (first entry)  
XX Human polypeptide SEQ ID NO 819.  
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
XX antiparkinsonian; antiepileptic; antianaemic; antiarthritic; cancer;  
XX antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
XX antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;  
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; nephrotropic; gene therapy; vaccine.  
OS Homo sapiens.  
XX US2002090672-A1.  
PN 11-JUL-2002.  
PD 17-JAN-2001; 2001US-00764853.  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.  
 PR 07-JUL-2000; 2000US-0216647P.  
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 PR 11-JUL-2000; 2000US-0217487P.  
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 PR 14-AUG-2000; 2000US-0224518P.  
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 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 XX (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 PI Rosen CA, Ruben SM, Barash SC;  
 XX WPI; 2002-681727/73.  
 DR N-PSDB; ABV84070.  
 XX Novel polypeptide useful for diagnosis, prognosis, prevention, and  
 PT treatment of immune, hyperproliferative, renal, respiratory,  
 PT cardiovascular, reproductive, endocrine, gastrointestinal and  
 PT neurological disorders.  
 XX Claim 11; SEQ ID NO 819; 369pp + Sequence Listing; English.  
 PS The invention relates to novel genes (ABV83682-ABV84101) and proteins  
 CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 722 AA;

## Alignment Scores:

Pred. No.: 0 Length: 722  
 Score: 3770.00 Matches: 717  
 Percent Similarity: 99.31% Conservative: 0  
 Best Local Similarity: 99.31% Mismatches: 5  
 Query Match: 63.77% Indels: 0  
 DB: 5 Gaps: 0

US-10-039-073-2 (1-3366) x ABP67098 (1-722)

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 Db 1 VallysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLys 20  
 Qy 920 ATGAGTACATACCTTGTAGCCTACATAGTTTGTGATTTCACACTCTCTGAGTGGCTTCACT 979  
 Db 21 MetSerThrTyrLeuValAlaTyrIleValIcysAspPheHisSerLeuSerGlyPheThr 40  
 Qy 980 TCATCAGGGTCAAGGTGTCCATCTATGCATCCCGACAGCAAAACGGAATCAACACATTAT 1039  
 Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60  
 Qy 1040 GCITTCGAGCATCAGTGAAGCTACTGATTTTATGAAAAGTACTTTGTATCTACTAT 1099  
 Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80  
 Qy 1100 CCACTCTCAAACCTGGATTAAATTGCTATTCTGACTTTTCACCTGGAGCATGGAAAAT 1159  
 Db 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100  
 Qy 1160 TGGGGCTCATATACATATAGGGAGACGTCACTGCTTTTTCACCCCAAGACCTCTTCTGCT 1219  
 Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120  
 Qy 1220 TCCGATAAACTGTGGGTCCACAGCATGACCCCATGAACTGGGCACCATGTTGGC 1279  
 Db 121 SerAspLysLeuTrpValThrArgValIleAlaHieGluLeuAlaHisGlnTrpPheGly 140  
 Qy 1280 AACCTGTCACAATGGAATGGTGAATGATATTGCTTAAGGAGGGTTTTGCAAAATAC 1339  
 Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160  
 Qy 1340 ATCGAACTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGT 1399  
 Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180  
 Qy 1400 AATGCTGTTTTCAGTAATTACAAAAGATTCAATTGAAATCCCGCCCTATCTCCAAA 1459  
 Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200  
 Qy 1460 CCAGCGGAACCCCGACTCAAATACAGGAAATGTTTGTGAAAGTTTCTCTATAACAAGGGA 1519  
 Db 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220  
 Qy 1520 GCTTGATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATA 1579  
 Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPhe\*\*\*LysGlyIle 240  
 Qy 1580 ATTCACTACTTAAGAGGTTTCAGCTATAGAAATGCTTAAGAAATCATGCTTGTGGAGCAGT 1639  
 Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer 260

QY 1640 CTGTCMAATAGTGTGTTTAAAGATGATTTTACATCTGGTGGAGTTGTGTCATTCGGATCCC 1699  
DB 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspPro 280  
QY 1700 AAGATTGACAAGTAACATGCTCCCTTCTCTGGGGGAAATGACAGAGGTCAAAGAGATGATG 1759  
DB 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGlu\*\*\*LysGluMetMet 300  
QY 1760 ACTACATGGACTCTCCAGAAAGGAATCCCTCGCTGGTGTAAACAAGACGGGTGTCA 1819  
DB 301 ThrThrTrpThrLeuGlnLysGlyLeuProLeuLeuValValLysGlnAspGlyCysSer 320  
QY 1820 CTCGACTGCAACAGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCCGAAATGGAGG 1879  
DB 321 LeuArgLeuGlnGlnArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340  
QY 1880 GCCCTGCGAGGAGGTACCTGGGATATCCCATTTGACCTACTCCACGAGTTCTCTTAAT 1939  
DB 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerSerSerAsn 360  
QY 1940 GTGATCCACAGACACATTTAAATCAAAAGACAGATCTCTGGATCTACCTGAAAAGACC 1999  
DB 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380  
QY 2000 AGTTGGGTGAATTTAATGTGACTCAAAATGTTACTACATCGTTTCACTATGAGGGTCAT 2059  
DB 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 400  
QY 2060 GGATGGGACCACTCATTAACAGCTGAATCAGAACCCACACTTCTCAGACCTAAGGAC 2119  
DB 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420  
QY 2120 AGAGTAGGTCTGATTCATGATGTGTTTTCAGCTAGTTGGTGCAGGAGACTGACCCCTAGAC 2179  
DB 421 ArgValGlyLeuIleHisValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440  
QY 2180 AAGCTCTTGACATGACTTACTCTTCAACATGAACAAAGCAGCGCCGCACTTCTCGAA 2239  
DB 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisLeuThrSerSerProAlaLeuLeuGlu 460  
QY 2240 GCTCTGAGTTACTTCCGATCGTTTACACATGATGGACAGAGCAATATTTACATATC 2299  
DB 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 480  
QY 2300 TCTGAAACCTCAAGCGTTACTCTTCTCAGTATTTTAAGCCAGTATTGACAGGCAAAAGC 2359  
DB 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500  
QY 2360 TGGAGTGACAAGGGCTCAGTCTGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGCC 2419  
DB 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520  
QY 2420 TGTGACCTGACCATGCTCTTGCATCCGAAGCTGCTGAACTCTTCTCCAGTGGATG 2479  
DB 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540  
QY 2480 GAATCCAGTGGAAAAATTAATATACCAACAGATGTTTTAAAGATTGTGTATTCTCGGT 2539  
DB 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560  
QY 2540 GCTCAGACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAATGTCAATGTCAAGT 2599  
DB 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580  
QY 2600 GCTGACACAAACAAATTTCTGTATGCTTGTCAAGCAGCAGCATCAGGAAAAGTACTG 2659  
DB 581 AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGlnLysLeuLeu 600  
QY 2660 AAGTTAATGAATAGGAATGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTC 2719  
DB 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeu 620

QY 2720 CTTTCATCGGATTGCCAGACGTCCAAAGGGGAGCAACTAGCATGGATTTTGTAAAGAA 2779  
DB 621 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640  
QY 2780 AATTGGACCCCATCTTCGAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATC 2839  
DB 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660  
QY 2840 TCTGCGCAACAGCTCACTTTTCTTCCAGGATTAAGTTGCAAGGTTGAACTATTTT 2899  
DB 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680  
QY 2900 GAATCTCTTGGGCTCAAGGATCACTGATATTTTCAACTGTTCTCGAAACGATA 2959  
DB 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700  
QY 2960 ACCAAAAATAAATGGCTGGAGAAGATCTCCGACTCTGAGGACTTGGCTAATGGTT 3019  
DB 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu\*\*\*\*\* 720  
QY 3020 AATACT 3025  
DB 721 \*\*\*Thr 722  
RESULT 10  
ADR41453  
ID ADR41453 standard; protein; 722 AA.  
XX AC ADR41453;  
XX DT 07-OCT-2004 (first entry)  
XX DE Human CD-like molecule HAIDK30, SEQ ID NO:252.  
XX KW Human; CD-like molecule; cluster of differentiation; diagnosis;  
KW prevention; immune disorder; immunodeficiency; autoimmune disorder;  
KW blood-related disorder; haematological disorder; haemostatic disorder;  
KW thrombolytic disorder; hyperproliferative disorder; cancer; tumour;  
KW apoptotic disorder; cardiovascular disorder; respiratory disorder;  
KW angiogenic disorder; neovascularisation; neurological disorder;  
KW endocrine disorder; reproductive system disorder; infectious disease;  
KW gastrointestinal disorder; drug screening; tissue regeneration;  
KW chemotaxis; gene therapy; antibody therapy; drug targeting;  
KW chromosome mapping; forensic analysis; immunophenotyping; cytostatic;  
KW haemostatic; tranquiliser; vulnery; antiinflammatory; nephrotropic;  
KW cardiant; antiallergic; anti-HIV; antirheumatic; antiarthritic;  
KW antipruritic; immunosuppressive; vasotropic; nootropic; neuroprotective;  
KW antithyroid; thyromimetic; gynaecological; virucide; hepatotropic;  
KW antibacterial; dermatological; chromosome 16.  
XX OS Homo sapiens.  
XX PN WO200226930-A2.  
XX PD 04-APR-2002.  
XX PF 25-SEP-2001; 2001WO-US029838.  
XX PP 26-SEP-2000; 2000US-0235484P.  
XX PR (HUMA-) HUMAN GENOME SCI INC.  
XX PA Rosen CA, Birse CE;  
XX PI WPI; 2002-405050/43.  
XX DR N-PSDB; ADR41277.  
XX PT Novel polynucleotides and polypeptides useful for treating, preventing or  
PT ameliorating cardiovascular, renal, neurovascular, and autoimmune  
XX disorders.  
XX PS Claim 11; SEQ ID NO 252; 1243pp; English.

CC The invention relates to 167 novel human CD (cluster of differentiation) -  
XX like molecules (ADR41388-ADR41563) and to cDNAs encoding them (seqid:11)-  
SQ Sequence 722 AA;

## Alignment Scores:

Pred. No.: 0 Length: 722  
Score: 3763.00 Matches: 717  
Percent Similarity: 99.31% Conservative: 0  
Best Local Similarity: 99.31% Mismatches: 5  
Query Match: 63.65% Indels: 0  
DB: 5 Gaps: 0

US-10-039-073-2 (1-3366) x ADR41453 (1-722)

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QY 860 GTTAAGACAATTGAACCTGAAGGAGCTCTTTTGGAGATCACTTTGAAACTACTGTAAAA 919
Db 1 VallysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrVallys 20
QY 920 ATGAGTACATACCTTGTAAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 979
Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40
QY 980 TCATCAGGGGCAAGGTCCTCATCTATGCATCTCCCGAGCAAAACGGAATCAAACACATTAT 1039
Db 41 SerSerGlyVallysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60
QY 1040 GCTTTGCAAGGCATCACTGAAGCTACTTGATTTTATGAAAGTACTTTGATATCTACTAT 1099
Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80
QY 1100 CCATCTCCAACTGGATTAAATGCTATTCTGACTTTGCACTTTGCACTGGAGCCATCGAAAAAT 1159
Db 81 ProluSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaIleGluAsn 100
QY 1160 TGGGCGCTCATTAATATAGGAGACGTCCTGCTGCTTTTGTACCCCAAGACCTCTCTGCT 1219
Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120
QY 1220 TCCGATAAAGCTGGGTCAACAGAGTCATAGCCCATGAGCTGGCGCCAGTGGTTGGC 1279
Db 121 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140
QY 1280 AACCTGGTCACAATGGAAATGGTGAATGATATTTGGCTTAAGAGGGTTTTGCAAAATAC 1339
Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160
QY 1340 ATGGAACCTTATCGCTGTTAAATGCTACATATCCAGAGCTGCATTTGATGACTATTTTGTG 1399
Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180
QY 1400 AATGCTGTTTGAAGTAATTAACAAGATTCATTGAATTCATCCCGCCCTATCTCCAAA 1459
Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200
QY 1460 CCAGCGAAACCCCGACTCAAAATACAGAAATGTTTGTATGAAGTTTCTATAACAAGGGA 1519
Db 201 ProAlaGluThrProThrGlnIleGlnGluMet***AspGluValSerTyrAsnLysGly 220
QY 1520 GCTTGATTTTGAATATGCTCAAGATTTTCTGGGTAGGAGAAATTCAGAAAGGAATA 1579
Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIle 240
QY 1580 ATTCACTACTTAACAGAGTTCAGCTATAGAATGCTAAGATGATGACTTGTGAGCAGT 1639
Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 260
QY 1640 CTGTCAAAATAGTGTGTAGAAAGTGAATTTACATCTGCTGGAGTTTGTCAATTCGGATCCC 1699
Db 261 LeuSerAsnSer***LeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 280
QY 1700 AAGATGACAAGTACATGCTCGCTTTCTGGGGGAAATATGACAGAGGTCAAAGATGATG 1759
Db 1759 AAGATGACAAGTACATGCTCGCTTTCTGGGGGAAATATGACAGAGGTCAAAGATGATG
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Db 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet 300
QY 1760 ACTACATGGACTCTCCAGAAAGGAATCCCTCTGCTGGTGTAAACAAAGCGGTGTCA 1819
Db 301 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 320
QY 1820 CTCGACTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCCCTGAATGAGG 1879
Db 321 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340
QY 1880 GCCTTCAGAGAGGTACTGTGGCATATCCCATTTGACCTACTCCACAGTCTTCTTAAT 1939
Db 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 360
QY 1940 GTGATCCACAGACACATCTTAAATCAAGACAGATACTCTGGATCTACCTGAAAAGACC 1999
Db 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380
QY 2000 AGTTGGGTGAAATTTAATGTGGACTCAAATGGTTTACTACATCGTTCACTATGAGGGTCA 2059
Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 400
QY 2060 GGATGGGACCAACTCAATTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGAC 2119
Db 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420
QY 2120 AGAGTAGGTCTGATTCATGATGTGTTTCAGCTAGTTGGTCAGGGAGACTGACCTAGAC 2179
Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440
QY 2180 AAAGCTCTTGACATGACTTACTACTCCAAACATGAAACAAAGCAGCCCCGACTTCTCGAA 2239
Db 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 460
QY 2240 GGTCTGAGTTACTTGAATCGTTTTTACCACATGATGACAGAGGAATATTTCCAGATATC 2299
Db 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 480
QY 2300 TCTGAAACCTCAAGCGTTACCTTCTCAGTATTTTAAAGCCAGTGTGACAGGCAAGC 2359
Db 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500
QY 2360 TGGAGTGACAAGGCGCTCAGTCTGGGACAGGATGCTCGCTCGGCTCTCTTTGAAAGCTGGCC 2419
Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520
QY 2420 TGTGACTGAACCATGCTCTCTGCAATCCAGAAAGCTGCTGAACTCTTCTCCAGTGTGATG 2479
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540
QY 2480 GAATCCAGTGGAAAATTAATATATACCAACAGATGTTTTTAAAGATTTGTGTTCTGTGGGT 2539
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560
QY 2540 GCTCAGACACAGCAGGATGGAATTAACCTTTTATAGCAATATGAACCTGTCAATGTCAAGT 2599
Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580
QY 2600 GCTGAACAAACAAAATTCGTATGCTTTGTCAACGAGCAGGATCAGGAAAAGTACTG 2659
Db 581 AlaGlnGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu 600
QY 2660 AAGTTAATTCAACTAGGAATGGAAGAAAGGTTTATCAAGACACAGAACTTTGGCAGCTCTC 2719
Db 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu 620
QY 2720 CTTTCATCGGATTCAGACGCTCCAAAGGCGCAGCAACTAGCATGGGATTTTGTAAAGAA 2779
Db 621 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640
QY 2780 AATTGACCCCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAAAGATGATCATC 2839
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660
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QY 2840 TCTGGCACAACAGCTCCTCTTTCTTCCAAAGGATAAGTTCCAAAGAGTGAACACTATTTTT 2899  
 DB 661 SerGlyThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680  
 QY 2900 GAATCTCTTGGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAAACGATA 2959  
 DB 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700  
 QY 2960 ACCAAAATATATAATGGCTGGAGAGAAATCTTCCGACTCTCGAGACTTGGCTAATGGTT 3019  
 DB 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu\*\*\*\*\* 720  
 QY 3020 AATACT 3025  
 DB 721 \*\*\*Thr 722  
 RESULT 11  
 AAU07829  
 ID AAU07829 standard; protein; 941 AA.  
 XX  
 AC AAU07829;  
 XX  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Human ARTS-1 polypeptide.  
 XX  
 KW Human; aminopeptidase regulator of type I; cytokine signalling; ARTS-1;  
 KW tumor necrosis factor receptor ectodomain shedding; interleukin-1;  
 KW interleukin-6; immune disorder; TNF-mediated immune disease;  
 KW inflammatory disorder; anti arthritic; vasotropic; immunomodulator;  
 KW immunosuppressive; antibacterial; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 350..361  
 FT /label= Zinc\_binding\_domain  
 FT Domain 353..376  
 FT /label= Zinc\_metalloproteinase\_catalytic\_motif  
 FT Domain 372..379  
 FT /label= Zinc\_binding\_catalytic\_site  
 XX  
 PN WO200164856-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US006464.  
 XX  
 PR 28-FEB-2000; 2000US-0185586P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Levine S;  
 XX  
 DR WPI; 2001-550175/61.  
 DR N-PSDB; AAS09227.  
 XX  
 PT Novel polypeptide useful for the regulation of ectodomain shedding of  
 PT type I, tumor necrosis factor receptor and other cytokine receptors and  
 PT for treating disorders and diseases of the immune system.  
 XX  
 PS Claim 2; Fig 1; 139pp; English.  
 CC  
 CC The present invention relates to the isolation of a novel human  
 CC polypeptide, defined as aminopeptidase regulator of type I, 55 kDa tumor  
 CC necrosis factor (TNF) receptor ectodomain shedding (ARTS-1), and the  
 CC polynucleotide sequence encoding for ARTS-1. The invention describes  
 CC compositions and methods for the regulation of cytokine signalling  
 CC through the TNF pathway. The ARTS-1 polypeptide and antibodies that bind  
 CC ARTS-1 are useful for regulating the shedding of the extracellular domain  
 CC of a cytokine receptor such as type-I tumor necrosis factor receptor,  
 CC type I or II interleukin-1 cytokine receptor and interleukin-6 cytokine

CC receptor alpha-chain gp80, by delivering the molecules to a tissue  
 CC comprising one or more cells expressing the cytokine receptor or their  
 CC plasma membrane extracellular surface. The ARTS-1 sequences are or  
 CC useful for treating a subject, preferably human, displaying, suspected  
 CC of, or at risk of displaying a pathology resulting from abnormal cytokine  
 CC activity, such as tumor necrosis factor alpha, interleukin-1alpha, beta  
 CC or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1  
 CC is useful in gene therapy. The ARTS-1 sequences are useful in diagnostic  
 CC and therapeutic regimens in treating immune disorders (e.g. TNF-mediated  
 CC immune diseases) and inflammatory disorders (e.g. rheumatoid arthritis).  
 CC The present sequence represents human ARTS-1 polypeptide  
 XX  
 SQ Sequence 941 AA;

## Alignment Scores:

Pred. No.: 3.54e-245 Length: 941  
 Score: 2516.50 Matches: 478  
 Percent Similarity: 69.34% Conservative: 171  
 Best Local Similarity: 51.07% Mismatches: 268  
 Query Match: 42.57% Indels: 19  
 DB: 4 Gaps: 7

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QY 212 TACTGCTTAACAGGCATCTTGCCCAATAATGCAATTTGTTCTCAGTTCTCAGTGCCATCT 271  
 DB 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal::: SerThrProSer 30  
 QY 272 AGTTATCATCTTCACTGAGGATCCTGGGGCTTTCCAGTAGCCACCTAATGGGGAACGATT 331  
 DB 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47  
 QY 332 CCTTGGCAGGAGCTAAGGCTCCCGAGTGTGTCTATTCTCTCCATTATGACCTCTTTGCT 391  
 DB 48 ProTrpAsnLysIleArgLeuProGluTyrrValIleProValHisTyrrAspLeuLeu 67  
 QY 392 CACCCCAATCTCCTCTCGGACTTTGTCATCTGAGAGATCGAAGTCTTGTCAGC 451  
 DB 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrLysValGluIleThrAlaSer 87  
 QY 452 AATGCTACCCAGTTTATCATCTTCACAGCAAGACTCTTGAATCAGCAATGCCACCTT 511  
 DB 88 GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107  
 QY 512 CAGTCAGAGGAAGATTCAAGATACATGAAACACAGGAAAGAACTTGAAGTTTGTGATTAC 571  
 DB 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125  
 QY 572 CCTGCTCATGAACAAATTCGCTCTGCTGTTCCAGAGAACTTACGCTCAGCTGAAATAC 631  
 DB 126 ProArgGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145  
 QY 632 TATGTGCTATGGACTTCCAGCCCAAGTTAGTGTGCTTTGAAGGGTTTTATAAAGC 691  
 DB 146 ThrValValIleHisTyrrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrrLysSer 165  
 QY 692 ACATACAGAACTCTTGTGTGTGAACAAGAAATCTTGCAGTAACAGATTTTTCAGCAACC 751  
 DB 166 ThrTyrrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185  
 QY 752 CAGCAGCATGGCTTCCCTTGTGTTGATGAACCGTTGTTCAAGGCCAACTTTCAATC 811  
 DB 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205  
 QY 812 AAGATACAGAGAGAGACGACGATATTCACATCCCAACATGCCAAGGTTTAAACACATT 871  
 DB 206 LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225  
 QY 872 GAACCTGAAGAGGCTTTTGGAGATCAGCTTTGAAACTACTGTAAAAAGAGTACATAC 931  
 DB 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245  
 QY 932 CTTGTAGCCTACATAGTATTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTC 991



[illegible]

QY 1472 CCGACTCAAAATACAGGAATCTTTGATGAAGTTTCCTATACAGGGAGCTTGATTG 1531  
DB ProlaGlnIleArgGluMetPheAspGlnValSerTyrAspLysGlyAlaCysIleLeu 445  
QY 1532 AATATGCTCAAGGAATTTCTGGGTGAGAGAAATTCAGAAAGGAATAAATCACTACTTA 1591  
DB AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465  
QY 1592 AAGAAGTTCAGCTATAGAAATCTAAGATGATGACTGTGGAGAGCTCTCTCAAAAGT 1651  
DB GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTyrAspSerMetAlaSerIle 485  
QY 1652 TGTTTAGAAAGTGAATTTACATCTGGT-----GGAGTTTCTCATTCGGATCCCAAGATG 1705  
DB Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503  
QY 1706 ACAAGTAACATGCTCGCTTTCTGGGGGAAATGACAGAGTCAAGAGATGATGACTACA 1765  
DB SerSerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr 523  
QY 1766 TGGACTCTCCAGAAAGGAATCCCTGCTGCTGTGGTTAAACAAGACGGGTGTTCACTCGA 1825  
DB TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543  
QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAGACCCCTGAATGGAGGCCCTG 1885  
DB MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlapro 557  
QY 1886 CAGGAGAGGTACCTGTGGCATATCCCAATGACCTACTCTACAGAGTTCTTCTTAATGTGATC 1945  
DB AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal 577  
QY 1946 CACAGACACATCTTAAATCAAGACAGATCTCTGGATCTACCTGAAAGACAGCTGG 2005  
DB HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluGluValGluTrp 597  
QY 2006 GTGAAATTTAATGTGAGCTCAAAATGTTTACTACATCGTTTCACTATGAGGGTCATGGATGG 2065  
DB IleLysPheAsnValGlyMetAsnGlyTyrTrpIleValHisTyrGluAspGlyTrp 617  
QY 2066 GACCAACTCATTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGATA 2125  
DB AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637  
QY 2126 GGTCTGATTCATGATGTTTTCAGCTAGTCTGGTCAGGAGACTGACCTAGACAAAGCT 2185  
DB SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657  
QY 2186 CTTCAGATGACTTACTCTCCATCAATGAAACAGACGCCCGCACCTTCTCGAAGGTCTG 2245  
DB LeuAspLeuSerLeuTyrLeuLysHisGluThrGluLeuMetProValPheGlnGlyLeu 677  
QY 2246 AGTTACTTTGGAATCGTTTACCACATGATGACAGAGGAATATTTTCAGATATCTCTGAA 2305  
DB AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697  
QY 2306 AACCTCAAGCTTACCTTCTCAGTATTTTAAAGCCAGTGATGACAGCAAGCTGAGT 2365  
DB GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717  
QY 2366 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2425  
DB AspGluGlySerValSerGluArgMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal 737  
QY 2426 CTGAACCATGCTCTTCATCCAGAAAGCTGCTGAACCTTCTTCCAGTGATGGAATCC 2485  
DB HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757  
QY 2486 AGTGGAAATTAATATACCAACAGATGTTTAAAGATTGTTATTCGTGGGTGCTCAG 2545  
DB AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777

QY 2546 ACAACACAGGATGGAATTAACCTTTTAGACAATATGAACTGTCAATGTCAAGTGTGCA 2605  
DB SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797  
QY 2606 CAAAACAAAATCTGTATGTTGTCAACGACGAGCATCAGGAAAAGTTACTCTGAAGTTA 2665  
DB LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817  
QY 2666 ATTGAAGTACGAATGGNAGGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2725  
DB LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837  
QY 2726 GCCATTCCAGAGCTGCCAAAGGGCGACAACTAGCATGGGATTTTGTAAAGAGAAAATTGG 2785  
DB LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857  
QY 2786 ACCCATCTTCTGAAAAAATTGACTTGGGTCATATACATAAGGATGATCATCTCTGGC 2845  
DB AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877  
QY 2846 ACAACAGCTCAGCTTTCTTCCAGGATAAGTTGCAAGGGTGAACCTATTTTGAATCT 2905  
DB ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897  
QY 2906 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTCTGGAACGATACCAAA 2965  
DB LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917  
QY 2966 AATATAAATGGCTGGAGAGAATCTTCGACTCTGAGGACTTGGCTA 3013  
DB AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933  
RESULT 13  
ID ADA56820 standard; protein; 941 AA.  
XX ADA56820;  
XX  
XX 20-NOV-2003 (first entry)  
XX Human secreted protein #103.  
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
XX cytosatic; cerebroprotective; neuroprotective; gene therapy;  
XX cardiovascular; antiarteriosclerotic; cancer; immune disorder; inflammation;  
XX human secreted protein; cancer; CNS disorder; neurodegenerative disorders;  
XX respiratory disorder; Crohn's disease; nephritis; Crohn's disease; asthma; allergy;  
XX inflammatory bowel disease; ischaemic brain injury; Parkinson's disease;  
XX multiple sclerosis; atherosclerosis; myocarditis; chromosome mapping;  
XX Alzheimer's disease; antisense gene therapy; forensic biology.  
OS Homo sapiens.  
XX  
XX WO2002102994-A2.  
XX  
XX 27-DEC-2002.  
XX  
XX 19-MAR-2002; 2002WO-US008278.  
XX  
XX 21-MAR-2001; 2001US-0277340P.  
XX 19-JUL-2001; 2001US-0306171P.  
XX 13-NOV-2001; 2001US-0331287P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
XX WPI: 2003-167512/16.  
XX N-PSDB; ADA55924.  
XX  
XX New human secreted polypeptides and polynucleotides, useful for  
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT

PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1010; 1754pp; English.

PS The invention relates to 592 new human secreted polypeptides useful for  
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 95% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for  
CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence data for  
CC this patent did form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 941 AA;

#### Alignment Scores:

Pred. No.:	4,47e-245	Length:	941
Score:	2515.50	Matches:	477
Percent Similarity:	69.34%	Conservative:	172
Best Local Similarity:	50.96%	Mismatches:	268
Query Match:	42.55%	Indels:	19
DB:	6	Gaps:	7

US-10-039-073-2 (1-3366) x ADA56820 (1-941)

QY	212	TACTGCTTAACGCCATCTGCCCAATATGCAATTTGTTCTCAGTTCTCAGTGCATCT	271
DB	15	PhelLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer	30
QY	272	AGTTATCACTTCACCTGAGGATCCTGGGCTTCCCGATGAGCACCATAATGGGAACGATTT	331
DB	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47
QY	332	CCTGGCAGGAGCTAAGCTCCCGAGTGGTGCATCTCTCCATATGACCTCTTTGTC	391
DB	48	ProTrpAsnLysIleArgLeuProGluLysValIleProValHisThrAspLeuLeu	67
QY	392	CACCCCATCTCACCCTCTGCACTTCTTGATCGATCGAGAGATCGAATCTTGGTCAGC	451
DB	68	HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
QY	452	AATGCTACCCAGCTTTATCATCTTGACAGCAAGAGATCTTGAATCACCAGATGCCACCTT	511
DB	88	GlnProThrSerThrIleLeuHisSerHisLeuGlnLeuSerArgAlaThrLeu	107
QY	512	CAGTCAGAGGAGATTCAGATACATGAACACGAGAAAGAACTGAAAGTTTGTGATTC	571
DB	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
QY	572	CCTGCTCATGAACAAATTTGCACTGCTGTTCCAGAGAAACCTTACGCCTCACCTGAAATAC	631

Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145
QY	632	TATGTGGCTATGGAGCTTCCAGCCCAAGTTAGGTGATGCTTTGAAGGGTTTTATAAAGC	691
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
QY	692	ACATACAGAACTCTGGTGGTGAACAAGAAATCTTGCAGTAACACAGATTTTGAGCCAAC	751
Db	166	ThrTyrArgThrLysGluGlyLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
QY	752	CAGCAGCATGGCTTCCCTTGTGATCAACCGTTGTTCAAGGCAACACTTTTCAATC	811
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
QY	812	AAGTACGAAGAGAGAGAGCATATTGCATCTCCAAATCCCAACATGCGCAAGGTTAAGA	871
Db	206	LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225
QY	872	GAACTTGAAGAGGCTTTTGGAGATCATTTCGAACTACTGTAAAATGATGATACATAC	931
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245
QY	932	CTTGTAGCTACATAGTTTGTGATTTCACCTCTCTGAGTGGCTTCACTTCATCAGGGTC	991
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
QY	992	AAGGTGTCATCTATGATCCCCAGACAAAGGAAATCAACACATATATGCTTTGCAGCA	1051
Db	266	LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla	285
QY	1052	TCACTGAAGTACTTGTATTTTATGAAAGTACTTTGATATCTACTACTCCTCCAAA	1111
Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305
QY	1112	CTGGATTTAATTGCTATTCTGACTTTGCCTCGAGCATGGGAAATTTGGGCGCTCAT	1171
Db	306	GlnAspLeuAlaIleIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325
QY	1172	ACATATAGGAGAGCGTCACTGCTTTTTCACCCCAAGAGACCTCTCTGCTTCGATAAATC	1231
Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345
QY	1232	TGGGTACACGAGATCATAGCCCATGAACCTGGCGCACAGTGGTTGGCAACTGGTCACA	1291
Db	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
QY	1292	ATGGAATGGTGGATATATTGGCTTAAGGAGGTTTTGCATAATACATCGAATCTATC	1351
Db	366	MetGluTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
QY	1352	GCTGTTAATGTCATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTGTGTTT	1411
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
QY	1412	GAAGTAATACAAAGATTCATGAATTCATCCCGCCCTATCTCCAAACCGCGGAAC	1471
Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425
QY	1472	CCGACTCAATACAGGAAATGTTTGATGAAGTTTTCTTATACAAAGGAGCTTGTGTTTG	1531
Db	426	ProIleGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
QY	1532	AATATGCTCAAGGATTTTTCGGGTGAGAGAAATTCAGAAAGGAATAATTCAGTACTTA	1591
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
QY	1592	AAGAGTTTCAGCTATAGAATCTAGAATGATGATCTTGGAGCAGCTCTGTCAAAATAGT	1651
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
QY	1652	TGTTTAGAAGTGAATTTTACATCTGGT-----GGAGTTGTTCATTCGGATCCCAAGAT	1705
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503

QY	1706	ACAAGTAACA	TGCTCGCCTTTCTGGGGGAA	AAATGCAGAGGTC	CAAGAGATC	GATGACTACA	1765
		::: :::	::: :::	::: :::	::: :::	::: :::	
Db	504	SerSerSerSer	HisTTrpHis	GlnGluGlyVal	AspVal	ValThrMetMet	AsnThr 523
QY	1766	TGGACTCTCC	AGAAAGNA	TCCCCTCTGGTGGT	TAAACAAGAC	CGGGTGTTC	ACTCCGA 1825
		:::	:::	:::	:::	:::	
Db	524	TrpThrLeu	GlnArgGlyPhe	ProLeu	ThrThrVal	ArgGlyVal	ArgAsnValHis 543
QY	1826	CTGCAACAGG	AGCCCTTCTCCACGGGGT	TTTCCAGGAAG	ACCCTGAATCG	AGGGCCCTG	1885
		::: :::	::: :::	::: :::	::: :::	::: :::	
Db	544	MetLysGln	GluHisTyrMet	LysGly	-----	-----Ser	AspGlyAlaPro 557
QY	1886	CAGGAGAGG	TACCTGTGGCATAT	CCCATCTGAC	TACTCCACGAG	TCTTCTTAATG	TGATC 1945
		:::	:::	:::	:::	:::	
Db	558	AspThrGly	TyrLeuTTrpHis	ValProLeu	ThrPheThrSer	LysSerAsp	MetVal 577
QY	1946	CACAGACAC	ATTCTTAATAA	CAAGACAGAT	CTCTGGATCTAC	CTGTAAGAAC	CCAGTGTG 2005
		:::	:::	:::	:::	:::	
Db	578	HisArgPhe	LeuLeuLysThr	LysThrAsp	ValLeuLeuPro	GluGluVal	Glutrrp 597
QY	2006	GTGAAATTT	TAATGTGGACT	CAAAATGGTTACT	TACATCGTTCA	TATGAGGTC	TATGATGG 2065
		:::	:::	:::	:::	:::	
Db	598	IleLysPhe	AsnValGlyMet	AsnGlyTyrTyr	IleValHisTyr	GluAsp	GlyTrrp 617
QY	2066	GACCAACT	CATTACACAG	CTGTAATCAGAA	CCACACACTCT	TCAGACCTA	AGGACAGATG 2125
		:::	:::	:::	:::	:::	
Db	618	AspSerLeu	ThrGlyLeuLeu	LysGlyThrHis	ThrAlaValSer	SerSerAsn	AspArgAla 637
QY	2126	GCTCTGAT	TTCATGATGTTT	CAGTCTAGTTGGT	CACGGAGACT	GCACCTAGACA	AAAGCT 2185
		:::	:::	:::	:::	:::	
Db	638	SerLeuLeu	AsnAsnAlaPhe	GlnLeuValSer	IleGlyLysLeuSer	IleGluLysAla	657
QY	2186	CTTGACATG	ACTTTACTCT	CCAAATCAATG	AAACAAGAC	AGCCCGCACTT	CTCGAAGTCGTG 2245
		:::	:::	:::	:::	:::	
Db	658	LeuAspLeu	SerLeuTyrLeu	LysHisGlnThr	GluIleMetPro	ValPheGln	GlyLeu 677
QY	2246	AGTTACTTG	NAATCGTTTACC	ACATGATGAC	AGAGAAGGA	TATTTTCAGAT	ATCTCTGAA 2305
		::: :::	::: :::	::: :::	::: :::	::: :::	
Db	678	AsnGluLeu	IleProMetTyr	LysLeuMet	GluLysArgAsp	MetAsnGlu	ValGluThr 697
QY	2306	AACCTCAAG	CGTTACCTTCT	TCCAGTATTTAAG	CCAGTGATGAC	GGCAAGAGCT	GCGAGT 2365
		:::	:::	:::	:::	:::	
Db	698	GlnPheLys	AlaPheLeu	IleArgLeuLeu	ArgAspLeuLeu	AspLysGlnThr	TrpThr 717
QY	2366	GACAAGGG	CTCAGTCTGG	GCACAGGATCT	CCGCTCGGCTCT	CTTTGAAG	CTGGCTGTGAC 2425
		:::	:::	:::	:::	:::	
Db	718	AspGluGly	SerValSerGlu	ArgMetLeu	ArgSerGluLeu	LeuLeuLeu	LeuAlaCysVal 737
QY	2426	CTGNAACAT	GCTCTCTGAT	CCAGAAAGCTG	CTGAACTCTT	CTCCCAGT	TGGATGCC 2485
		:::	:::	:::	:::	:::	
Db	738	HisAsnTyr	GlnProCysVal	GlnArgAlaGlu	GlyTyrPheArg	LysTrrpLys	GluSer 757
QY	2486	AGTGGAAAA	TTAAATATAC	CAACAGATGTTT	TAAAGATTGT	GTATTTCTG	TGGGTGCTCAG 2545
		:::	:::	:::	:::	:::	
Db	758	AsnGlyAsn	LeuSerLeuPro	ValAspValThr	LeuAlaValPhe	AlaValGlyAla	Gln 777
QY	2546	ACAACACAG	AGATGAATAC	CTTTTAGCA	CAATATGAACTG	TCAATGTCA	AGTGTGTA 2605
		:::	:::	:::	:::	:::	
Db	778	SerThrGlu	GlyTrrpAspPhe	LeuTyrSer	LysTrrpGlnPhe	SerLeuSerSer	ThrGlu 797
QY	2606	CAAAACAAA	ATTCGTATG	CTTTCTCA	CAGCAAGCAT	CAGGAAAAG	TACTGCAAGTTA 2665
		:::	:::	:::	:::	:::	
Db	798	LysSerGln	IleGluPheAlaLeu	CysArgThrGln	AsnLysGluLysLeu	GlnTrpLeu	817
QY	2666	ATTGAACT	AGGAAATGGA	AGAAAGTTAT	CAAGACAC	AGAACTTGG	CAGCTCTCTTCAT 2725
		:::	:::	:::	:::	:::	
Db	818	LeuAspGlu	SerPheLysGlyAsp	LysIleLysThrGln	PheProGln	IleLeuThr	837
QY	2726	CGGATTCG	CACACTCCAA	AGGGCCAGCA	ACTAGCAT	GGGATTTT	TGTAAGAAAAATGG 2785
		:::	:::	:::	:::	:::	
Db	838	LeuIleGly	ArgAsnPro	ValGlyTrrp	LeuAlatrrpGln	PheLeuLysGly	AsnTrp 857

Qy	2786	ACCCATCTTCTGAAAAAATTGTACTTGCGGCTCATATGACATAAGGATGCATCTCTGGC	2845
Db	858	AsnLysLeuValGlnPheGluLeuLysSerSerIlealaHisMetValMetGly	877
Qy	2846	ACAACAGCTCACCTTTCTTCCAAGGATAAGCTTCGAAGAGCTGAACTATTTTTTGAATCT	2905
Db	878	ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer	897
Qy	2906	CTTGAGGCTCAAGGATCACATCTGGATATTTTTCAAACCTCTTCTGGAACGATAACCAA	2965
Db	898	LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu	917
Qy	2966	AATATAAAATGGCTGGAGAAGAATCTTCCGACTCTGAGGACTTGGCTPA	3013
Db	918	AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu	933
<b>RESULT 14</b>			
ABR47686			
ID	ABR47686	standard; protein; 941 AA.	
XX	AC	ABR47686;	
XX	XX		
DT	12-JUN-2003	(first entry)	
DE	Human secreted protein, SEQ ID 577.		
XX	KW	Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;	
KW	KW	vulnerary; antiinflammatory; nootropic; neuroprotective;	
KW	KW	antiparkinsonian; gene therapy; human; cardiovascular disorder.	
XX	OS	Homo sapiens.	
XX	XX		
PN	WO200295010-A2.		
XX	PD	28-NOV-2002.	
XX	PF	19-MAR-2002; 2002WO-US009785.	
XX	PR	21-MAR-2001; 2001US-0277340P.	
PR	PR	19-JUL-2001; 2001US-0306171P.	
PR	PR	13-NOV-2001; 2001US-0331287P.	
XX	XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	PI	Rosen CA, Ruben SM;	
XX	XX	WPI; 2003-129429/12.	
DR	XX		
PT	PT	Novel human secreted proteins, useful for detecting, preventing,	
PT	PT	diagnosing, prognosticating, treating and/or ameliorating cardiovascular	
PT	PT	disorders such as arrhythmia.	
XX	FS	Claim 13; SEQ ID NO 577; 1881pp; English.	
XX	XX		
CC	CC	The present invention relates to novel human secreted proteins (ABR47633-	
CC	CC	ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins	
CC	CC	and their coding sequences are useful for the preparation of a diagnostic	
CC	CC	or pharmaceutical composition for diagnosing or treating a cardiovascular	
CC	CC	disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary	
CC	CC	arteriosclerosis and myocardial ischaemia), neural disorders, immune	
CC	CC	system disorders, muscular disorders, reproductive disorders,	
CC	CC	gastrointestinal disorders, pulmonary disorders, renal disorders,	
CC	CC	proliferative disorders and/or cancerous diseases and conditions, for	
CC	CC	wound healing and epithelial cell proliferation, to treat inflammation or	
CC	CC	infection, for treating thrombosis and arteriosclerosis, for treating or	
CC	CC	preventing neural damage which occurs in neuronal disorders or	
CC	CC	neurodegenerative conditions such as Alzheimer's disease and Parkinson's	
CC	CC	disease, to enhance bone and periodontal regeneration and aid in tissue	
CC	CC	transplants or bone grafts, to prevent skin aging or hair loss, to	
CC	CC	stimulate growth and differentiation of haematopoietic cells and bone	
CC	CC	marrow cells when used in combination with other cytokines, to maintain	
CC	CC	organs before transplantation or for supporting cell culture of primary	
CC	CC	tissues, to increase or decrease differentiation or proliferation of	

CC embryonic stem cells, or to modulate mammalian characteristics or  
 CC metabolism. Note: The sequence data for this patent was published in  
 CC electronic format and is available from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 941 AA;

# Alignment Scores:

Pred. No.: 4,476-245 Length: 941  
 Score: 2515.50 Matches: 477  
 Percent Similarity: 69.34% Conservative: 172  
 Best Local Similarity: 50.96% Mismatches: 268  
 Query Match: 42.55% Indels: 19  
 Gaps: 7

US-10-039-073-2 (1-3366) x ABR47686 (1-941)

QY 212 TACTGCTTAACAGCCATCTTGCCCAATATGATGTTGTTCTCAGTGTCCAGTGCACCT 271  
 Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30  
 QY 272 AGTTATCACTTCACTCAGGATCCTGGGCTTTCCAGTAGCCACTAAATGGGGAACGATTT 331  
 Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47  
 QY 332 CTTGGCAGGAGCTAAGGCTCCCGAGTGGTGCATCTCTCCATATGACCTCTTTGTC 391  
 Db 48 ProTrpAsnLysIleArgLeuProGluTrpValIleProValHisTrpAspLeuLeuIle 67  
 QY 392 CACCCCAATCTCCTCTGACCTTGTGTCATCTGAGAGATCGAAGTCTTGTCAGC 451  
 Db 68 HisAlaAsnLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87  
 QY 452 AATGCTACCACCTTTATCATCTTGACAGCAAGACTCTTGAATCAGCAATGCCACCTT 511  
 Db 88 GlnProThrSerThrIleIleLeuHisSerHisHisLeuGlnIleSerArgAlaThrLeu 107  
 QY 512 CAGTCAGAGGAAGATTCAGATPACATGAACACGAGGAAGAACTGAAAGTTTGTAGTTC 571  
 Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125  
 QY 572 CTTGCTCATGACAAATGCACTGCTGGTTCAGAGAACTTACCCCTCAGTCAAGATAC 631  
 Db 126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTrp 145  
 QY 632 TATGTGGCTATGCACTTCCAGCCCAAGTTAGTGTGCTTTGAAGGTTTATAAAGC 691  
 Db 146 ThrValValIleHisTrpAlaGlyAsnLeuSerGluThrPheHisGlyPheTrpLysSer 165  
 QY 692 ACATACAGAACTTTGGTGGTGAACAAGAAATCTTGCAAGTAAACAGATTTGAGCCAAC 751  
 Db 166 ThrTrpArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185  
 QY 752 CAGGCACCGATGCTTCCCTGCTTGTGATGACCGTGTTCAGAGCAACCACTTTCAATC 811  
 Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysLeuAlaSerPheSerIle 205  
 QY 812 AAGATACGAAGAGAGAGGAGGATATGCACTATCAACATGCCAAAGGTTAAGCAAT 871  
 Db 206 LysIleLeuArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225  
 QY 872 GAATCGAAGGAGGCTTTTGGAGATCACTTTGAACTACTGTGTAATAATGAGTACATAC 931  
 Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTrp 245  
 QY 932 CTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCAGGGTC 991  
 Db 246 LeuValAlaPheIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265  
 QY 992 AAGGTGCTCATCTATGATCCCGACAAACCGAATCAACACATATGCTTTGACGCA 1051  
 Db 266 LysValSerValTrpAlaValProAspLysMetAsnGlnAlaAspTrpAlaLeuAspAla 285

QY 1052 TCACTGAAGCTACTGATTGTTTATGAAAGTACTTTTGATATCTACTATCTCCACTCTCCAAA 1111  
 Db 286 AlaValThrLeuLeuGluPheTyrGluAspTrpPheSerIleProTrpLeuProLys 305  
 QY 1112 CTGGATTAAATGCTATTCTGACTTTGACCTCGAGCCATGGAAATATGGGGCTCAT 1171  
 Db 306 GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325  
 QY 1172 ACATATAGGAGAGCTCACTGCTTTTGAACCCCAAGACCTCTCTGCTTCGATAAATG 1231  
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 QY 1232 TGGGTCAACAGCATAGCCCATCACTGGCGACCACTGGTGTGGCAACTGGTCA 1291  
 Db 346 GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365  
 QY 1292 ATGCAATGGTGAATGATATTGGCTTAAGGAGGTTTGCAAAATACATACGAACTATC 1351  
 Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385  
 QY 1352 GCTGTTAATGTCATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTT 1411  
 Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTrpPhePheGlyLysCysPhe 405  
 QY 1412 GAAGTAATCAAAAGATTCAATTCATCCCGCCCTATCTCCAAACCCAGCGAACC 1471  
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 QY 1472 CCGACTCAATACAGGAAATGTTTGTGAGTGTCTTATACAAAGGAGCTGTGATTTG 1531  
 Db 426 ProAlaGlnIleArgGluMetPheAspValSerTrpAspLysGlyAlaCysIleLeu 445  
 QY 1532 AATATGCTCAAGGATTTTCTGGTGAGGAGAAATTTCCAGAAAGGAATAATTCAGTACTTA 1591  
 Db 446 AsnMetLeuArgGluTrpLeuSerAlaAspAlaPheLysSerGlyIleValGlnTrpLeu 465  
 QY 1592 AAGAAGTTCAGTATAGAAATCTAAGAAATGACTGTGTCGAGCAGTCTGTCAATAGT 1651  
 Db 466 GlnLysHisSerTrpLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485  
 QY 1652 TGTTTAGAAAGTGTATTTACATCTGGT-----GGAGTTTGTCTTCAGTCCCAAGATG 1705  
 Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerAspSerGlnHis 503  
 QY 1706 ACAAGTAACTGCTGCTTCTGGGGGAAATGCAGAGGTCAAAGATGATGACTACA 1765  
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 QY 1766 TGGACTCTCCAGAAAGAAATCCCTCTGCTGTGTGTTAAACAAGCGGTGTCTACTCGA 1825  
 Db 524 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543  
 QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAGAACCTCGAATGAGGGCCCTG 1885  
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 QY 1886 CAGGAGAGGTACCTGTGGCATATCCCATGACCTACCTCCAGAGTTCCTTAATGTATC 1945  
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 QY 1946 CACAGACACATCTTAAATCAACAACAGATCTGTGATCTACCTCGAAGAACCCAGTTGG 2005  
 Db 578 HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluGluValGluTrp 597  
 QY 2006 GTGAAATTAATGAGGACTCAATGGTTTACTACATCGTTTACTATGAGGGTCATGGATGG 2065  
 Db 598 IleLysPheAsnValGlyMetAsnGlyTrpTrpIleValHisTrpGluAspAspGlyTrp 617  
 QY 2066 GACCAACTCATACAGCTGAATCAGAACCCACACTTCTCAGACCTTAAGCAGAGATA 2125  
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Qy	392	CACCCCAATCTCACCTCTCTGAGCTTTTGGTGCATCTGAGAAGATCGAAGTCTTGGTCAGC	451
Db	68	HisAlaAsnLeuThrLeuLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
Qy	452	AATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAATCAGCAATGCCACCTT	511
Db	88	GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107
Qy	512	CAGTCAGGAGAGATTCAAGATACATGAACACAGGAAAGAACTCAAAAGTTTTCAGTTAGT	571
Db	108	ArgLysGlyAlaGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
Qy	572	CTGTCTCATGAACAAATTCGACTGTCTGGTTCAGAGAAACTTACGCCTCACCTGAAATAC	631
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuValGlyLeuProTyr	145
Qy	632	TATGTGGCTATGGACTTCCAGGCCAAGTTAGTGTGATGGCTTTGAAGGGTTTTATAAAGC	691
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
Qy	692	ACATACAGAATCTCTGGTGGTGAACAACAAGATTCTTGCAGATAACACAGATTTTTCAGCC	751
Db	166	ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
Qy	752	CAGGCACGCATGGCTTCCCTTGGTTGATGAACCGTTGGTTCAAGCCAACTTTTCAATC	811
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
Qy	812	AAGATACCAAGAGAGACGACATATTCGACTATCCACATGCCCAAGGTTTAAGCAATT	871
Db	206	LysIleArgArgGluProArgHisIleuAlaIleSerAsnMetProLeuValLysSerVal	225
Qy	872	GAACTTGAAGAGGTCCTTTTGAAGATCACCTTTGAACAATACTGTGTAAAAATCAGTACATAC	931
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245
Qy	932	CTTTGAGCTCATAGTTTGTGATTTCCACTCTCTGAGTGCTTCACCTTCATCAGGGGTC	991
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
Qy	992	AAGGTGTCATCTATGCATCCCGACACAAACGGATCAACACATATGTCCTTTCAGGCA	1051
Db	266	LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla	285
Qy	1052	TCACTTGAAGCTACTGTGATTTTATGAAAAGTACTTTGATATCTACTATCCACTCTCCAAA	1111
Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305
Qy	1112	CTGGATTAAATTGCTATTCTGACTTTGCACCTGGAGCCATGGAAAAATTTGGGGCTCAT	1171
Db	306	GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAenTrpGlyLeuThr	325
Qy	1172	ACATATAGGGAGAGCTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGATAAATCG	1231
Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345
Qy	1232	TGGGTCCACGAGTCAATAGCCCATCAACTGGCGCACCACTGGTTTGGCAACTCGTCCACA	1291
Db	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
Qy	1292	ATGGAATGGTGAATGATATTGCTTAAAGAGGGTTTTGCAAAATACATGAACTTATC	1351
Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
Qy	1352	GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTTTGAATGCTGTTTT	1411
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
Qy	1412	GAAGTAATTACAAAAGATTCAATTGAATTCATCCCGCCCTATCTCCAAACACGCGCAACC	1471
Db	406	AspAlaMetGluValAspAlaLeuAsnSerHisProValSerThrProValGluAsn	425
Qy	1472	CCGACTCAAAATACAGGAAATGTTTGATGAAGCTTTCCTATATAACAGGGAGCTTGTATT	1531

Db	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
QY	1532	AATATGCTCAAGGATTTTCTGGTGGAGGAGAAATCCAGAAAGAAATAATTCAGTACTTA	1591
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
QY	1592	AAGAAGTTTCAGCTATAGAAATGCTAAGAATGATGACTGTGGAGCAGCTCTGTCAAATAGT	1651
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTyrAspSerMetAlaSerIle	485
QY	1652	TGTTTAGAAGATGATTTTACATCTGGT-----GGAGTTTGTCATTTCGGATCCCAAGATG	1705
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
QY	1706	ACAAGTAAACATGCTCGCTTCTGGGGGAAAAATGCAGAGGTCAAAGAGATGATGACTACA	1765
Db	504	SerSerSerSerHisIstPheHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
QY	1766	TGGACTCTCCAGAAAGGAATCCCTCTGCTGGTGGTTAAACAAGACGGGTGTTCACTCCGA	1825
Db	524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
QY	1826	CTGCAACAGAGACGCTTCTCCAGGGGGTTTTTCCAGGAAGACCTGTAATGGAGGGCCCTG	1885
Db	544	MetLysGlnGluHisIstYrMetLysGly-----SerAspGlyAlaPro	557
QY	1886	CAGGAGAGGTACCTGTCGCATATCCCAATTGCACCTTCCACGAGTCTCTTAATGTGATC	1945
Db	558	AspThrGlyTyrLeuIstPheIstValProLeuThrPheIleThrSerLysSerAspMetVal	577
QY	1946	CACAGACACATTTCAAATCAAAACAGACAGATACTCTGGATCTACTCGTAAAAAGACCGATTGG	2005
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluValGluTyr	597
QY	2006	GTGAAATTTAATGTGGACTCAATGGTTACTACATCGTTCTCACTATGAGGGTCAATGGATGG	2065
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisIstYrGluAspAspGlyTyr	617
QY	2066	GACCAACTATTACACAGCTGAATCAGAACCCACACACTCTCTCAGACCTAAGGACAGATGA	2125
Db	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
QY	2126	GGTCTGATTCATGATGTGTTTCAGCTAGTTGGTGCAGGGAGACTGACCTTAGACAAAGCT	2185
Db	638	SerLeuIleAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657
QY	2186	CTTGACATGACTTACTACCTCCAACATGAACAAAGCAGCCCGCAGCTTCTCGAAGGTCGTG	2245
Db	658	LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu	677
QY	2246	AGTTACTTGGAATCGTTTACCACATGTCGACAGAGGAATATTTCCAGATATCTCTGAA	2305
Db	678	AsnGluLeuLeuProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr	697
QY	2306	AACTCAAGCGTTACCTTCTTCAGTATTTTAAAGCCAGTGAATTCACAGCGCAAGCTGGAGT	2365
Db	698	GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr	717
QY	2366	GACAAAGGGCTCAGTCTGGGACAGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC	2425
Db	718	AspGluGlySerValSerGluArgMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal	737
QY	2426	CTGACCACTGCTCTTCTGCATCCAGAAAGCTGCTGAACCTCTTCCAGCTGGATGGAAATCC	2485
Db	738	HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysIstPyrLysGluSer	757
QY	2486	AGTGGAAAAATAAATATACCACACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAG	2545
Db	758	AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln	777
QY	2546	ACAACAGCAGATGGAATTACCTTTTAGAGCAATATGAATGTCTCAATGTCTCAAGTCTGAA	2605



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: September 26, 2005, 06:43:03 ; Search time 431.186 Seconds  
(without alignments)  
6354.782 Million cell updates/sec

Title: US-10-039-073-2  
Perfect score: 5912  
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Scoring table:  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 3653108

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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Database :  
Published Applications AA:  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5052	85.5	960	13	US-10-039-073-1	Sequence 1, Appli
2	5052	85.5	960	14	US-10-168-425-6	Sequence 6, Appli
3	4141	70.0	785	15	US-10-363-616-459	Sequence 459, App
4	3799	64.3	728	9	US-09-764-853-646	Sequence 646, App
5	3770	63.8	722	9	US-09-764-853-819	Sequence 819, App
6	2516.5	42.6	941	15	US-10-220-443-2	Sequence 2, Appli
7	2515.5	42.5	941	15	US-10-264-237-2723	Sequence 2723, Ap
8	2515.5	42.5	941	18	US-10-472-533-329	Sequence 329, App
9	2515.5	42.5	944	14	US-10-106-698-6381	Sequence 6381, Ap
10	2512.5	42.5	941	9	US-09-989-722-353	Sequence 353, App
11	2512.5	42.5	941	9	US-09-989-723-353	Sequence 353, App
12	2512.5	42.5	941	12	US-09-989-279-353	Sequence 353, App
13	2512.5	42.5	941	9	US-09-989-727-353	Sequence 353, App
14	2512.5	42.5	941	9	US-09-989-731-353	Sequence 353, App
15	2512.5	42.5	941	9	US-09-989-732-353	Sequence 353, App
16	2512.5	42.5	941	9	US-09-991-073-353	Sequence 353, App
17	2512.5	42.5	941	9	US-09-990-442-353	Sequence 353, App
18	2512.5	42.5	941	18	US-09-991-163-353	Sequence 353, App
19	2512.5	42.5	941	9	US-09-993-604-353	Sequence 353, App
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21	2512.5	42.5	941	9	US-09-989-721-353	Sequence 353, App
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44	2512.5	42.5	941	10	US-09-991-157-353	Sequence 353, App
45	2512.5	42.5	941	10	US-09-997-514-353	Sequence 353, App

ALIGNMENTS

RESULT 1  
US-10-039-073-1  
; Sequence 1, Application US/10039073  
; Publication No. US20020098177A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: 17867, A No. US20020098177A1el Human Aminopeptidase  
; FILE REFERENCE: 35800/240749(5800-36  
; CURRENT APPLICATION NUMBER: US/10/039,073  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 09/345,650  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-039-073-1

## Alignment Scores:

Pred. No.: 0 Length: 960  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 85.45% Indels: 0  
DB: 13 Gaps: 0

US-10-039-073-2 (1-3366) x US-10-039-073-1 (1-960)

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DB 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40
QY 266 CCATCTAGTATCACTTCACCTGAGGATCCTCGGGGCTTTCCAGTAGCCACTAAATGGGAA 325
DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
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QY 386 TTTGTCCACCCCAATCTCACCCTCTGACCTCTGACATTTGTCATCTGAGAGATCGAAGTCTTG 445
DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
QY 446 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACCAATGCC 505
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DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
QY 686 AAAAGCACATACAGAACTCTTTGGTGGTGAACAAGAATTCTTGCAAGTAAACAGATTTGAG 745
DB 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
QY 746 CCNACCCAGGCATGCTTCCCTTCTGTTGATGNAACCGTTGTTCAAGGCCAATTT 805
DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
QY 806 TCAATCAAGATACGAAGAGAGAGGAGCATATTGCACATATCAACATGCCAAAGGTTAAG 865
DB 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240
QY 866 ACAATTGAACCTTGAGAGAGGCTTTTGGAGAGATCACTTTGAAACTACTGTGTAATAAGT 925
DB 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260
QY 926 ACATACCTGTAGCTACATGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCA 985
DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280
QY 986 GGGGTCAAGGTGCTCATCTATGATCCCGCAGCAAAACGGAATCAAAACATATTATGCTTTG 1045
DB 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300
QY 1046 CAGGCATCACTGAAGCTACTTGATTTTATGAAAAGTACTTTGATATCTACTCCACTC 1105
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DB 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320
QY 1106 TCCAAACTGGATTTAATTGCTATTCTTGATCTTTCACCTCGAGCCATGGAAAAATTTGGGC 1165
DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340
QY 1166 CTCAATTACATATAGGAGAGCTCACTGCTTTTTCACCCCAAGAGCTCTTCTGCTTCCGAT 1225
DB 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360
QY 1226 AAATGTGGGTCCACGAGTCATAGCCCATGAATGGCGCACCAAGTGGTTGGCAACCTG 1285
DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380
QY 1286 GTCACATGAAGTGGTGAATGATATTGCTTAAGGAGGGTTTTCAAAATAATCATCGAA 1345
DB 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrIleGlu 400
QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTG 1405
DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420
QY 1406 TGTTTTGAAGTAATTACAAAGATTCAATGAATTCATCCCGCCCTATCTCCAAACACGCG 1465
DB 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440
QY 1466 GAAACCCCGACTCAAATACAGGAAATGTTTGATGAAGTTTCTTATAACAAGGAGCTTGT 1525
DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460
QY 1526 ATTTTGAATATGCTCAAGGATTTTTCGGGTGAGGAGAAATTCAGAAAGGAATAATTCAG 1585
DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln 480
QY 1586 TACTTAAAGAGTTCAGCTATAGAAATGCTAAGAATGATGACTTGTGGAGAGTCTGTCA 1645
DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSerLeuSer 500
QY 1646 AATAGTTGTTTGAAGAGTGTATTCATCTGGTGGAGTTTGTCAATCCGATCCCAAGATG 1705
DB 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520
QY 1706 ACAAGTAACTATGCTCGCCTTTCTGGGGGAAAAATGCAGAGGTCAAAGAGATGATCTACA 1765
DB 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThr 540
QY 1766 TGAATCTCCAGAAAGAAATCCCGCTGCTGGTGTAAACAAGACGGGTGTTCACTCGGA 1825
DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560
QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCAGGAAGACCCCTGAATGAGGGCCCTG 1885
DB 561 LeuGlnGlnLysArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580
QY 1886 CAGGAGAGTACCTGTGGCATATCCCATTCACCTTCCACGAGTCTTCTTAATGTGATC 1945
DB 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600
QY 1946 CACGACACATCTTAAATCAAAGACAGATACTCTGATCTACTCTGAAAGACCACTGG 2005
DB 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
QY 2006 GTGAAATTTAATGTGGACTCAAATGGTTTACTACATCGTTTCACTATGAGGGTCACTGGATGG 2065
DB 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
QY 2066 GACCACTCAATTACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGAGTA 2125
DB 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
QY 2126 GGTCTGATTCATGATGTTTTCAGCTAGTTGGTGCAGGAGACTGACCCCTAGACCAAGCT 2185
DB 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
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QY 2186 CTTGACATGACTTACTTACCTCAACATGAAGAACAGCAGCCCCGCACTTCTCGAAGGTCTG 2245
Db |||||
QY 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
Db |||||
QY 2246 AGTTACTTGGATCGTTTACCATGATGGACAGAGAAATATTTTCAGATATCTCTGAA 2305
Db |||||
QY 701 SerTyrLeuGluSerPheTyrHisMetMetAspA-gA-gAsnIleSerAspIleSerGlu 720
Db |||||
QY 2306 AACCTCAAGCGTTACCTCTTCAGTATTTTAAAGCCAGTGAATGACAGGCAAAAGCTGGAGT 2365
Db |||||
QY 721 AsnLeuLeuArgTyrTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
Db |||||
QY 2366 GACAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGGCTGTGAC 2425
Db |||||
QY 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
Db |||||
QY 2426 CTGAACCATGCTCCTGTCATCCAGAAAGCTGCTGAACCTCTCCAGTGGATGGAATCC 2485
Db |||||
QY 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
Db |||||
QY 2486 AGTGAAATTAATATATACCAACAGATGTTTAAAGATTGTATTCTGTGGGTGCTCAG 2545
Db |||||
QY 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
Db |||||
QY 2546 ACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAACCTGCTCAATGTCAAGTCTGAA 2605
Db |||||
QY 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
Db |||||
QY 2606 CAAACAAATTCGTATGCTTTTGCACAGCAGCATCAGGAAAGTTACTGAAGTTA 2665
Db |||||
QY 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
Db |||||
QY 2666 ATTGAACTAGGAATGGAAGAAAGTTATCAAGACACAGAACTCTGCAGCTCTCCTTCAT 2725
Db |||||
QY 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
Db |||||
QY 2726 GCGATTGCCAGACGTCCTCAAGGGGCGAGCAACTAGCATGGATTTTGTGAAGAGAAATGG 2785
Db |||||
QY 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
Db |||||
QY 2786 ACCCATCTCTCAAAAATTTGACTTGGCTCATATGACATAAGCATCATCTCTGGC 2845
Db |||||
QY 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900
Db |||||
QY 2846 ACAACAGCTCACTTTTCTTCCAGGATAGTTGCAAGAGTCAAACTATTTTTCAACTCT 2905
Db |||||
QY 901 ThrThrAlaHisPheSerSerLysSerLysAspLysLeuGlnGluValLysLeuPheGluSer 920
Db |||||
QY 2906 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTTCTCGAAACGATAACCAAA 2965
Db |||||
QY 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
Db |||||
QY 2966 ATATATAATGCTGGAGAGAAATCTTCGACTCTGAGACTTGGCTTAATGTTACT 3025
Db |||||
QY 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
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RESULT 2

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US-10-168-425-6
; Sequence 6, Application US/10168425
; Publication NO. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.
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; APPLICANT: LAL, Preeti
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
; PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 960
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124706A1 60116897CD1
US-10-168-425-6

Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5052.00 Matches: 960
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 85.45% Indels: 0
DB: 14 Gaps: 0

US-10-039-073-2 (1-3366) x US-10-168-425-6 (1-960)
QY 146 ATGTTCATTCCTCTGCAATGTTAAATTCACACAGAAACCAATGTTTAAACATTCACAGA 205
Db |||||
QY 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
Db |||||
QY 206 GGATTTTACTCTCTTAACAGCCATCTTGCCCAAAATATGCAATTTGTTCTCAGTCTCAGTG 265
Db |||||
QY 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysLeuSerGlnPheSerVal 40
Db |||||
QY 266 CCATCTAGTATTCATCTCAGTACAGATCTCTGGGCTTTCCAGTAGCCACCAATCGGAA 325
Db |||||
QY 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60
Db |||||
QY 326 CGATTTCTCTCGCAGGAGCTAAGCTCCAGTGGTGCATTCTCTCCATTATCACCTC 385
Db |||||
QY 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80
Db |||||
QY 386 TTTGTCCACCCCAATCTCACCTCTCTGACATTTGTTGCATCTCGAAGATCGAAGTCTTG 445
Db |||||
QY 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100
Db |||||
QY 446 GTCAGCAATGTCATCCAGTTTATCATCTTGACACAGCAAGATCTTGAATTCACGAATGCC 505
Db |||||
QY 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120
Db |||||
QY 506 ACCCTTCAGTCAGAGGAGATTCAAGATACATGAAACCCAGGAAAGAACTGAAAGTTTG 565
Db |||||
QY 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140
Db |||||
QY 566 AGTTACCCCTGCTCATGAACAAATTCACCTGCTGTTCCAGAGAAACTTACGCTCACCTG 625
Db |||||
QY 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160
Db |||||
QY 626 AAATACTATGTGGCTATGGACTTCCAGCCCAAGTAGTGTAGTGGCTTTGAAGGGTTTAT 685
Db |||||
QY 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180
Db |||||
QY 686 AAAAGACATACAGAACTCTTGGTGGTGAACAAAGAAATTTCTGCAGTAAACAGATTTTCAG 745
Db |||||
QY 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200
Db |||||
QY 746 CCAACCCAGGACGATGCTTTCCTCTTGTGTTGATGAACCGTGTGTTCAAAGCCCACTTT 805
Db |||||
QY 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220
Db |||||
QY 806 TCAATCAAGATACGAAGAGAGAGAGGCGATATTGTCATCTATCCAAATCCCAAGGTTAAG 865
Db |||||
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Db 221 SerIleuYsIleAArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
QY 866 ACAATTGAACCTGAAGAGGCTCTTTGGAAGTACACTTTGAACTACTGTAAAAATGAGT 925  
Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260  
QY 926 ACATACCTTGTAGCCTACATAGTTGTGATTTTCACATCTCTGAGTGGCTTCACATTCATCA 985  
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
QY 986 GGGGTCAAGGTGTCATCTATGCAATCCCGACAGCAAAACGGAATCAACACATATGCTTTG 1045  
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
QY 1046 CAGGCATCACATGACCTACTGATTTTATGAAAGTACTTTGATATCTACTACTCCACTC 1105  
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
QY 1106 TCCAAACTGGATTTAATTGCTATTCTGACTTTGCCTGGAGCATGGAAAAATGGGGC 1165  
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
QY 1166 CTCATTACATATAGGAGACGTCACTGCTTTTTCACCCCAAGACCTCTCTGCTTCCGAT 1225  
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
QY 1226 AAATGCTGGGTCACGAGTCCATAGCCCATCACTGGCGCACAGTGGTTTGGCAACCTG 1285  
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
QY 1286 GTCACAAATGGAAATGGTGAATGATATTTGGCTTAAGGAGGGTTTTGCAAAATACATGGAA 1345  
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400  
QY 1346 CTTATCGCTGTAAATGCTACATATCCAGAGCTGCAATTTGATGATGACTATTTTGAATGTG 1405  
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420  
QY 1406 TGTTTGAAGTAATTACAAAGATTCAATTGAATTCATCCGCGCCCTATCTCCCAACACGCG 1465  
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
QY 1466 GAAACCCGACTCAAAATACAGAAATGTTTGATGAAGTTTCTCTATAACAAGGGAGCTTGT 1525  
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
QY 1526 ATTTTGAATATGCTCAAGGATTTCTGGTGAGGAGAAATTCAGAAAGGAATTAATTCAG 1585  
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480  
QY 1586 TACTTAAAGAAGTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGAGCAGTCTGTCA 1645  
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500  
QY 1646 AATAGTCTTTAGAAAGTATTTACATCTCGTGGAGTTTCTCATTCGGATCCCAAGATG 1705  
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520  
QY 1706 ACAAGTAACTGCTGCGCTTTCTGGGGGAAATGCAAGGTCAAAGATGATGACTACA 1765  
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540  
QY 1766 TGGACTCTCCAGAAGGAATCCCTGCTGCTGTTAAACAAGCGGGTTCCTCCGA 1825  
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560  
QY 1826 CTGCAACAGGAGCGCTTCCCTCAGGGGTTTTCCAGGAAGACCTCGAATGAGGGCCCTG 1885  
Db 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580  
QY 1886 CAGGAGAGTACCTGTGGCATATCCATGACCTTACTCCAGAGTCTCTCTAATGTGATC 1945

Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600  
QY 1946 CACAGACACATCTAAATCAAAAGACAGATACTCTGATCTACTCTGAAAAACAGATTGG 2005  
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
QY 2006 GTGAAATTTTAAATGTGACTCAAAATGGTTACTACATCCTTACATCTATGAGGTCATGGATGG 2065  
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
QY 2066 GACCAACTCATTTACACAGCTGAATCAGAACACACACTTCTCAGACCTAAGGACAGAGTA 2125  
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
QY 2126 GGTCTGATTCATGATGTGTTTTCAGCTAGTTGGTCAGGGAGACTGACCTTAGACAAAGCT 2185  
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
QY 2186 CTTGACATGACTTACTACCTCCAAACATGAAACAGCAGCCCCGACCTTCTCGAAGGCTG 2245  
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700  
QY 2246 AGTTACTTGGAAATCGTTTACACATGATGCGACAGAGGAATATTTTTCAGATATCTCTGAA 2305  
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720  
QY 2306 AACCTCAAGCTTACCTTCTTCACTATTTTAAAGCCAGTGAATGACAGGCAAGCTGGAGT 2365  
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
QY 2366 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGGCTGTGAC 2425  
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
QY 2426 CTGACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTCGATGGAATCC 2485  
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
QY 2486 AGTGGAAATTAATATACCAACAGATGTTTAAAGATTCTGTATTCTGTGGGTGCTCAG 2545  
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800  
QY 2546 ACAACGACAGGATGGAATTAACCTTTTAGACAAATATGAACCTGTCATGTCAAGTCTGAA 2605  
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820  
QY 2606 CAAAACAAATTCGTATGCTTGTCTCAACGACGACATCAGGAAAGTTACTGAACTTA 2665  
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QY 2666 ATTGAACCTAGGAATGGAAGGAAAGGTTTATCAAGACACAGAACTTGGCAGCTCTCCTTCAT 2725  
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QY 2726 GCGATTCCAGACGCTCAAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAAAATGG 2785  
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QY 2786 ACCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGGC 2845  
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900  
QY 2846 ACAACAGCTCACCTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAAACTTATTTTTGAATCT 2905  
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QY 2906 CTTGAGGCTCAAGATCACATCTGGATATTTTCAAACCTGTTCTTGAAAACGATTAACCAA 2965  
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QY 2966 AATATAAATGCGTGGAGAGAATCTTCCGACTCTGAGGACTTGGCTTAATGTTAATCT 3025  
Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960

## RESULT 3

US-10-363-616-459  
; Sequence 459, Application US/10363616  
; Publication No. US20040044181A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-113 (793)  
; CURRENT APPLICATION NUMBER: US/10/363,616  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 09/654,935  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 490  
; SEQ ID NO 459  
; LENGTH: 785  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-363-616-459

## Alignment Scores:

Pred. No.:	0	Length:	785
Score:	4141.00	Matches:	782
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	2
Query Match:	70.04%	Indels:	0
DB:	15	Gaps:	0

US-10-039-073-2 (1-3366) x US-10-363-616-459 (1-785)

QY	146	ATGTTCCATTCTTCGCAATGTTAATTCACAGAAAACCAATGTTTAACTTCACAGA	205
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QY	206	GGATTTTACTGCTTAACGCCATCTGCCCAAAATGCAATGTTGTTCTCAGTGT	265
DB	21	GlyPheThrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
QY	266	CCATCTAGTTATCACTTCACTGAGGATCCTGGGGCTTTCCACAGTACCACTAATGGGAA	325
DB	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	326	CGATTTCTTGGCAGAGTAAGGCTCCCACTGGTGGTCAATTCCTCTCCATTATGACCTC	385
DB	61	ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu	80
QY	386	TTTGTCCACCCCAATCTCACCTCTCTGGACTTGTGTGCATCTGAGAAGTCCAGTCTTG	445
DB	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	446	GTCAGCAATGCTACCCAGTTTATCATCTTGCAACAGAAAGATCTTGAATCACGAATGCC	505
DB	101	ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
QY	506	ACCTTTCAGTCAGAGAAGATTCAAGATACATGAAACCCAGGAAAGAACTGAAAGTTTG	565
DB	121	ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140
QY	566	AGTTACCTGCTCATGACAAATTCGACTGCTGGTTCAGAGAACTTACGCTCACCTG	625
DB	141	SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160
QY	626	AAATACTATGTGGCTATGACTTCCAAGCCAAGTTAGGTGATGGCTTTGAAGGGTTTAT	685
DB	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	686	AAAAGCACATACAGAACTCTTGGTGGTGAACAAGAAATTTCTGCACTAACAGATTTGAG	745
DB	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	746	CCAAACCCAGGACGCATGGCTTCCCTTGTGATGAACCGTGTGTTCAAGCCAACTTT	805
DB	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220

QY	806	TCAATCAAGATACGAAGAGAGAGAGAGGCGATATTGCACTATCCAAACATGCCAAAGGTTAAG	865
DB	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
QY	866	ACAATTGAACCTGAAGGAGGCTCTTTGCAAGCATCACTTTGAAACTACTGTAAATAAGT	925
DB	241	ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260
QY	926	ACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA	985
DB	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	986	GGGTCAAGGTGTCATCTATGCAATCCCGACAGAAAACGGAATCAACACATATATCTTTG	1045
DB	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	1046	CAGCATCACCTGAAGCTACTTGTATTTATCAAAAGTACTTTGATATCTACTATCTACCTC	1105
DB	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
QY	1106	TCCAAACTGGGATTTAAATGCTATTCTGACTTTTGCACTGGAGCCATCGAAAATTTGGGC	1165
DB	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
QY	1166	CTCATTTACATATAGGAGACGCTCACTGCTTTTTCACCCCAAGACCTCTCTGCTTCCGAT	1225
DB	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
QY	1226	AACTGTGGTCCACAGAGTCATAGCCCATCACTGGCGCACCGAGTGTGGCAACCTG	1285
DB	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
QY	1286	GTCAAAATGGAATCGTGAATGATATTGGCTTAAGGAGGGTTTTGCAAAATACATCGAA	1345
DB	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
QY	1346	CTTATCGCTGTTAATGTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG	1405
DB	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
QY	1406	TGTTTGAAGTAATACAAAAGATTCATTAATTCATCCCGCCCTATCTCCAAACACGG	1465
DB	421	CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla	440
QY	1466	GAACCCCGACTCAAAATACAGAAATGTTTCATGAAGTTTCTTAAACAAGGAGCTTGT	1525
DB	441	GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
QY	1526	ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAAGGAATATTCAG	1585
DB	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln	480
QY	1586	TACTTAAAGAAGTTCAGCTATAGAAATGCTTAAGATGATGATGATCTGTGAGCAGCTGTCA	1645
DB	481	TyrLeuLysLysPheSerTyrArgAsnAlaAsnAsnAspAspLeuTrpSerSerLeuSer	500
QY	1646	AATAGTTGTTTGAAGAAGTATTTTACATCTGGTGGAGTTTCTCATTCGGATCCCAAGATG	1705
DB	501	AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet	520
QY	1706	ACAAAGTAACTGCTCGCTTTCTGGGGGAAATTCAGAGGTCAAAGAGATGATGACTACA	1765
DB	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAlaAsnAlaGluValLysGluMetMetThrThr	540
QY	1766	TGGACTCTCCAGAAAGGAATCCCTGCTGGTGTGTTAAACAAGACGGGTGTTCATCCGA	1825
DB	541	TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg	560
QY	1826	CTGCAACAGGAGCGCTTCTCCAGGGGTTTTTCCAGGAAGACCCCTGAATGAGGCGCCCTG	1885
DB	561	LeuGlnGlnArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	580

Qy 1886 CAGGAGAGTACCTGTGGCATATCCCATGTGACCTACTCCAGAGTCTCTTAATGTGATC 1945  
Db |||||||  
Qy 1946 CACGACACATTCATAAATCAAGACAGATACTCTGGATCTACCTGAAAAACAGATTGG 2005  
Db |||||||  
Qy 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
Qy 2006 GTGAAATTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCATGGATGG 2065  
Db |||||||  
Qy 621 VallysPheAsnValAspSerAsnGlyTyrTyrIleValHisIstYrGluGlyHisGlyTrp 640  
Qy 2066 GACCAACTCATTACACAGCTCAATCAGAAACACACACTCTTCAGACCTTAAGGACAGAGTA 2125  
Db |||||||  
Qy 2126 GGTCTGATTCATGATGTCTTTCAGCTAGTTGGTGCGAGGAGACTGACCCCTTAGACAAAGCT 2185  
Db |||||||  
Qy 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
Qy 2186 CTTGACATGACTTACTACTCTCAACATGAAACAAAGCAGCCCGCACTTCTCGAAGGCTG 2245  
Db |||||||  
Qy 681 LeuAspMetThrTyrTyrLeuGlnHisGlnThrSerSerProAlaLeuLeuGluGlyLeu 700  
Qy 2246 AGTTACTTGGAAATCGTTTTACCACATGATGACAGAGAAGAAATATTTACAGATATCTCGAA 2305  
Db |||||||  
Qy 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720  
Qy 2306 AACCTCAAGCGTTACCTTCTTCAGTATTTTAAGCCAGTGATGACAGGCAAGCTGGAGT 2365  
Db |||||||  
Qy 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
Qy 2366 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTTTGAAGCTGGCTGTGAC 2425  
Db |||||||  
Qy 741 AspyLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
Qy 2426 CTGAACCATGCTCTTCATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATGGAATCC 2485  
Db |||||||  
Qy 2486 AGTGAAAAATTA 2497  
Db |||||||  
781 SerGlyLysLeu 784

RESULT 4  
US-09-764-853-646  
; Sequence 646, Application US/09764853  
; Patent No. US20020090672A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJ206  
; CURRENT APPLICATION NUMBER: US/09/764,853  
; PRIORITY FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 939  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 646  
; LENGTH: 728  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-853-646

Alignment Scores:  
Pred. No.: 0 Length: 728  
Score: 3799.00 Matches: 722  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 64.26% Indels: 0  
DB: 9 Gaps: 0

US-10-039-073-2 (1-3366) x US-09-764-853-646 (1-728)

Qy 860 GTTAAGACAAATTGAACCTTGAGGAGGTCTTTTGAAGATCACCTTTGAAACACTACTGTAAAA 919  
Db |||||||  
7 VallysThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLys 26  
Qy 920 ATGAGTACATACCTTGATGCTTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 979  
Db |||||||  
27 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 46  
Qy 980 TCATCAGGGTCAAGGTGCTCCATCTATGCATCCCCACAGAAACCGAATCAAAACACATTAT 1039  
Db |||||||  
47 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 66  
Qy 1040 GCTTTGCGAGCATCACCTGAAGTACTTTGATTTTTATGAAAAGTACTTTTGATATCTACTAT 1099  
Db |||||||  
67 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 86  
Qy 1100 CCACTCTCCAAACTGGATTTAATTGCTATTTCTGACTTTCACCTGAGCCATCGGAAAT 1159  
Db |||||||  
87 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 106  
Qy 1160 TGGGGCTCATATTACATAGGGAGCGTCACTGCTTTTTCACCCCAAGACCTCTTCTGCT 1219  
Db |||||||  
107 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 126  
Qy 1220 TCCGATAAACTGTGGGTCAACGAGTCATAGCCCATGAACCTGGCGCACCACTGTTTGGC 1279  
Db |||||||  
127 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 146  
Qy 1280 AACCTGCTCAATCGAATCGTGGATGATATTTGGCTTAAGGAGGTTTTGCAAAATAC 1339  
Db |||||||  
147 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 166  
Qy 1340 ATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGTG 1399  
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167 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 186  
Qy 1400 AATGTGTGTTTGAAGTAAATTAACAAAGATTCATATGAATTCATCCGCCCTATCTCAAA 1459  
Db |||||||  
187 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 206  
Qy 1460 CCAGCGAAACCCGACTCAATACAGGAAATGTTGATGAAGTTCCTATACAAAGGA 1519  
Db |||||||  
207 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 226  
Qy 1520 GCTTGATTTTGAATATGCTCAAGGATTTTCTGGTGAGGAGAAATCCAGAAAGGAATA 1579  
Db |||||||  
227 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyLe 246  
Qy 1580 ATTCAGTACTTAAAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGAGCAGT 1639  
Db |||||||  
247 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer 266  
Qy 1640 CTGTCAAATAGTTGTTTAGAAAGTGATTTTACATCTGCTGGAGTTCCTCATTCGGATCCC 1699  
Db |||||||  
267 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 286  
Qy 1700 AAGATGACAAAGTAACTGCTCGCTTCTGGGGGAAAAATGCAGAGGTCAAGAGATGATG 1759  
Db |||||||  
287 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet 306  
Qy 1760 ACTACATGGACTCTCCAGAAAGGAATCCCTGCTGCTGGTTTAAACAGACGGGTGTTC 1819  
Db |||||||  
307 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 326  
Qy 1820 CTCGAGCTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCCCTGAATGAGG 1879  
Db |||||||  
327 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 346  
Qy 1880 GCCCTGAGGAGAGGTACTCTGTGGCATATCCATTGACCTACTCCAGAGTCTTCTTAAT 1939  
Db |||||||  
347 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 366  
Qy 1940 GTGATCCACAGACACATTTCAAAATCAAGACAGATACTCTGGATCTACTCTGAAAAGACC 1999

Db	367	ValIleHisArgHisIleLeuLeuYssrLysThrAspThrLeuAspLeuProGluLysThr	386	
Qy	2000	AGTGGGTGAAATTAATGTGACCAAAATGCTTACTACATCGTTCACTATGAGGTCAT	2059	
Db	387	SerTrpValLysPheAsnValAspSerAsnGlyTyTyTyIleValHisTyGluGlyHis	406	
Qy	2060	GGATGGGCAACTCATATACACAGCTGAATCAGAACCCACACTCTCTCAGACCTAAGGAC	2119	
Db	407	GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp	426	
Qy	2120	AGAGTAGGTCTGATTCATGATCTGTTTCAGCTAGTTGTGTCAGGCGAGACTGACCTAGAC	2179	
Db	427	ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	446	
Qy	2180	MAAGCTCTTGACATGACTTACTCTCAACATGAACAAGCAGCCCGCACTTCTCGAA	2239	
Db	447	LysAlaLeuAspMetThrTyTyTyLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	466	
Qy	2240	GCTCTGAGTTACTTGGAAATCGTTTTCACATGATGGACAGAAATATTTTCAGATATC	2299	
Db	467	GlyLeuSerTyLeuGluSerPheTyHisMetMetAspArgAsnIleSerAspIle	486	
Qy	2300	TCTGAACCTCAAGCTTACCTTCTTCAGTATTTTAAGCCAGTATTACACAGCAAGC	2359	
Db	487	SerGluAsnLeuLysArgTyTyLeuLeuGlnTyPheLysProValIleAspArgGlnSer	506	
Qy	2360	TGGAGTGACAGGGCTCAGCTGGGACAGAGATGCTCCGCTCGCTCTTGAAGCTGGCC	2419	
Db	507	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	526	
Qy	2420	TGTGACCTGAACCATGCTCTTTCGATCCAGAAAGCTGTGAATCTTTCCTCCAGTGATG	2479	
Db	527	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	546	
Qy	2480	GAATCCAGTGGAAATTAATATATACCAACAGATGTTTAAAGATTGCTGATCTCTGGGT	2539	
Db	547	GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTySerValGly	566	
Qy	2540	GCTCAGACAAACAGCAGATGGAATACCTTTTGAAGCAATATGAATGTCAATGTCAAGT	2599	
Db	567	AlaGlnThrThrAlaGlyTrpAsnTyLeuLeuGluGlnTyTyGluLeuSerMetSerSer	586	
Qy	2600	GCTGAACAAACAAATCTGTATGCTTTGTCAACAGCAAGCATCAGGAAAGTTACTG	2659	
Db	587	AlaGluGlnAsnLysIleLeuTyTyAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	606	
Qy	2660	AGTTAATTAAGTAACTAGGAATGCAAGGAAAGTTATCAACACACAGAACTTGGCAGCTCTC	2719	
Db	607	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu	626	
Qy	2720	CTTCATGCGATTGCCAGACGCTCCAAAGGGGCGACCACTAGCATGGGATTTTCTAAGAGAA	2779	
Db	627	LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	646	
Qy	2780	AATGGACCCATCTTCTGAAAAATTTGACTTGGGCTCATATGACATAAGGATGATATC	2839	
Db	647	AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyTyAspIleArgMetIleIle	666	
Qy	2840	TCGGCACAACAGCTCAGCTTTTCTCCAGGATAGTTGCCAGAGGTGAACCTATTTT	2899	
Db	667	SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe	686	
Qy	2900	GAATCTCTTGAGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTCGAAACGATA	2959	
Db	687	GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle	706	
Qy	2960	ACCAAAATATAAATGGCTGGAGAGAAATCTTCCGACTCTCAGGACTTGGCTAATGGTT	3019	
Db	707	ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetVal	726	
Qy	3020	ATAACT 3025		

Db

727

AsnThr

728

RESULT 5

US-09-764-853-819

Sequence 819, Application US/09764853

Patent No. US20020090672A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: P206

CURRENT APPLICATION NUMBER: US/09/764,853

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 939

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 819

LENGTH: 722

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (237)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (296)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (719)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (720)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (721)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-853-819

Alignment Scores:

Pred. No.: 0

Length: 722

Score: 3770.00

Matches: 717

Percent Similarity: 99.31%

Conservative: 0

Best Local Similarity: 99.31%

Mismatches: 5

Query Match: 63.77%

Indels: 0

Gaps: 9

US-10-039-073-2 (1-3366) x US-09-764-853-819 (1-722)

Qy

860

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919

Db

1

VallysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLys

20

Qy

920

ATGAGTACATACCTTGTAGCCTACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCACT

979

Db

21

MetSerThrTyLeuValAlaTyIleValCysAspPheHisSerLeuSerGlyPheThr

40

Qy

980

TCATCAGGGGTCAAGGTGTCATCTATGCATCCCCAGACAAACGGAATCAACACATTAT

1039

Db

41

SerSerGlyValLysValSerIleTyTyAlaSerProAspLysArgAsnGlnThrHisTy

60

Qy

1040

GCTTTGAGGCGCACCTGCAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTAT

1099

Db

61

AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyTyGluLysTyTyPheAspIleTyTy

80

Qy

1100

CCACTCTCCAAACTGGGATTTAATTTGCTATTCTCTGACTTTTGACCTGGAGCCATCGAAAT

1159

Db

81

ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn

100

Qy

1160

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1219

Db

101

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Qy

1220

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1279

Db 121 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140  
Qy 1280 AACCTGGTCAACAATCGAATGGTAATGATATTTGGCTTAAGAGGGGTTTTGCAAAATAC 1339  
Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160  
Qy 1340 ATGGAACHTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGTG 1399  
Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180  
Qy 1400 AATGCTGTTTGAAGTAATTCACAAAGATTCATGAATTCATCCCGCCCTATCTCCAAA 1459  
Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200  
Qy 1460 CCAGCGGAAACCCGAGCTCAAAATACAGAAATGTTTGATGAAGTTTCTCTATAACAAGGGA 1519  
Db 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220  
Qy 1520 GCTTGATTTTGAATATGCTCAAGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATA 1579  
Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPhe\*\*LysGlyIle 240  
Qy 1580 ATTCACTACTTAAAGAGTTTCAGCTATAGAATCTTAAGATGATGACTTGTGCGACAGT 1639  
Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 260  
Qy 1640 CTGTCAAAATAGTGTGTTAGAAAGTATTTTACATCTGGTGGAGTTTGCATTCGGATCCC 1699  
Db 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 280  
Qy 1700 AAGATGACAAATACATGCTCCCTTCTGGGGGAAATGCGAGGTCAAAGAGATGATG 1759  
Db 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGlu\*\*LysGluMetMet 300  
Qy 1760 ACTACATGCACTCCAGAAAGGAATCCCCCTGCTGGTGTAAACAAGACGGGTGTCA 1819  
Db 301 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSer 320  
Qy 1820 CTCGGACTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCCCTGAATGGAGG 1879  
Db 321 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340  
Qy 1880 GCCTGCGAGGAGAGGTACCTGTGGCATATCCATGTGACCTACTCCACGAGTTCCTTAAT 1939  
Db 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsn 360  
Qy 1940 GTGATCCACACACATCTTAAATCAAGACACATCTCTGGATCTACCTGAAAGACACC 1999  
Db 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380  
Qy 2000 AGTTGGGTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAT 2059  
Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 400  
Qy 2060 GGATGGGACCAACTCATTACACAGCTGAATCAGAACCAACACACTTCTCAGACCTTAAGGAC 2119  
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Qy 2120 AGAGTAGTCTGATTCATGATGTGTTTCAGTAGTGTGGTGAGGAGACTGACCCCTAGAC 2179  
Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440  
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Db 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 460  
Qy 2240 GGTCTGAGTTACTTGGAAATCGTTTTTACCACATGATGACAGAGAAATATTTTCAGATATC 2299  
Db 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 480  
Qy 2300 TCTGAAAACCTCAAGCGTTACTCTTCTCAGTATTTTAAAGCAGTATGACAGGCAAGC 2359  
Db 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500

Qy 2360 TGGAGTGCACAGGCTCAGTCTGGGACAGGATCTCGCTCGGCTCTCTTTGAAGCTGGCC 2419  
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Qy 2420 TGTGACCTGAACCATGCTCTTGTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATG 2479  
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540  
Qy 2480 GAATCCAGTGGAAATTAATATACCAACAGATGTTTAAAGATTTGTGATTTCTGTCGGT 2539  
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560  
Qy 2540 GCTCAGACAAACAGCAGGATGGAATTTACTTTTAGAGCAATATGAACCTGTCAATGCTCAAGT 2599  
Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580  
Qy 2600 GCTGAACAAACAAAATTCGTATGCTTTGTTCACACGAGCAAGCATCAGGAAAAGTTACTG 2659  
Db 581 AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu 600  
Qy 2660 AAGTTAATTGAATAGGAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTC 2719  
Db 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu 620  
Qy 2720 CTTTCATCGCATTCGCCAGACGTCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAGAA 2779  
Db 621 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640  
Qy 2780 AATTGACCCCATCTTCGAAAAATTTGACTTGGGCTCATATGACATAGAAGATGATCATC 2839  
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660  
Qy 2840 TCTGGCACACACGCTCACTTTCTTCCAGGATAAGTTGCAAGGGTGAACTATTATTTT 2899  
Db 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680  
Qy 2900 GAATCTCTTGGAGCTCAAGGATCACATCTCGATATTTTCAAACTGTTCGGAACCATATA 2959  
Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700  
Qy 2960 ACCAAAAATATAAATGGCTGGGAGAGAAATCTTCCGACTCTGAGGACTTGGCTAATGGTT 3019  
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu\*\*\*\*\* 720  
Qy 3020 AATACT 3025  
Db 721 \*\*\*Thr 722  
RESULT 6  
US-10-220-443-2  
; Sequence 2, Application US/10220443  
; Publication No. US20030215820A1  
; GENERAL INFORMATION:  
; APPLICANT: Levine, Stewart  
; TITLE OF INVENTION: REGULATORS OF TYPE-1 TUMOR NECROSIS FACTOR RECEPTOR AND OTHER CYT  
; TITLE OF INVENTION: RECEPTOR SHEDDING  
; FILE REFERENCE: 218732  
; CURRENT APPLICATION NUMBER: US/10/220,443  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/06464  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/185,586  
; PRIOR FILING DATE: 2000-02-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 941  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-220-443-2  
Alignment Scores:

Pred. No.: 7,628-224 Length: 941  
Score: 2516.50 Matches: 478  
Percent Similarity: 69.34% Conservative: 171  
Best Local Similarity: 51.07% Mismatches: 268  
Query Match: 42.57% Indels: 19  
DB: 15 Gaps: 7

US-10-039-073-2 (1-3366) x US-10-220-443-2 (1-941)

QY 212 TACTGCTTAACAGCCATCTTGCCCAATATATGATTTGCTCAGTTCCTCAGTGCATCT 271  
DB 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal : : : : : SerThrProSer 30  
QY 272 AGTTATCACTTCCATGAGATCCTGGGCTTCCAGTAGCCACTAATGGGGAACGATT 331  
DB 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47  
QY 332 CTTGGCAGGAGCTAAGCTCCCAAGTGTGGTCTCTCCATATGACTCTTTGTC 391  
DB 48 ProTrpAsnLysIleArgLeuProGluTyValIleProValHisThrAspLeuLeu 67  
QY 392 CACCCCAATCTCACCTCTGACCTTTGTCATCTGAGAGATCGAAGTCTTGTGTCAGC 451  
DB 68 HisAlaAsnLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87  
QY 452 AATGCTACCCAGTTTATCATCTTGACAGCAAGACTTGTGAATCAGCAATGCCACCTT 511  
DB 88 GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107  
QY 512 CAGTCAGAGGAGATTCAAGATACATGAACCCAGGAAAGAACTGAAAGTTTGTGTTAC 571  
DB 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125  
QY 572 CTGCTCATGAACAAATGCACTGTGGTTCAGAGAAACTTACGCCCTCACCTGAAATAC 631  
DB 126 ProArgGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTy 145  
QY 632 TATGTGGCTATGAGCTTCCAGCCCAAGTTAGTGTGAGTGTGAGGGTTTATAAAGC 691  
DB 146 ThrValValIleHisTyAlaGlyAsnLeuSerGluThrPheHisGlyPheTyLysSer 165  
QY 692 ACATACAGACTCTTGGTGTGAACAAAGAAATCTTGCAAGTAACAGATTGTGAGCCAACC 751  
DB 166 ThrTyArgThrLysGluGlyLeuArgIleLeuAlaSerThrGlnPheGluProThr 185  
QY 752 CAGGCACGATGCTTCCCTTCTGATGAACCGTTGTTCAAGCCAACTTTCAATC 811  
DB 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205  
QY 812 AAGATACGAAGAGAGCAGGCATATTGCATATCCAAATGCGCCAAAGGTTAAGACAAT 871  
DB 206 LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225  
QY 872 GNACTTGAAGAGGCTTTTGGAGATCACCTTTGAACTACTGTGTAATAATGATGATAC 931  
DB 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTy 245  
QY 932 CTGTGAGCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCCACTTCATCAGGGTC 991  
DB 246 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265  
QY 992 AAGGTGTCCATCTATGCAATCCCAAGCAAAAGCAATATGCTTTTGGAGCA 1051  
DB 266 LysValSerValTyAlaValProAspLysIleAsnGlnAlaAspTyAlaLeuAspAla 285  
QY 1052 TCACGTAGCTACTGATTTTATGAAGTACTTTGATATCTACTACTCCTCCTCCAAA 1111  
DB 286 AlaValThrLeuLeuGluPheTyGluAspTyPheSerIleProTyProLeuProLys 305  
QY 1112 CTGGATTAATGCTATCTCCTCCTTGCACCTTGAGCAGCATGGAAATGGGGCCTCATT 1171  
DB 306 GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325

QY 1172 ACATATAGGAGAGCGTCACCTCTTTTGAACCCCAAGACCTCTTCTGCTTCGATAACTG 1231  
DB 326 ThrTyArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345  
QY 1232 TGGGTCAACAGAGTCATAGCCCATGCGCAGCAGTGTGTTGGCAACTGTGTGTCACA 1291  
DB 346 GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365  
QY 1292 ATGGAATGTGGGAATGATATTGGCTTAAAGAGGGTTTGCAAAATACATCGAACTTATC 1351  
DB 366 MetGlnTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385  
QY 1352 GCTGTTAATGTCATATCCAGAGCTGCAATTTGATGACTATTTTTCGAATGTGTGTTT 1411  
DB 386 SerValSerValThrHisProGluLeuLysValGlyAspTyPhePheGlyLysCysPhe 405  
QY 1412 GAAGTAATTAACAAAGATTTCATTCATCCCGCCCTATCTCCAAACACGAGCGAAACC 1471  
DB 406 AspAlaMetGluValAlaAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 425  
QY 1472 CCGACTCAAAATACAGGAAATGTTTGAATGAACTTCTATAACAAGGGAGCTTGTATTTG 1531  
DB 426 ProAlaGlnIleArgGluMetPheAspAspValSerTyAspLysGlyAlaCysIleLeu 445  
QY 1532 AATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTA 1591  
DB 446 AsnMetLeuArgGluTyLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyLeu 465  
QY 1592 AAGAAGTTCAGTATAGAAATGCTAAGAAATCATGACTTGTGAGCAGTCTGTCAATAGT 1651  
DB 466 GlnLysHisSerTyLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485  
QY 1652 TGTTTAGAAAGTGAATTTTACATCTGGT-----GGAGTTTGTCTCATTCGGATCCCAAGATG 1705  
DB 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503  
QY 1706 ACAAGTAACATGCTCGCCTTCTCGGGGAAATGCAGAGGTCAAGAGATGATGACTACA 1765  
DB 504 SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr 523  
QY 1766 TGGACTCTCCAGAAAGNAATCCCTCTGCTGTGTTAAACAAGCGGTGTTCACTCCGA 1825  
DB 524 TrpThrLeuGlnLysGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543  
QY 1826 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCCCTGAATGAGGCGCCCTG 1885  
DB 544 MetLysGlnGluHisTyMetLysGly-----SerAspGlyAlaPro 557  
QY 1886 CAGGAGAGGTACCTGTGGCATATCCCATTTGACCTTCCAGAGTCTTCTTAATGTGATC 1945  
DB 558 AspThrGlyTyLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal 577  
QY 1946 CACAGACATCTTAAATCAACACAGATACTCTGGATCTACTCTACCTGAAAGACCACTGGG 2005  
DB 578 HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuLeuProGluGluValGluTrp 597  
QY 2006 GTGAAATTTAATGTGGACTCAAATGGTTTACTTACATCGTTTCACTATGAGGGTCATGGATGG 2065  
DB 598 IleLysPheAsnValGlyMetAsnGlyTyTyIleValHisTyLysGluAspGlyTrp 617  
QY 2066 GACCACTCATTAACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGCAGCAGTA 2125  
DB 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637  
QY 2126 GGTCTGATTCATGATGTTTTCAGTAGTGGTGCAGGAGACCTAGACCTAGACAAAGCT 2185  
DB 638 SerLeuIleAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657  
QY 2186 CTTGACATGACTTACTACCTCCAAACATCAACAGCAGCCCGCAGCTTCTCGAAGGCTG 2245  
DB 658 LeuAspLeuSerLeuTyLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677  
QY 2246 AGTTACTTGGAAATCGTTTTACCACATGATGACAGAGGAATATTTTCAGATATCTCTGAA 2305





; ORGANISM: Homo sapiens									
US-10-472-533-329									
Alignment Scores:									
Pred. No.:	9.44e-224	Length:	941						
Score:	2515.50	Matches:	477						
Percent Similarity:	69.34%	Conservative:	172						
Best Local Similarity:	50.96%	Mismatches:	268						
Query Match:	42.55%	Indels:	19						
DB:	18	Gaps:	7						
US-10-039-073-2 (1-3366) x US-10-472-533-329 (1-941)									
Qy	212	TACTGCTTAACAGCCATCTTCCCAATATGCAATTTGTTCTCAGTTCTCAGTGCCCATCT	271						
Db	15	PhelLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer	30						
Qy	272	AGTTATCACTTCATCTGAGGATCCTGGGCTTCCCAAGTAGCCATTAATGGGAACGATTT	331						
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47						
Qy	332	CCTTGGCAGAGCTAAGGCTCCCAAGTGTGGTCTATCTCTCCATTTATGACCTTTTGTGTC	391						
Db	48	ProTrpAsnLysIleArgLeuProGluTrpValIleProValHisTyrAspLeuLeuIle	67						
Qy	392	CACCCCAATCTCACTCTCTGCACTTGTTCATCTGAGAGATCGAAGTCTTGGTCAGC	451						
Db	68	HisAlaAsnLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87						
Qy	452	AATGCTACCCAGTTTATCATCTTGACAGCAAGAACTCTTGAATACAGAAATGCCCCTT	511						
Db	88	GlnProThrSerThrIleIleLeuHisSerHisIleLeuGlnIleSerArgAlaThrLeu	107						
Qy	512	CAGTCAGAGGAGATTCAAGATACATGAAACCAGGAAAGAACTGAAAGTTTCAGTTAC	571						
Db	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125						
Qy	572	CCTGCTCATGAACAAATGCACTGCTGGTTCAGAGAAACTTACGCCTCACTCAAAATAC	631						
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145						
Qy	632	TATGTGCTATGACTTCCAAACCAAGTTAGTGATGGCTTTGAAGGTTTATAAAGC	691						
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165						
Qy	692	ACATACAGAACTCTTGGTGGTGAACAGAAATCTTTCGAGTAAACAGATTTTGACCCAAC	751						
Db	166	ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185						
Qy	752	CAGGCACGCATGGCTTCCCTTGTCTTGTGATGAACCGTTGTTCAAAGCCAACTTTCAATC	811						
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205						
Qy	812	AAGTACGAAGAGAGAGCATATGCACTATCCCAACATGCCAAAGGTTAAGACAATT	871						
Db	206	LysIleArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225						
Qy	872	GAACTTGAAGGAGCTTTTGAAGATCACATTGAACTACTGTAAATAACAGTACATAC	931						
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245						
Qy	932	CTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGATGGCTTCACTTCAATCAGGSGTC	991						
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265						
Qy	992	AAGTGTCTATCTATGATCCCGACAGAAACGGAATCAAAACATATGCTTTGCGAGCA	1051						
Db	266	LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla	285						
Qy	1052	TCACGTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCTCCACTCTCCAAA	1111						
Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305						
Qy	1112	CTGGAATTAATGCTATTCTGACTTTGCACCTGGAGCCATGGAAAATTTGGGCGCTCAT	1171						
Db	306	GlnAspLeuAlaIleIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325						
Qy	1172	ACATATAGGAGAGAGCTCCTGCTTTTGTGACCCCAAGACCTCTTCTGCTTCGATAAATG	1231						
Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345						
Qy	1232	TGGGTCAACAGAGCTATAGCCCATGAACTGCGCCAGCTGGTTTGGCAACCTCGTCCACA	1291						
Db	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365						
Qy	1292	ATGGAATGGTGGAAATGATATTTGGCTTAAGAGAGGGTTTTGCAAAATACATGGAACTTATC	1351						
Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385						
Qy	1352	GCTGTTAATCTCATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTTT	1411						
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405						
Qy	1412	GAAAGTAATTACAAAGATTCAATTGAAATTCCTCCGCTTATCTCCAAACAGCGGAAACC	1471						
Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425						
Qy	1472	CCGACTCAAAATACAGGAAATGTTTGAAGTTTCTTATAAACAGGAGCTTGTATTTTG	1531						
Db	426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445						
Qy	1532	AATATGCTCAAGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATAATTCAGTACTTA	1591						
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465						
Qy	1592	AAGAAGTTCACTATGAAATGCTAAGAATGATGACTTGTGGAGCAGCTCTGCAAAATAGT	1651						
Db	466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485						
Qy	1652	TGTTTGAAGAGTGAATTTACATCTGGT-----GGAGTTTGTCTCGATGCCAAGATG	1705						
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503						
Qy	1706	ACAAGTAAACATGCTCGCTTCTGGGGGAAATGCAGAGCTCAAGAGATGATGACTACA	1765						
Db	504	SerSerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523						
Qy	1766	TGACTCTCCAGAAAGAAATCCCTCTGCTGGTTTAAACAAGACGGGTGTTCTCACTCCGA	1825						
Db	524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543						
Qy	1826	CTGCAACAGAGCGCTTCTCCAGGGGGTTTCCAGGAAGACCTTGAATGGAGGGCCCTG	1885						
Db	544	MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro	557						
Qy	1886	CAGGAGGAGTACCTGGCGCATATCCCATTCACCTACTCCACGAGTCTTCTTAATGTGATC	1945						
Db	558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal	577						
Qy	1946	CACAGACACATCTTAAATCAAACAGACATCTCTGATCTCTACCTGAAAAACAGTTGG	2005						
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuLeuProGluGluValGluTrp	597						
Qy	2006	GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACATGAGGGTCAATGG	2065						
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp	617						
Qy	2066	GACCACTCATTACACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGGACAGATA	2125						
Db	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637						
Qy	2126	GGTCTGATTCATGATGGTTTTCAGCTAGTTGGTGCAGCGAGACTGACCCTAGACAAAGCT	2185						
Db	638	SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657						
Qy	2186	CTTGACATGACTTACTACTCCCAACATGAAACAGACGCCCGCCACTTCTCGAAGGCTG	2245						

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Db 658 LeuAspLeuSerLeuTyrLeuIleHisGluThrGluLeuMetProValPheGlnGlyLeu 677
Qy 2246 AGTTACTTGGAAATCGTTTACACATGATGAGCAGAGAAGAAATATTTTCAGATCTCTCGAA 2305
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
Qy 2306 AACCTCAACGGTACCTTCTTCAGTATTTTAAGCAGAGTATGACAGCAAGCTGGAGT 2365
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuLeuAspLysGlnThrTrpThr 717
Qy 2366 GACAAGGCTCAGTCGGACAGGATGCTCGCTCTCTCTCAAGCTGGCCGTGAC 2425
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal 737
Qy 2426 CTGAACCATGCTCTTGGCATCCAGAAAGCTGCTGAACCTTCTCCAGTGGATGGAATCC 2485
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
Qy 2486 AGTGAAAAATTAATATACCAACAGATGTTTAAAGATTGTATTTCTGTGGTCTCAG 2545
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
Qy 2546 ACAACAGCAGGATGAATTACCTTTAGAGCAATATGAACCTCAATGTCAGTCTGAA 2605
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797
Qy 2606 CAAACAAAAATTCGTATGCTTTGCAACGACCAAGCATCAGAAAAAGTTACTGAAGTTA 2665
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
Qy 2666 ATTGAACATAGGAAAGGAAAGGTTATCAAGACACAGCAAGCTTGGCAGCTCTCTTCAT 2725
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
Qy 2726 GCGATTGCCAGCTGCCAAGGGGAGCAACTAGCATGGATTTTGTAAAGAGAAATGG 2785
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
Qy 2786 ACCCATCTTCGAAAAATTTGACCTGGCTCATATGACATAAGGATGATCATCTCTGGC 2845
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
Qy 2846 ACAACAGCTCACTTTTCTCCAGGTAAGTTGCAAGAGTGAAGAACTATTTTGAATCT 2905
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
Qy 2906 CTTGAGGCTCAAGGATCATCTCGATATTTTCAAACTGTTCTCGAAACGATACCAAA 2965
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
Qy 2966 AATATAAAATGGCTGGAGAAGAACTCTCCGACTCTGAGGACTTGGCTA 3013
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

RESULT 9
US-10-106-698-6381
; Sequence 6381, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
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; SEQ ID NO 6381
; LENGTH: 944
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6381

Alignment Scores:
Pred. No.: 9,45e-224 Length: 944
Score: 2515.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 42.55% Indels: 19
Db: 14 Gaps: 7

US-10-039-073-2 (1-3366) x US-10-106-698-6381 (1-944)
Qy 212 TACTGCTTAACAGGCATCTTGCCTCCCAATATGCAATTTGTTCTCAGTCTCTCAGTGCATCT 271
Db 18 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 33
Qy 272 AGTTATCACTTCACTGAGGATCTCTGGGCTTTCCAGTAGCCACTTAATGGGGAAGATTT 331
Db 34 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 50
Qy 332 CTTGGCAGGAGCTAAGGCTCCCGAGTGTGCTCCTCTCCATTATGATGACCTCTTGTCTC 391
Db 51 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle 70
Qy 392 CACCCCAATCTCACTCTCTGACTTTGTCATCTGAGAAGATCGAAGTCTTGGTCAGC 451
Db 71 HisAlaLeuLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 90
Qy 452 AATGCTACCCAGTTTATCATCTTCACAGCAAGATCTTGAATCACAATGCCACCTT 511
Db 91 GlnProThrSerThrIleIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 110
Qy 512 CAGTCAGAGGAAAGTTCAGATACATGAAACCAGGAAAGAACTGAAAGTTTGTGATTAC 571
Db 111 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 128
Qy 572 CTTGCTCATGAACAAATGCACTCTGTTCCAGAGAACTTACGCCCTCAGCTGAAATAC 631
Db 129 ProGlnGlnGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 148
Qy 632 TATGTGCTATGACTTCCAAAGCAAGTTAGTATGGCTTTGAGGGTTTATATAAGC 691
Db 149 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 168
Qy 692 ACATACAGAACTCTGGTGGTGAACAAAGAAATCTTCGCAAGTAAACAGATTTTGAGCAACC 751
Db 169 ThrTyrArgThrLysGluGlyLeuArgIleLeuAlaSerThrGlnPheGluProThr 188
Qy 752 CAGGCAGCATGGCTTTCCCTTGTGTTGATCAACCGTTGTTCAAGCCAACTTTTCAATC 811
Db 189 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 208
Qy 812 AAGATACGAAGAGAGAGCAGCATATTCGACTATCCAACTGCCAAAGGTTAAGACAAT 871
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APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Best Local Similarity: 50.36% Mismatchches: 268
Query Match: 42.50% Indels: 19
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US-10-039-073-2 (1-3366) x US-09-989-722-353 (1-941)

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1172	ACATATAGGAGGACGTCACCTGCTTTTGTGACCCCAAGACCTCTCTGCTCCGATAAACTG	1231
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1232	TGGGTCCACAGAGTCATAGCCCATGAACCTGGCGCACAGTGGTTCGGCAACCTGGTCACA	1291
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1352	GCTGTTAATGCTACATATCCAGAGCTGCAAATTTGATGACTATTTTGAATGTGTGTTTT	1411
386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
1412	GAAGTAATTACAAAGACTCATTGAATTCATCCCGCCCTATCTCCAAACACAGCGGAAC	1471
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1652	TGTTTGAAGAAGTCATTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1705
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1826	CTGCAACAGAGCGCTTCCTCCAGGGGGTTCCTCCAGGAAGACCTCAATGGAGGGCCCTG	1885
544	MetLysGlnGlnHisTyrMetLysGly-----SerAspGlyAlaPro	557
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598	IleLysPheAenValGlyMetAenGlyTyrTyrIleValHisTyrGluAspAspGlyTrp	617
2066	GACCAACTCATTACACAGCTGAATCAGAACACCACTTCTCAGACTTAAAGCAGAGTA	2125
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2126	GGTCTGATTCATGATGTTGTTTTCAGCTAGTGTGGTGGAGGAGCTAGACCTTAGCAAGCT	2185
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Alignment Scores:
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Score:          2512.50        Matches:    477
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Best Local Similarity: 50.96%  Mismatches: 268
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RESULT 13
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC65
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity: 50.96%  Mismatches: 268
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Qy 272 AGTTATCACTTCACTGAGGATCCTGGGGCTTCCAGTAGCCACTAATGGGGAACGATTT 331
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
Qy 332 CCTTGGCAGGAGCTAAGGCTCCCGAGTGGTGTATTCCTCTCCATTATGACCTTTTGTC 391
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; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Gurney, Austin L.  
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; APPLICANT: Roy, Margaret Ann  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
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; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1,798-223 Length: 941
Score: 2512.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 42.50% Indels: 19
Db: 9 Gaps: 7

US-10-039-073-2 (1-3366) x US-09-989-731-353 (1-941)
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QY 1052 TCAGTGAAGCTACTTGTATTTTATGAAAGTACTTTGTATCTACTATCTCCTCACTCTC 1111
Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305
QY 1112 CTGGATTTAATTTGCTATTCTCAGCTTTGCACCTCGAGCCATGGAAATTTGGGGCTCAT 1171
Db 306 GlnAspLeuAlaIleIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325
QY 1172 ACATATAGGAGAGCTCACTGCTTTTGGACCCCAAGACCTCTTCTGCTCCGATAAATCG 1231
Db 326 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345
QY 1232 TGGGTCAACAGAGTCATAGCCCATGAAGTGGCGCACACAGTGGTTGGCAACTGTGTACA 1291
Db 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY 1292 ATGGAATGGTGGAAATGATATTGCTTTAAGGAGGGTTTTCGAAAATACATGGAATATC 1351
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385
QY 1352 GCTGTTAATGTCATCATCCAGAGCTGCAATTTGATGACTATATTTTGAATGTGTGTTT 1411
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405
QY 1412 GAAGTAATTACAAAGATTCATGAATTCATCCCGCCTATCTCCAAACACAGCGAAACC 1471
Db 406 AspAlaMetGluValAspAlaLeuAsnSerHisProValSerThrProValGluAsn 425
QY 1472 CCGACTCAAAATACAGGAAATGTTTGTAGTGAAGTTTCTTATACAAAGGGAGCTTGTATTTG 1531
Db 426 ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 445
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QY 1592 AAGAAGTTACGATATGAAATGCTAAGATGATGACTTGTGGAGCAGTCTGTCAATAGT 1651
Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485

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[illegible]

; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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US-10-039-073-2 (1-3366) x US-09-989-732-353 (1-941)

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Qy	272	AGTTATCACTTCACCTAGGATCTCTGGGCTTCCAGTAGCCATTAATGGGAACGATT	331
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47
Qy	332	CTTGGCAGGAGCTAAGCTCCAGTGTGCTCATTCTCTCCATTATGACCTCTTTGTC	391
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Qy	392	CACCCCAATCTCACCTCTCGACTTCTTGTCATCTGAGAAGATCGAAGTCTTGGTCAGC	451
Db	68	HisAlaLeuLeuThrLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
Qy	452	AATGCTACCCAGTTTATCATCTTCACAGCAAAAGATCTTGAATACAGAAATGCCACCTT	511
Db	88	GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107
Qy	512	CAGTCAGAGGAGATTCAGATACATGAACACGAGAAAGAAAGACTGAAAGTTTTCAGTTAC	571
Db	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
Qy	572	CCTGCTCATGAACAAATGCACTGCTGTTCCAGAGAACTTACGCCCTCACCTGAAATAC	631
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145
Qy	632	TATGTGCTATGGACTTCCAAACCAAGTATAGTATGCTTGAAGGTTTATAAAGC	691
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
Qy	692	ACATACAGAACTCTGGTGTGAACACAGATTTCTTCAGTAAACAGATTTTGACCAACC	751
Db	166	ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
Qy	752	CAGGCACGATGGCTTTCCCTTGTGTTGATGAACCGTGTGTTCAAAGCCAACTTTCAATC	811
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Qy	812	AAGTACGAAGAGAGAGAGGATATTCATATCCCAATGCCAAAGTTTAAACAAAT	871
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Qy	872	GNACTTGAAGGCTTTTTCGAGATCACATCTTGAACCTACTGTAAATATGATGATACATAC	931
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Qy	932	CTTGTAGCTCATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCAGGGGTC	991
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
Qy	992	AAGGTGCTCATATGATCCCAACAAACGGAATCAACACATTAATGCTTTCCAGGCA	1051
Db	266	LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla	285
Qy	1052	TCAGTGAAGCTACTGATTTTATGAAAGTACTTTGATATCTACTACTCTCCACTCTCCAA	1111
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Qy	1112	CTGGATTAAATGCTATTCTGACTTTGACCTGGAGCCATGGAAAATTTGGGCTCATTT	1171
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Qy	1232	TGGGTACACAGAGCTATAGCCCATGAACTGGCCGACCACTGGTTTGGCAACCTGGTCACA	1291
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Qy	1292	ATGGAATGGTGGATGATATTTGGCTTAAGGAGGGTTTTGCAAAATACATGGAATCTATC	1351
Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
Qy	1352	GCTGTTAATGCTCATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTTT	1411
Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
Qy	1412	GAAGTAATTACAAAGATTCATTGAAATTCATCCGCCCTATCTCCAAACGACGGAACCC	1471
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Qy	1472	CCGACTCAAAATACAGGAAATGTTTGAAGTTTCTTATACAGGAGGAGCTTGTATTTTG	1531
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Qy	1532	AATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGAAATAATTCAGTACTTA	1591
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Qy	1592	AAGAGTTACGCTATAGAAATGCTAAGATGACTTGTGGAGCAGCTCTGCAAAATAGT	1651
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Qy	1706	ACAAGTAACTGCTGCGCTTTCTGGGGGAAATGCAGAGGTCAAGAGATGATGACTACA	1765
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Qy	1826	CTGCAACAGGAGGCTTTCTCCAGGGGGTTTTCCAGGAAGACCTCGAATGGAGGGCCCTG	1885
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Qy	1886	CAGAGAGGTACCTGTGGCATATCCCATTTGACTCTCCAGGAGTCTTCTTAATGTGATC	1945
Db	558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal	577
Qy	1946	CACAGACACATCTTAAATCAAAACAGACATCTCTGGATCTACTCTGAAAACAGCAGTTGG	2005
Db	578	HisArgPheLeuLeuLysThrLysThrAspValIleLeuLeuProGluGluValGluTrp	597
Qy	2006	GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTTCACTATGAGGGTCAATGGATGG	2065
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp	617
Qy	2066	GACCAACTTATCACAGCTGAATCAGAACCAACACATCTTCTCAGACCTTAAGGACAGAGTA	2125
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Qy	2126	GGTCTCATCTCATGTGTTTTCAGTAGTTGGTGCAGGAGACTGACCCCTAGACAAAGCT	2185
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Qy      2306 AACCTCAAGCGTTACCTTCTCAGTATTTTAAAGCCAGTATTGACAGGCAAGCTGGAGT 2365
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Qy      2366 GACAAGGCTCAGTCTGGACAGGATGCTCGCTCGCTCTTGAAGCTGGCTGTGAC 2425
Db      718 AspGluGlySerValSerGluGlnMetLeuArgSerGluLeuLeuLeuAlaCysVal 737
Qy      2426 CTGAACCATCTCTTGTGATCCAGAAAGCTGCTGAACCTCTCTCCAGTGGATGGAATCC 2485
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Qy      2486 AGTGGAAATTAATATACCAACAGATGTTTAAAGATTGTATTTCTGTGGTGTCTCAG 2545
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Qy      2786 ACCCATCTTCTGAAAAAATTTGACTTGGCTCATATGACATAAGGATGATCATCTCTGCGC 2845
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Qy      2906 CTTGAGGCTCAAGGATCAGATCTGGATATTTTTCAACTGTTCTCGAAACGATAACCAA 2965
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Qy      2966 AATATAAATGGCTGGAGAGAAATCTTCGACTCTGAGGACTTGGCTA 3013
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 26, 2005, 06:11:31 ; Search time 82.6822 Seconds  
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Searched: 513545 seqs, 74649064 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2507.5	42.4	948	4	US-09-620-312D-1105
3	2027	34.3	1025	2	US-08-530-792D-23
4	2016.5	34.1	1026	2	US-08-530-792D-22
5	1444	24.4	957	4	US-09-949-016-6154
6	1440	24.4	964	4	US-09-949-016-7431
7	1264.5	21.4	967	3	US-09-139-802-201
8	1264.5	21.4	967	4	US-09-659-786-201
9	1225	20.7	919	4	US-09-919-039-222
10	1165	19.7	977	3	US-08-335-844A-22
11	1165	19.7	977	4	US-08-129-366-22
12	1117	18.9	972	3	US-08-335-844A-24

13	1117	18.9	972	4	US-09-129-366-24	Sequence 24, Appl
14	1100	18.6	972	3	US-08-335-844A-23	Sequence 23, Appl
15	1100	18.6	972	4	US-09-129-366-23	Sequence 23, Appl
16	1083	18.3	699	4	US-09-270-767-45507	Sequence 45507, A
17	986	16.7	593	4	US-08-637-670-38	Sequence 38, Appl
18	908	15.4	608	4	US-08-637-670-36	Sequence 36, Appl
19	884	15.0	850	4	US-09-902-540-10199	Sequence 10199, A
20	865.5	14.7	990	4	US-09-657-931A-11	Sequence 11, Appl
21	867	14.7	848	4	US-09-583-110-2738	Sequence 2738, Ap
22	863	14.6	995	4	US-09-657-931A-1	Sequence 1, Appl
23	844	14.3	815	4	US-09-107-433-5059	Sequence 5059, Ap
24	841.5	14.2	946	4	US-09-657-931A-10	Sequence 10, Appl
25	820.5	13.9	1009	4	US-09-657-931A-13	Sequence 13, Appl
26	818.5	13.8	986	4	US-09-657-931A-12	Sequence 12, Appl
27	785.5	13.3	942	4	US-09-657-931A-9	Sequence 9, Appl
28	711.5	12.0	616	4	US-08-637-670-26	Sequence 26, Appl
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37	477.5	8.1	346	4	US-08-637-670-24	Sequence 24, Appl
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40	459	7.8	350	4	US-08-637-670-39	Sequence 39, Appl
41	458	7.7	350	4	US-08-637-670-25	Sequence 25, Appl
42	440	7.4	680	4	US-09-902-540-11278	Sequence 11278, A
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44	379.5	6.4	242	4	US-09-248-796A-18160	Sequence 18160, A
45	364.5	6.2	380	4	US-09-270-767-44186	Sequence 44186, A

ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/09345650  
; Patent No. 6362324  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: 17867, A No. 6362324el Human Aminopeptidase  
; FILE REFERENCE: 5800-36  
; CURRENT APPLICATION NUMBER: US/09/345.650  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-345-650-1

Alignment Scores:  
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Best Local Similarity: 100.00%  
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Mismatch: 0  
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US-10-039-073-2 (1-3366) x US-09-345-650-1 (1-960)

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QY 1106 TCCAACTGGATTAAATGCTATTCTGACTTTGCACTTGGACCTGAGGCATGGAATTTGGGC 1165  
DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
QY 1166 CTCATTACATATAGGAGACGCTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTCCGAT 1225  
DB 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
QY 1226 AAATGTGGGTACACAGAGTCAATGCCATGAATGGCGCACCGAGTGGTTGGCAACTG 1285  
DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
QY 1286 GTCACAAATGGATGGTGAAGTATTTGGCTTAAAGGAGGCTTTTGCAAAATACATGAA 1345  
DB 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400

QY 1346 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG 1405  
DB 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420  
QY 1406 TGTTTTGAAGTAATTACAAAAGATTCAATGAATTCATCCCGCCCTATCTCCAAACACGCG 1465  
DB 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
QY 1466 GAAACCCCGACTCAATACAGGAAATGTTTGTGATGAAGTTCCTATATAACAAGGGAGCTTGT 1525  
DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
QY 1526 ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGAGAAATTCAGAAAGGAATAATTCAG 1585  
DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480  
QY 1586 TACTTAAAGAAGTTCACTATAGAAATGCTAAGAATGATGACTTGTGGAGAGTCTGTCA 1645  
DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500  
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DB 501 AsnSerCysLeuGluSerAspPheThrSerGlyLysValCysHisSerAspProLysMet 520  
QY 1706 ACAAGTAACATGCTCGCTTTTCTGGGGGAAAATGCAAGAGTCAAGAGATGATGACTACA 1765  
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QY 1766 TGACTCTCCAGAAAGGAATCCCTCTGCTGCTGGTGTAAACAAGACGGGTGTCTACTCCGA 1825  
DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560  
QY 1826 CTCACACAGGAGCGCTTCTCCAGAGGGTTCCTCAGGAAGACCTGAAATCAGAGGCCCTG 1885  
DB 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580  
QY 1886 CAGGAGAGGTACCTGTGGCATATCCCATTTGACCTACTCTCCACGAGTTCCTTAATGTGATC 1945  
DB 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600  
QY 1946 CACAGACACATTTCAAATAACAAAGACAGATACCTCTGATCTACTGAAAAGACAGTTGG 2005  
DB 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
QY 2006 GTCAAAATTTAATGTGAGCTCAAAATGTTACTACATGTTTCACTATGAGGTCATGGATGG 2065  
DB 621 ValLysPheAsnValAspSerAsnGlyTyrTrpIleValHisTyrGluGlyHisGlyTrp 640  
QY 2066 GACCAACTCAATTAACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAGGACAGAGTA 2125  
DB 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
QY 2126 GGTCTGATTCATGATGTGTTTACAGTAGTTGGTGCAGGAGACTGACCTTAGACAAAGCT 2185  
DB 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
QY 2186 CTTTGACATGACTTACTACCTCCAAACATGAACAGCAGCCCCGACCTTCTCGAAGTCTG 2245  
DB 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700  
QY 2246 AGTTACTTGGAAATCGTTTTTACCACATGATGGACAGAGGAATATTTTTCAGATATCTCGAA 2305  
DB 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720  
QY 2306 AACCTCAAGGTTTACCTTCTTCAAGTATTTTAAGCCAGTGTGATTCACAGGCAAGCTGAGT 2365  
DB 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
QY 2366 GACAAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGGCTGTGAC 2425  
DB 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
QY 2426 CTGAACCATGCTCTCTTGCATCCAGAAAGCTGTGCTGAACTCTTCTCTCCAGTGGATGCC 2485



Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305  
QY 1112 CTGATTAATAATGCTATTCCTGACCTTCGACCTCGAGCCATGGAATTCGGGCTCAT 1171  
Db 306 GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAenTrpGlyLeuThr 325  
QY 1172 ACATATAGGGAGAGCTCACTCTCTTTTACCCCAAGACCTCTCTGCTTCGATAAACTG 1231  
Db 326 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345  
QY 1232 TGGGTCAACAGATCATAGCCATGAATCTGCGCCACAGATGTTTGGCAACCTGGTCACA 1291  
Db 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365  
QY 1292 ATGNAATGCTGGAATGATATTTGCTTAAGAGAGGTTTGCARAATACATGGAATTC 1351  
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385  
QY 1352 GCTGTTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTGTGTTT 1411  
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405  
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QY 1472 CCGACTCAATACAGGAATCTTTGATCAAGTTTCTTATACAGAGGAGCTTGATTTTG 1531  
Db 426 ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 445  
QY 1532 AATATGCTCAAGGATTTTCTGGTGAGAGAAATTCAGAAAGGAATAAATTCAGTACTTA 1591  
Db 446 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465  
QY 1592 AAGAAGTTCAGTATAGAAATGCTAAGATGATGACTTGAGGACGATCTGTCNAATAGT 1651  
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QY 1766 TGGACTCTCCAGAAAGAAATCCCTCTGCTGTGTGTTAAACAGACGGGTCTACTCCGA 1825  
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Db 544 MetLysGlnGluHisTrpMetLysGly-----SerAspGlyAlaPro 557  
QY 1886 CAGGAGAGGTACCTGTGGCATATCCATTTGACCTACTCCAGAGTCTCTTAATGTGATC 1945  
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QY 1946 CACAGACACATCTTAAATCAAGACAGATACTCTGGATCTACTCTGAAAGACACAGTTGG 2005  
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QY 2006 GTGAAATTTAATGTGGACTCAATGTTTACTACATCGTTTCACTATGAGGGTCAATGG 2065  
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QY 2066 GACCAACTCATTAACAGCTGAATCAGAACCCACACACTTCTCAGACCTTAAGGACAGATA 2125  
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637  
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QY 2186 CTTGACATGACTTTACTACCTCCCAACATGAACAAGCAGCCCCGACCTTCTCGAAGGCTG 2245  
Db 658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677  
QY 2246 AGTTACTTGGAAATCGTTTTTACCACATGATGACGACAGGAATATTTTCAGATATCTCTGAA 2305  
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697  
QY 2306 AACCTCAAGCTTACCTTCTTCACTATTTTAAACCCAGTGTATTCACAGGCAAGCTGGAGT 2365  
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717  
QY 2366 GACAAGGGCTCAGCTCTGGGACAGATGCTCCGCTCGCTCTCTTGAAGCTGGCTGTGAC 2425  
Db 718 AspGluLysSerValSerGluGlnMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal 737  
QY 2426 CTGAACCATGCTCTCTTGCATCCAGAAGCTGCTGAACTCTTCTCCAGAGTGGATGCC 2485  
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757  
QY 2486 AGTGGAAATTAATATACCAACAGATGTTTTTAAAGATTGTGTATCTGTGGGTGCTCAG 2545  
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777  
QY 2546 ACAACAGCAGGATGGAATTACCTTTTAGAGCAATATGAACCTGTCATGTCAAGTGTGAA 2605  
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTrpGlnPheSerLysSerSerThrGlu 797  
QY 2606 CAAAACAAAATTCGTATGCTTTGTCAACGACGACGATCATCAGAAAGATTACTGAAAGTTA 2665  
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817  
QY 2666 ATTGAACATAGGAATGGAAGAAAGTTATCAACAGACAGAACTTGGCAGCTCTCTTCAT 2725  
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837  
QY 2726 GCATTTCGACAGCTCCAAAGGGGAGCAACTAGCATGGGATTTTGTAAAGAGAAATTTGG 2785  
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QY 2786 ACCCATCTTGTAAAAAATTTGCTTGGCTCATATGACATAAAGGATGATCATCTCTGGC 2845  
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877  
QY 2846 ACAACAGCTCAGCTTTTCTCCAGGATAGTTTCAAGAGGTGAACTATTTTGTGATCT 2905  
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897  
QY 2906 CTTGAGGCTCAAGGATCAGATCTGGATATTTTCAAACTGTTCTGAAACGATAACCAAA 2965  
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917  
QY 2966 AATATAAATTTGGTGGAGAGAATCTTCGACTCTCGAGCTTGGCTA 3013  
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

## RESULT 3

US-08-530-792D-23  
; Sequence 23, Application US/08530792D  
; Patent No. 5972680  
; GENERAL INFORMATION:  
; APPLICANT: Knowles, W. J.; Guralski, D.; Haigh, W.; Letsinger, J. T.;  
; APPLICANT: Clairmont, K.; and Hart, J.  
; TITLE OF INVENTION: Glucose Transporter Vesicle Aminopeptidase  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bayer Corporation  
; CITY: West Haven  
; STATE: Connecticut  
; COUNTRY: U.S.A.  
; ZIP: 06516

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb Storage
; COMPUTER: Dell Windows 95 PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,792D
; FILING DATE: 09/19/95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/309,232
; FILING DATE: 09/20/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Brewer, Alice A.
; REGISTRATION NUMBER: 32888
; REFERENCE/DOCKET NUMBER: MMH 323P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 812-2705
; TELEFAX: (203) 812-5492
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1025 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein;
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; DEVELOPMENTAL STAGE: adult
; TISSUE TYPE: skeletal muscle
; IMMEDIATE SOURCE:
; LIBRARY: Clontech rat skeletal muscle cDNA library in lambda
; LIBRARY: gt11 and mRNA isolated from rat skeletal muscle
; CLONE: 12.1 (from lambda gt11 library), PCR product clones 5,
; CLONE: 334, and KC44.
; FEATURE:
; NAME/KEY: complete amino acid sequence for GTVap, long version
; IDENTIFICATION METHOD: translation from cDNA
; US-08-530-792D-23

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Alignment Scores:
Pred. No.: 3,148-199 Length: 1025
Score: 2027.00 Matches: 402
Percent Similarity: 61.81% Conservative: 158
Best Local Similarity: 44.37% Mismatches: 310
Query Match: 34.23% Indels: 36
DB: 2 Gaps: 5

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US-10-039-073-2 (1-3366) x US-08-530-792D-23 (1-1025)

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QY 305 CCAGTAGCCTAAATGGGGAACGATTTCTTGGCAGGAGCTAAGGCTCCCGAGTGTGTC 364
DB 153 ProlieAlaThrAsnGlyLeuValPheProTrpAlaGlnIleArgLeuProThrAlaIle 172
QY 365 ATTCTCTCCATATGACTCTTTGTCCACCCCAATCTCACTCTCTGGACTTTGTCA 424
DB 173 IleProGlnArgTyrrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
QY 425 TCTGAGAGAGTCGAAGTCTTGTGTCAGCAATGCTACCCAGTTTATCATCTTCACACGCAA 484
DB 193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleLeuHisSerThr 212
QY 485 GATCTTGAATACCAAGTCCACCCCTTCAGTCAGAGGAAGATTCAAGATACATGAACCA 544
DB 213 GlyHisAsnIleSerSerValThrPheMetSerAlaValSerGln----- 228
QY 545 GGAAAGAACTGAAGTTTGTAGTTACCTGCTCATGAACAATTCGACTGCTGTTCCA 604
DB 229 GluLeuGlnValGluLeuGluTyrrProTyrrHisGluGlnIleAlaValAlaPro 248
QY 605 GAGAACTTACCCCTCACCTGAATACTATGTGGCTATGGACTTCCAGCCCAAGTTAGGT 664

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DB 249 GluSerLeuLeuThrGlyHisAsnTyrrThrLeuLysIleGluTyrrSerAlaAsnIleSer 268
QY 665 GATCGCTTTGAAGGGTTTTATATAAAGCACATACAGAACTCTTGGTGGTGAACAAGAATT 724
DB 269 AsnSerTyrrGlyPheTyrrGlyIleThrThrAspLysSerAsnGlyLysAsn 288
QY 725 CTTGCAGTAAACAGATTTTGGAGCAACCCAGCAGCATGGCTTCCCTTGGCTTTTCATGAA 784
DB 289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCyPheAspGlu 308
QY 785 CCGTTGTTCAAGGCAACTTTTCAATCAAGATACGAGAGAGAGCAGCATATTTCACATA 844
DB 309 ProAlaPheLysAlaThrPheIleLysIleThrArgAspGluHisThrAlaLeu 328
QY 845 TCCAACATGCCAAAGGTTTAAAGCAATTAAGACTTGAAGGAGGTCTTTTGGAGAGATCAC 904
DB 329 SerAsnMetProLysLysSerSerValProThrGluGluGlyLeuIleGlnAspGluPhe 348
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DB 349 SerGluSerValLysMetSerThrTyrrLeuValAlaPheIleValGlyGluMetArgAsn 368
QY 965 CTGAGTGGCTTCACTTTCATCAGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACGG 1024
DB 369 LeuSerGln---AspValAsnGlyThrLeuValSerValTyrrAlaValProGluLysIle 387
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DB 388 AspGlnValTyrrHisAlaLeuAspThrThrValLysLeuLeuGluPheTyrrGlnAsnTyrr 407
QY 1085 TTTGATATCTACTATCCACTTCCAAACTGATTTAATGTCTATTCCTGACTTTGCACCT 1144
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QY 1145 GGAGCCATGGAAATTTGGGGCTCATATACATATAGGAGAGCTCACTGCTTTTTCACCCC 1204
DB 428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrrAspAsn 447
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DB 448 AlaThrSerSerValAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
QY 1265 CACCAGTGGTTTGGCAACCTGGTCACATGAATGGTGGATGATATTTGGCTTAAGGAG 1324
DB 468 HisGlnTrpPheGlyAsnLeuValThrMetGlnTrpTrpAsnAspLeuTrpLeuAsnGlu 487
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DB 488 GlyPheAlaThrPheMetGluTyrrPheSerValGluLysIlePheLysGluLeuAsnSer 507
QY 1385 GATGACTATTTTGAATGTGTGTTTGAAGTAATACAAAAGATTTCATTTGAATTCATCC 1444
DB 508 TyrGluAspPheLeuAspAlaArgPheLysThrMetArgLysAspSerLeuAsnSerSer 527
QY 1445 CGCCTATCTCCAAACCGGAAACCCCGACTCAATACAGGAAATTTTGTATCAAGTT 1504
DB 528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluMetPheAspSerLeu 547
QY 1505 TCCTATAACAGGAGGCTTGTATTTGAATATGCTCAAGGATTTTCTGGTGAGGAGAA 1564
DB 548 SerTyrrPheLysGlyAlaSerLeuLeuLeuMetLeuLysSerTyrrLeuSerGluAspVal 567
QY 1565 TTCCAGAAAGGAATTAATTCAGTACTTAAAGAAAGTTCAGCTATAGAAATGCTTAAGAATGAT 1624
DB 568 PheGlnHisAlaIleLeuTyrrLeuHisAsnHisSerTyrrAlaAlaIleGlnSerAsp 587
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DB 588 AspLeuTrpAspSerPheAsnGlu----- 595
QY 1685 TGTCTTCGGATCCCAAGATGACAAGTAACATGCTCGCTTCTTGGGGGAAATGCGAG 1744
DB 596 -----ValThrGlyLysThrLeuAsp 602

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Qy	1265	CACCAGTGGTTTGGCAACCTGGTGCACAAATGGAAATGGTGGAAATGATATATTTGGCTTAAGGAG	1324
Db	468	HisGlnTrpPheGlyAsnLeuValThrMetGlnTrpTrpAsnAspLeuTrpLeuAsnGlu	487
Qy	1325	GGTTTTGGCAAAATACATCAAGCACTTATCGCTGTGTTAAATGCTACATATCCAGAGCTCGCAATTT	1384
Db	488	GlyPheAlaThrPheMetGluTrpPheSerValGluLysIlePheLysGluLeuAsnSer	507
Qy	1385	GATGACTATTTTGAATGTGCTGTTTGAAGTAATTAACAAAGATTCATTGAATTCATCC	1444
Db	508	TyrGluAspPheLeuAspAlaAaGpPheLysThrMetArgLysAspSerLeuAsnSerSer	527
Qy	1445	CGCCCTATCTCCAAACACGCGGGAACCCCGACTCAAAATACAGCAAAATGTTTGATGAAGTT	1504
Db	528	HisProIleSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu	547
Qy	1505	TCCTATAACAAG--GAGAGTCTGTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAG	1561
Db	548	SerTrpPheLysGlnGlyAlaSerLeuLeuMetLeuLysSerTrpLeuSerGluAsp	567
Qy	1562	AAATTCAGAAAGGAATAATTTCAGTAGTACTTAAAGAAGTTCAGCTATAGAAATGCTAAGAAT	1621
Db	568	ValPheGlnHisAlaIleIleLeuTrpLeuHisAsnHisSerTrpAlaAlaIleGlnSer	587
Qy	1622	GATGACTTGTGGAGCAGTCTGTCOAATAGTGTGTTTGAAGTGAATTTTATCATCTGGTGGGA	1681
Db	588	AspAspLeuTrpAspSerPheAsnGlu-----	596
Qy	1682	GTTTGTTCATTCGGATCCCAAGATGCACNAGTAACATGCTCGCCTTCTGGGGGAAATGCA	1741
Db	597	-----ValThrGlyLysThrLeu	602
Qy	1742	GAGTCAAGAGAGATGATGACTACATGAGTCTCCAGAAAGGAATCCCTCTGCTGGTGTT	1801
Db	603	AspValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrVal	622
Qy	1802	AAACAAGACGGGTGTTTCATCTCCAGTGCACACAGAGCGCTTCTCCAGGGGGTTTTCCAG	1861
Db	623	GlnArgLysGlyThrGluLeuLeuLeuGlnGlnGluArgPhePheProSerMet-----	640
Qy	1862	GAAGACCTCAATCGAGGGCCCTCGAGGAGAGTACTGTGGCATATCCCATTTGACCTAC	1921
Db	641	---GlnProGlnLeuGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTrp	659
Qy	1922	TCCACAGAGTCTTCTAATGTGATCCACAGACAC-----ATTCTAAATCAAAAGACA	1972
Db	660	ValThrAspGlyArgAsnTrpSerGluTrpArgSerValSerLeuLeuAspLysLysSer	679
Qy	1973	GATACCTCTGGATCTACTGAAAGACACAGTGGTGGTGAAATTTAATGTGGACTCAAAATGGT	2032
Db	680	AspValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGly	699
Qy	2033	TACTACATCGTTCATCTAGGGGTCTAGATGGGACCACTCATTACACAGCTGAATCAG	2092
Db	700	TyrTyrlleValHisTrpAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArg	719
Qy	2093	AACACACACTCTCAGACCTAAGGACAGAGTAGGTCTGATTCATGATGTTTTCAGTCA	2152
Db	720	AsnProTrpValLeuSerAspLysAspAlaAsnLeuIleAsnAsnIlePheGluLeu	739
Qy	2153	GTTGGTGCAGGAGACTGACCCCTAGACAAAGCTCTTTGACATGACTTACTACCTCCCAACAT	2212
Db	740	AlaGlyLeuGlyLysValProLeuGlnMetAlaPheAspLeuIleAspTrpLeuArgAsn	759
Qy	2213	GAACAACAGACGCCCCGACTCTCTCGAAGGTCTGAGTTACTTGGAAATCGTTTTACCAACATG	2272
Db	760	GluThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTrpAsnLeu	779
Qy	2273	ATGCACAGAGGAATATTTTCAGATATCTCTGAAACCTCAAGCGTTTACCTTCTTCAGTAT	2332
Db	780	LeuGluLysLeuGlyHisMetAspLeuSerSerArgLeuValThrArgValHisLysLeu	799

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Qy 2333 TTTAAGCCAGTATTGACAGGCAAGCTGGAGTGACAAAGGCTCAGTCTGGGACAGGATG 2392
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
800 LeuGlnAenGlnIleGlnGlnThrPrpThrAspGluGlyThrProSerMetArgGlu 819
Qy 2393 CTCGGCTCGGCTCTCTTGAAGCTGCTGTGACCTGAAACCATGCTCTTGTGATCCAGAAA 2452
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
820 LeuArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAenCysThrThrMet 839
Qy 2453 GCTGCTGAACCTCTCTCCAGTGGATGGAATCCAGTGGAAAAATTAATATACCAACAGAT 2512
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
840 AlaThrLysLeuPheAenGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAsp 859
Qy 2513 GTTTTAAAGATTGTGATTCTGTGGTGCTCAGACAAACAGCAGGATGAAATTACTTTTA 2572
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
860 ValMetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLeuPhe 879
Qy 2573 GAGCAATATGAATGCTCAATGCTCAAGTCTGGAACAAACAAAATCTGTATGCTTTGTCA 2632
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
880 SerMetTyrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAla 899
Qy 2633 ACGAGCAAGCATCAGGAAAGTTACTGAAGTTAATTGAACCTAGGAATCGAAGGAAGGTT 2692
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
900 SerSerAlaAspAlaHisLysLeuTyrTrpLeuMetLysSerSerLeuAspGlyAspIle 919
Qy 2693 ATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATTGCCAGACGTCCTCAAGGGGCGAG 2752
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
920 IleArgThrGlnLysLeuSerLeuIleIleArgThrValGlyArgGlnPheProGlyHis 939
Qy 2753 CAATAGCATGGATTGTTGAAGAGAAATTTGGACCCCATCTCTTGAAAAAATTTGACTTG 2812
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
940 LeuLeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeu 959
Qy 2813 GCCTCATATGACATAAGGATCATCTCTCGCACACAGCTCATCTTCTTCTTCCCAAGAT 2872
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
960 GlySerTyrThrIleGlnSerIleValAlaGlySerThrHisLeuPheSerThrLysThr 979
Qy 2873 AAGTTGCAAGAGGTGAACATAATTTTGAATCTCTTGAGGCTCAAGGATCATCTCTGGAT 2932
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
980 HisLeuSerGluValGlnGluPheGluAsnGlnSerGluAlaThrLeuGlnLeuArg 999
Qy 2933 ATTTTCAAACTGTTCTGGAACGATACCAAAAATATATAAATGGCTGGAGAAATCTT 2992
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1000 CysValGlnGlnAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeu 1019
Qy 2993 CCGACTCTGAGGACTTGCGCTA 3013
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1020 LysThrLeuThrLeuTrpLeu 1026
```

## RESULT 5

```
US-09-949-016-6154
; Sequence 6154, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6154
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6154
```

```
Alignment Scores:
Pred. No.: 3,43e-139 Length: 957
Score: 1444.00 Matches: 323
Percent Similarity: 53.07% Conservative: 178
Best Local Similarity: 34.22% Mismatches: 361
Query Match: 24.42% Indels: 82
DB: 4 Gaps: 19

US-10-039-073-2 (1-3366) x US-09-949-016-6154 (1-957)
Qy 263 GTGCCATCTAGTTATCTTCACTGAGGATCTCTGGGGCTTTTCCAGTA----- 310
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
60 LeuProSerSer-----ThrAlaSerProSerGlyProAlaGlnAspGlnAsp 76
Qy 311 -----CCCACTAATGGGGAACGATTTCTTGGCAGGAGCTAAGGCTCCCAAGTGTG 361
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
77 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 96
Qy 362 GTCATTTCTCTCCATTATGACCTTCTTGTCCACCAATCTCACCTCTCTGGACTTTGTT 421
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
97 ValAsnProValHisTyrAspLeuHisValLysProLeuLeuGluAspThrTyrThr 116
Qy 422 GCATCTGAGAAGATCGAAGTCTTGTGTCAGCAATGCTACCCAGTTTATCATCTTGACAGC 481
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
117 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 136
Qy 482 AAGATCTTGAATCAGCAATGCCACCTTTCAGTCAGAGGAAGATTCAAGATACATGAAA 541
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
137 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 149
Qy 542 CCA---GGAAAAGAACTGAAAGTT-----TTGAGTTACCTCTGCTCATGAACAAAT 589
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
150 ProSerGlyAspGlnValGlnValArgCysPheGluTyrLysLysGlnGluTyrVal 169
Qy 590 GCATCTGCTGTTCCAGAGAACTTACGCCTCACCTG-----AAATCTATGTGGCT 640
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
170 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 189
Qy 641 ATGCATCTCCCAAGCCCAAGTTAGTGCTGCTTTGAAGGGTTTATATAAAGCACATACAGA 700
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
190 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr- 208
Qy 701 ACTCTTGGTGGTGAACAAGAATTTTGCAGTAACAGATTTTGAGCCCAACCCAGGCACGC 760
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
209 ThrGluAsnGlyArgValLysSerIleAlaAlaThrAspHisGluProThrAspAlaArg 228
Qy 761 ATGGCTTTCCTTGGTGTGTAAGACCGTTGTTCAAGCCCAACTTTTCAATCAAGATACGA 820
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
229 LysSerPheProCysPheAspGluProAsnLysAlaThrTyrThrIleSerIleThr 248
Qy 821 AGAGAGAGCAGGCATATTGCACTATCAACATGCCAAAGGTTAAGACAATTAAGTGAAC 880
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
249 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluLysValAsp 268
Qy 881 GGAGGCTTTTGAAGATCACTTTGAAACTACTGTAAAAATAGTACATACCTTGTAGCC 940
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
269 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 288
Qy 941 TACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGTGTC 1000
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
289 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 308
Qy 1001 ATCTATGTCATCCCGACAGCAACCGAATCAACACATTTATCTTTGCGGCGATCACTGA 1060
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
309 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 328
Qy 1061 CTACTTGAATTTTATGAAAAGTACTTTGATATCTTACTTCACTCTCCAAACTGGATTTA 1120
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
329 ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys 348
Qy 1121 ATTGCTATTCTCAGCTTTGCACCTGGAGCCCATGGAAAATTTGGGCGCTCATATAGG 1180
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
349 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 368
```



```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7431
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7431

Alignment Scores:
Pred. No.:      8,89e-139      Length:      964
Score:          1440.00        Matches:      322
Percent Similarity: 52.97%      Conservative: 378
Best local Similarity: 34.11%    Mismatches:  162
Query Match:      24.36%      Indels:       82
DB:               4           Gaps:         19

US-10-039-073-2 (1-3366) x US-09-949-016-7431 (1-964)

QY 263 GTGCCAATCTAGTTATCACTTCACGTAGGATCCTGGGGCTTTCCAGTA----- 310
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 67 LeuProSerSer-----ThrAlaSerProSerGlyProProAlaGlnAspGlnAsp 83
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 311 -----GCCACTAATGGGGAACGATTCTCTGGCAGGAGCTAAGCTCCCGAGTGTG 361
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 84 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheA:GLeuProAspPhe 103
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 362 GTCATTCCTCTCCATTATGACTCTCTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTT 421
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 104 ValAsnProValHisTyrAspLeuHisValLysProLeuLeuGluGluAspThrTyrThr 123
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 422 GCATCTGAGAAGATGAAGATCTTGCTGACGAATGCTACCCAGTTTATCATCTTCACAGC 481
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 124 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 143
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 482 AAAGATCTTGAATCACAAGTCCACCCCTTCAGTCAGGAGGAGATTCAAGATACATGAAA 541
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 144 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 156
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 542 CCA---GGAAAGAACTGAAAGTT-----TTGAGTTACCTGCTCATGAACAATTT 589
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 157 ProSerGlyAspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal 176
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 590 GCATCTGCTGTTCCAGAGAACTTACGCTCACCTG-----AAATACTATGTGGCT 640
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 177 ValValGluAlaGluGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 196
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 641 ATGGACTTCCAGCCCAAGTTAGTGTGATCGCTTTGAGGGTTTATAAAGCACATACAGA 700
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 197 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr--- 215
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 701 ACTCTTGCTGTGAAACAAGAAATCTTGCAGTAACAGATTTTGAGCCAAACCCAGGCACGC 760
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 216 ThrGluAsnGlyArgValLysSerIleValAlaThrAspHisGluProThrAspAlaArg 235
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 761 ATGGCTTTCCCTTGTGTTGATGAACCGTTGTTCAAGCCAACTTTCAATCAAGATACGA 820
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 236 LysSerPheProCysPheAspGluProAsnLysLysAlaThrTyrThrIleSerIleThr 255
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 821 AGAGAGACGCGCATATTGCACTATCCAAATGCCAAAGGTTAGACAAATGAACCTTGA 880
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 256 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluLysValAsp 275
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 881 GGAGGTCTTTTGGGAAGATCACTTTGAAACTACTGTAAAAATGAGTACATACCTTTGTAGCC 940
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 276 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 295
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 941 TACATAGTTTGTGATTTCCATCTCTCTGAGTGGCTTCTCACTTCATCAAGGGTCAAGGTGCC 1000
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 296 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 315
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1001 ATCTATGATCCCCAGACAAACGGAATCAACACATATTATGCTTTGCGGCACTCACTAAG 1060
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 316 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 335
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
```

```
QY 1061 CTACTTGATTTTATGAAAAAGTACTTTTGATATCTTACTATCTCCACTCTCCAAACTCGAATTTA 1120
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 336 ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys 355
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1121 ATTGCTATTCTGACTTTGTCACCTGGAGCCCATGAAATTTGGGGCTCATTTACATATAGG 1180
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 356 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 375
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1181 GAGACGTCACCTGCTTTTGGACCCAGACCTCTTCTGCTCCGATAAATCTGGGTCCACC 1240
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 376 GluThrAsnLeuLeuTyrAspProLysGluSerAlaSerSerAsnGlnGlnArgValAla 395
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1241 AGAGTCATAGCCCATGAACCTGGCGCCACCTGAGTGTGTTGGCAACCTGGTGCACAAATGGAATGG 1300
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 396 ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAspTrp 415
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1301 TGGAAATGATATTTGGCTTAAAGAGGGTGTTCGAAAAATACATGAACTTATCGCTGTTAAT 1360
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 416 TrpGluAspLeuTrpLeuAsnGluGlyPheAlaSerPhePheGluPheLeuGlyValAsn 435
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1361 GCTACATATCCAGAGCTGCAATTT---GATGACTATTTTGAATGTGTCTTTTGAAGTA 1417
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 436 HisAlaGluThrAspTrpGlnMetArgAspGlnMetLeuLeuGluAspValLeuProVal 455
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1418 ATTACAAAAGATTCATTGAATTCATCCCGCCTTATCTCCAAACCCAGCGGAAACCCCGACT 1477
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 456 GlnGluAspAspSerLeuMetSerSerHisProIleValThrValThrThrProAsp 475
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1478 CAAATACAGAAATGTTTGTATGAAGTTTCTTATAACAGAGGAGCTGTATTTGATATG 1537
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 476 GluIleThrSerValPheAspGlyIleSerTyrSerLysGlySerSerIleLeuArgMet 495
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1538 CTCAGAGATTTCTGGGTGAGGAGAAATTCACAAAGAGGATAATTCAGTACTTTAAAGAAG 1597
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 496 LeuGluAspTrpIleLysProGluAsnPheGlnLysGlyCysGlnMetTyrLeuGluLys 515
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1598 TTCAAGCTATAGAAATGCTAAGAAATGATGCTTGTGGAGCAGTCTGTCCAAATAGTTGTTA 1657
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 516 TyrGlnPheLysAsnAlaLysThrSerAspPheTyrAlaAlaLeuGluGluAla--- 533
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1658 GAAAGTGATTTTACATCTGGTGAGTTGTTCATTCGATCCCAAGATGACAAGTAACATG 1717
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 533 ----- 533
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1718 CTCGCTTTCTGGGGGAAAATGCAGAGGTCAAAGAGATGATGACTACATGCACTCTCCAG 1777
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 534 -----SerArgLeuProValLysGluValMetAspThrTrpThrArgGln 548
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1778 AAAGGAATCCCTGCTGGTGGTTAAACAAGACGGGTGTTCACTCCGACTGCAACAGGAG 1837
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 549 MetGlyTyrProValLeuAsnVal-----AsnGlyValLys---AsnIleThrGlnLys 565
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1838 CGCTTCTCCAGGGGTTTTCAGGAGAACCTGTAATGGAGGGCCCTCGCAGGAG----- 1891
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 566 ArgPheLeuLeu-----AspProArgAlaAsnProSerGlnProProSer 580
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1892 -----AGGTACTGTGGCATATCCCATTCACCTAC-----TCACGAGGTCTTCT 1936
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 581 AspLeuGlyTyrThrTrpAsnIleProValLysTrpThrGluAspAsnIleThrSerSer 600
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1937 AATGTGATCCACAGACACATTTCTAAATCAAAGACAGATACTCTGGATCTTCACTGAAAG 1996
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 601 ValLeuPheAsnArgSerGluLysGluGlyIleThrLeuAsnSerSerAsnProSerGly 620
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 1997 ACAGTTGGTGAAATTAATGGACTCAATGGTTACTACATCGTTCACTATGAGGT 2056
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 621 AsnAlaPheLeuLysIleAsnProAspHisIleGlyPheTyrArgValAsnTyrGluVal 640
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 2057 CATGGATGGACCAACTCATTACACAGCTGAATCAGAACCCACACACTTCTCAGACCTAAG 2116
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 641 AlaThrTrpAspSerIleAlaThrAlaLeuSerLeuAsnHisLysThrPheSerSerAla 660
Db  :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
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QY 2117 GACAGTAGGTCGATTCATGATGTTTACAGTAGTTGGTGCAGGAGACTGACCCCTA 2176
Db 661 AsparGalaSerLeuileAspAspAlaPheAlaLeuAlaArgAlaGlnLeuLeuAspTyr 680
QY 2177 GACAAAGCTCTGACATGACTTACTACCTCCCAACATGAACAACAGCAGC-----CCC 2227
Db 681 LysValAlaLeuAsnLeuThrLysTyrLeuLysArgGluGluAsnPheLeuProTrpGln 700
QY 2228 GCATCTTCGAAGGCTGAGTTACTTGGAAATCGTTTACCACATGATGGACAGAAGGAT 2287
Db 701 ArgValIleSerAlaValThrTyrIleIleSerMetPhe-----GluAsp 715
QY 2288 ATTTCCAGATATCTCGAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAAGCCAGTAT 2347
Db 716 AspLysGluLeuTyrProMetIleGluGluTyrPheGlnGlyValLysPheProIleAla 735
QY 2348 GACAGGCAAAAGCTGGAGTGACAAGGCTCAGCTGGACAGGATGCTCGCTCGGCTCTC 2407
Db 736 AspSerLeuGlyTrpAsnAspAlaGlyAspHisValThrLysLeuLeuArgSerVal 755
QY 2408 TTGAAGCTGGCTGTGACCTGAACCATGCTCCTTCATCCAGAAAGCTGCTGAATCTTC 2467
Db 756 LeuGlyPheAlaCysLysMetGlyAspArgGluAlaLeuAsnAsnAlaSerSerLeuPhe 775
QY 2468 TCCAGTGATGGAATCCAGTCGAAATTAATATATACACAGATGTTTAAAGATTG 2527
Db 776 GluGlnTrpLeu-----AsnGlyThrValSerLeuProValAsnLeuArgLeuVal 793
QY 2528 TATTCGTGGGGCTCAGACAACAGCA-----GGATGAAATTTACCTTTTAGAGCAA 2578
Db 794 TyrArgTyrGlyMetGlnAsnSerGlyAsnGluIleSerTrpAsnTyrThrLeuGln 813
QY 2579 TATGAATCTGTAATGCAAGTCTGAAACAAAATAATCTGTATGCTTTGTCAAGAGC 2638
Db 814 TyrGlnLysThrSerLeuAlaGlnGluLysGluLysLeuLeuTyrGlyLeuAlaSerVal 833
QY 2639 AAGCATCAGAAAGTTACTGAAGTAAATGAACATAGGAATGGAAGGAAGTTATCAAG 2698
Db 834 LysAsnValThrLeuLeuSerArgTyrLeuAspLeuLeuLysAspThrAsnLeuIleLys 853
QY 2699 ACACAGAACTTGGCAGCTCTCCTCATGCGATTGGCCAGACGTCACAAAGGGGACGACTA 2758
Db 854 ThrGlnAspValPheThrValIleArgTyrIleSerTyrAsnSerTyrGlyLysAsnMet 873
QY 2759 GCATGGGATTTTGAAGAAATTTGGACCCATCTTCTGAAATAATTTGACTTTGGGCTCA 2818
Db 874 AlaTrpAsnTrpIleGlnLeuAsnTrpAspTyrLeuValAsnArgTyrThrLeuAsnAsn 893
QY 2819 TATGACATAAGGATGATCATCTCTGGCACACAGCTCACTTTTCTCCAGGATAGTTG 2878
Db 894 ArgAsnLeuGlyArgIleValThr---IleAlaGluProPheAsnThrGluLeuGlnLeu 912
QY 2879 CAAGAGGTGAACATATTTTCAATCTCTTGAGGCTCAAGGATCATCTGGATATTTT 2938
Db 913 TrpGlnMetGluSerPhePheAlaLysTyrProGlnAlaGlyAlaGlyGluLysProArg 932
QY 2939 CAAACTGTTCTGGAACACATACCAAAATAATGCTCGGAGAGAAGAAATCTCCGACT 2998
Db 933 GluGlnValLeuGluThrValLysAsnAsnIleGluTrpLeuLysGlnHisArgAsnThr 952
QY 2999 CTGAGGACTTGG 3010
Db 953 IleArgGluTrp 956
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## RESULT 7

```
US-09-139-802-201
; Sequence 201, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
```

```
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-139-802-201

Alignment Scores:
Pred. No.: 1,07e-120 Length: 967
Score: 1264.50 Matches: 325
Percent Similarity: 46.62% Conservative: 158
Best Local Similarity: 31.37% Mismatches: 386
Query Match: 21.39% Indels: 167
Gaps: 26
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US-10-039-073-2 (1-3366) x US-09-139-802-201 (1-967)

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QY 203 AGAGATTTTACTGCTTAACAGCCATC-----TTGCCCAA 238
Db 3 LysGlyPheTyrIleSerLysSerLeuGlyIleLeuGlyIleLeuGlyValAlaAla 22
QY 239 ATATGCATTTGTTCTCAGTCTCAGTCCCATCTAGTTATCTACTTCACGTGAGGATCCTGGG 298
Db 23 ValCysThrIleIleAlaLeuSerValValTyrSerGlnGluLysAsnLysAsnAlaAsn 42
QY 299 GCTTTCACGATGACC----- 313
Db 43 SerSerProValAlaSerThrThrProSerAlaSerAlaThrThrAsnProAlaSerAla 62
QY 314 ---ACTAATGGGAACGATTTCTTGGCAGAGCTAGGCTCCCGAGTGTGCTTCTCT 370
Db 63 ThrThrLeuAspGlnSerLysAlaTrpAsnArgTyrArgLeuProAsnThrLeuLysPro 82
QY 371 CTCCATTTAGCTCTTGTGTCACCCCAATCTCACCTCTCTGGAC----- 415
Db 83 AspSerTyrGlnValThrLeuArgProTyrLeuThrProAsnAspArgGlyLeuTyrVal 102
QY 416 TTTGTTGCATCTGAGAAGATCGAAGTCTTGTGTCAGCAATGCTTACCAGTTTATCATCTTTG 475
Db 103 PheLysGlySerSerThrValArgPheThrCysLysGluAlaThrAspValIleIleIle 122
QY 476 CACAGCAAGATCTTGAATCAGCAATGCCACCTTCAGTCAGAGGAAGATTCAAGATAC 535
Db 123 HisSerLysLysLeuAsnTyrThr----- 130
QY 536 ATGAACCCAGAAAGAACTCAAAAGTTTGTAGTTAC-----CCTGCTCAT 580
Db 131 LeuSerGlnGlyHisArgValValLeuArgGlyValGlyGlySerGlnProProAspIle 150
QY 581 GAACAAATTCACCTGCTGGTTCCA--GAGAAATCTACGCCCTCACCTGAAA----- 628
Db 151 AspLysThrGluLeuValGluProThrGluTyrLeuValValHisLeuLysGlySerLeu 170
QY 629 -----TACTATGTGCTATGAGCTTCCAAAGCCAAAGTTAGGTGATGGCTTT 673
Db 171 ValLysAspSerGlnTyrGluMetAspSerGluPheGluGlyGluLeuAlaAspAspLeu 190
QY 674 GAAGGTTTTATAAAGCACATACAGAACTCTTGGTGTGGAACACAGAAATTTCTTCAGTA 733
Db 191 AlaGlyPheTyrArgSerGluTyrMetGlu---GlyAsnValArgLysValValAlaThr 209
QY 734 ACAGATTTTGTAGCCAAACCCAGGACGATGCTTCCCTTCTTGTGTAACCCGTTGTTTC 793
Db 210 ThrGlnMetGlnAlaAlaAspAlaArgLysSerPheProCysPheAspGluProAlaMet 229
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QY 1475 ACTCAATACAGGAATGTTTGTATGAAGTTTCTTATACAAAGGAGCTGTGTAATTTGAAT 1534
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
466 AlaGlnIleSerGluLeuPheAspAlaIleSerTyrSerLysGlyAlaSerValLeuArg 485
QY 1535 ATGCTCAAGGATTTTCTGGGTGAGAGAAATTCAGAAAGAAATAATTCAGTACTTAAG 1594
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
486 MetLeuSerSerPheLeuSerGluAspValPheLysGlnGlyLeuAlaSerTyrLeuHis 505
QY 1595 AAGTTTCAGTATAGAAATGCTAAGAAATGATGACTTGTGGACACTCTG----- 1642
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
506 ThrPheAlaIleGlnAsnThrIleTyrLeuAsnLeuTrpAspHisLeuGlnGluAlaVal 525
QY 1643 TCAATAGTCTGTTAGAAAGTGAATTTTACATCTCGTGGAGTTTGTCTATTCGATCCCAAG 1702
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
536 AsnAsnArgSerIleGlnLeuProThrThr----- 535
QY 1703 ATGACAGTAACATGCTCGCCTTTCTGGGGGAAATGACAGGTCAAAGAGATGATGACT 1762
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
536 -----ValArgAspIleMetAsn 541
QY 1763 ACATGGACTCTCCAGAAAGGAATCCCTCGTGTGGTTTAAACAAGACGGGTGTTCACTC 1822
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
542 ArgTrpThrLeuGlnMetGlyPheProValIleThrVal-----AspThrSerThrGly 559
QY 1823 CGACTGCAACAGGACGCTTCTCCAGGGGCTTTTCCAGGAAGACCCCTGAA----- 1873
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
560 ThrLeuSerGlnGluHisPheLeuLeu-----AspProAspSerAsnVal 574
QY 1874 TGGAGGGCCCTGCGAGGAGAGTACTCTGTGGCATATCCATTGACC----- 1918
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
575 ThrArgProSerGluPheAsnTyrValTrpIleValProIleThrSerIleArgAspGly 594
QY 1919 -----TACTCCACG 1927
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
595 ArgGlnGlnGlnAspTyrTrpLeuIleAspValArgAlaGlnAsnAspLeuPheSerThr 614
QY 1928 AGTTCTTCTAATGTATCCACAGACACATTTCTAAATCAAAAGACAGATACTCTGGATCTA 1987
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
615 SerGlyAsn----- 617
QY 1988 CCTGAAAGACCAGTTGGGTGAATTTAATGTGACTCAATATGTTACTATCATCTGTTCAAC 2047
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 -----GluTrpValLeuLeuAsnLeuAsnValThrGlyTyrTyrArgValAsn 633
QY 2048 TATGAGGTCTGATGATGGACCACTCATTAACAGCTGAATCAGAACCAACACACTTCTC 2107
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
634 TyrAspGluGluAsnTrpArgLysIleGlnThrGlnLeuGlnArgAspHisSerAlaIle 653
QY 2108 AGACCTAAGGACAGAGTAGTCTGATTCATGATCTGTTTCAGCTAGTGTGTGCGAGGAGA 2167
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
654 ProValIleAsnArgAlaGlnIleAsnAspAlaPheAsnLeuAlaSerAlaHisLys 673
QY 2168 CTGACCTTAGACAAGCTCTTGACATGACTTACTCTCCACATGAAACAGCAGGCCCC 2227
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
674 ValProValThrLeuAlaLeuAsnAsnThrLeuPheLeuIleGluGluArgGlnTyrMet 693
QY 2228 GCACCTTCGAAAGTCTGAGTTACTTGAATCGTTTACACATGATGACAGCAAGGAAT 2287
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
694 ProTrpGluAlaLeuLeuSerSerLeuSerTyrPheLysLeuMetPheAspArg----- 711
QY 2288 ATTTTCAGATATCTCTGAAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAAGCCAGTGATT 2347
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
712 ---SerGluValTyrGlyProMetLysAsnTyrLeuLysLysGlnValThrProLeuPhe 730
QY 2348 -----GACAGGCAAGCTGGAGTGAC---AAGGCTCAGTCTGGGACAGG 2389
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
731 IleHisPheArgAsnAsnThrAsnAsnTrpArgGluIleProGluAsnLeuMetAspGln 750
QY 2390 ATGCTCCGCTCGGCTCTCTTGAAGCTGCGCTGTGACCTGACCAACCATGCTCTTCATCCAG 2449
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
751 TyrSerGluValAsnAlaIleSerThrAlaCysSerAsnGlyValProGluCysGluGlu 770
QY 2450 AAAGCTGCTGAATCTTCTCCAGTGGATGGAATCCAGTGGAAAAATTAATATATACCAACA 2509
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Db 771 MetValSerGlyLeuPheLysGlnTrpMetGluAsnProAsnAsnProIleHisPro 790
QY 2510 GATGTTTTAAAGATTGTGAT-----TCTGTGGTGCTCAGACAACAGCAGGATGAAT 2563
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 AsnLeuArgSerThrValTyrCysAsnAlaIleAlaGlnGlyGlyGluGluTrpAsp 810
QY 2564 TACCTTTTACAGCAATATGAATGTCATGTCAAGTGTCAAGTGTCAACAAACAAATTTCTGTAT 2623
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
811 PheAlaTrpGluGlnPheArgAsnAlaThrLeuValAsnGluAlaAspLysLeuArgAla 830
QY 2624 GCTTTGTCAACGACGATCATCGAAAGATTACTGAAGTTAATTAAGTGAAGTGAAGTGA 2683
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
831 AlaLeuAlaCysSerLysGluLeuTrpIleLeuAsnArgTyrLeuSerTyrThrLeuAsn 850
QY 2684 GGAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATCGGATGCCACAGCTCCA 2743
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
851 ProAspLeuIleArgLysGlnAspAlaThrSerThrIleIleSerIleThrAsnAsnVal 870
QY 2744 AAGGGCGACCACTAGCATGGGATTTTGAAGAGAAAAATTTGGACCATCTTCTGAAAAA 2803
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
871 IleGlyGlnGlyLeuValTrpAspPheValGlnSerAsnTrpLysLysLeuPheAsnAsp 890
QY 2804 TTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCAACAACAGCTCACTTTCT 2863
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 TyrGlyGlySerPheSerPheSerAsnLeuIleGlnAlaValThrArgArgPheSer 910
QY 2864 TCCAAGGTAAGTTCGAAGAGGTGAAACTATTTTTTGAATCTCTTGAGGCTCAA----- 2917
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
911 ThrGluTyrGluLeuGlnGlnLeuGlnPheLysLysAspAsnGluGluThrGlyPhe 930
QY 2918 GGATCATCTCGATATTTTTCAACTGTTCTCGAAACGATAACCAAAATATAAAATGG 2977
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
931 GlySerGlyThrArgAlaLeuGluAlaLeuGluLysThrLysAlaAsnIleLysTrp 950
QY 2978 CTGAGAGAAGATCTTCGACTCTCGAGGACTTGGCTAATGTTAATACT 3025
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
951 ValLysGluAsnLysGluValValLeuGlnTrpPheThrGluAsnSer 966

RESULT 9
US-09-919-039-222
; Sequence 222, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919, 039
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 222
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 2278688CD1
US-09-919-039-222

Alignment Scores:
Pred. No.: 1,21e-116 Length: 919
Score: 1255.00 Matches: 309
Percent Similarity: 49.74% Conservative: 163
Best Local Similarity: 32.56% Mismatches: 351
Query Match: 20.72% Indels: 126
DB: 4 Gaps: 26

US-10-039-073-2 (1-3366) x US-09-919-039-222 (1-919)
QY 308 GTAGCCACTAATGGGGAACGATTTCTTGGCAGAGCTAAGGCTCCCGCATTTGGTCAATT 367
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QY 2405 CTCTTGAAGCTGGCTGTGACCTGAACCATCTCTCTTGCATCCAGAAAGCTGCTGAATC 2464
Db :|||
709 valLeuGlyLysLeuGlyLysAlaGlyHisLysAlaThrLeuGluGluAlaArgArg 728
:|||||
2465 TTCTCCAGTGGATGGAATCCAGTGGAAATTAATATATACCAACAGATGTTTTAAAGATT 2524
Db :|||
729 PheLysAspHisValGlu-----GlyLysGlnIleLeuSerAlaAspLeuAspSerPro 746
:|||||
2525 GTGTATTCTGTG-----GGTCTCAGACCAACAGCAGGATGGAATTACCTTTTA 2572
Db :|||
747 ValTyrLeuThrValLeuLysHisGlyAspGlyThrThrLeu-----AspIleMetLeu 764
:|||||
2573 GAGCAATATGAATGCTCAATGCTCAAGTCTGAACAAACAAAATTCGTATGCTTCTGCA 2632
Db :|||
765 LysLeuHisLysGlnAlaAspMetGlnGluGluLysAsnArgIleGluArgValLeuGly 784
:|||||
2633 ACGAGCAAGCATCAGGAAAGTTACTGAAGTTAATGAACCTAGGAATGGAAGAAAGTT 2692
Db :|||
785 AlaThrLeuLeuProAspLeuIleGlnLysValLeuThrPheAlaLeuSerGluGluVal 804
:|||||
2693 ATCAAGACACAGAACTGGCGACTCTCTTCATCGGATTGCCAGACGTCCAAAG---GGG 2749
Db :|||
805 ---ArgProGlnAspThrValSerValIleGlyValAlaGlyLysSerLysHisGly 823
:|||||
2750 CAGCAACTAGCATGGGATTTTGTAAAGAAATTTGGACCCCATCTTCTGAAAAATTTGAC 2809
Db :|||
824 ArgLysAlaAlaThrLysPheIleLysAsnAsnIleGluGluLeuTyrAsnAsnGlyGln 843
:|||||
2810 TTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAAACAGCTCACTTTCTTCCAAG 2869
Db :|||
844 ---GlyGlyPheLeuIleSerArgLeuIleLysLeuSerValGluGlyPheAlaValAsp 862
:|||||
2870 GATAAGTTGCAAGAGGTGAACACTATTTTGAATCTCTTGAGGCTCAAGATCACATCTG 2929
Db :|||
863 LysMetAlaGlyGluValLysAlaPhePheGluSerHisProAlaProSerAlaGluArg 882
:|||||
2930 GATATTTTCAAACTGTTCTGGAACGATACCAACAAAATATAAAATGAGTGGGAGGAAT 2989
Db :|||
883 ThrIle---GlnGlnCysCysGluAsnIleLeuLeuAsnAlaAlaThrPleuLysArgAsp 901
:|||||
2990 CTTCGACTCTGAGGACTTGGCTAATG 3016
Db :|||
902 AlaGluSerIleHisGlnTyrLeuLeu 910
:|||||

RESULT 10
US-08-335-844A-22
; Sequence 22, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-335-844A-22

Alignment Scores:
Pred. No.: 1,91e-110 Length: 977
Score: 1165.00 Matches: 280
Percent Similarity: 49.22% Conservative: 192
Best Local Similarity: 29.20% Mismatches: 411
Query Match: 19.71% Indels: 76
DB: 3 Gaps: 21

US-10-039-073-2 (1-3366) x US-08-335-844A-22 (1-977)
QY 260 TCAGTGCCATCTAGTTATCATCTTCACT-----GAGGAT 292
Db 41 SerIleGlyLeuThrTyrPheThrArgLysAlaPheAspThrThrGlyGlyAsnGly 60
QY 293 CCTGGGGCTTCCAGTAGCCACTAATGGGAACGATTTCTTGGCAGGAGCTAAGGCTC 352
Db 61 LysGlyAspGlnProIleValAspAsnSerProSerAla---GluGluLeuArgLeu 79
QY 353 CCAGTGTGTGTCATCTCTCCATTATGACCTTTTGTCCAC-----CCCAATCTC 403
Db 80 ProThrThrIleLysProLeuThrThrAspLeuValIleLysThrTyrLeuProAsnTyr 99
QY 404 ACCTCTCTG-----GACTTT-----GTTGATCTGAG 430
Db 100 ValAsnTyrProProGluLysAspPheAlaIleAspGlyThrValValIleAlaMetGlu 119
QY 431 AAGATCGAAGTCTTGTGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTT 490
Db 120 ValValGlu-----ProThrLysSerIleValLeuAsnSerLysAsnIle 134
QY 491 GAAATCACGAATGCCCCCTTCAGTCAGAGGAAGATTCAAGATACATGAACACCGAGAAA 550
Db 135 ProVal-----IleAlaAspGlnCysGluLeuPheSerAsnAsnGlnLysLeuAspIle 152
QY 551 GAATCGAAAGTTTGTAGTTACCTGCTCATGAACAAATGCACTGCTGTTCCAGAGAAA 610
Db 153 Glu---LysValValAspGlnProArgLeuGluLysValGluPheValLeuLysLysLys 171
QY 611 CTTACGCCCTCACCTGAATACTATGTGGCTATGTGCTTCCAGCCCAAGTTAGGTGATGGC 670
Db 172 LeuGluLysAsnGlnLysIleThrLeuLysIleValTyrIleGlyLeuIleAsnAspMet 191
QY 671 TTTGAAGGGTTTATAAAGACATACAGAACTCTTGTGGTGGTGAACAAAGAATTTCTGCA 730
Db 192 LeuGlyGlyLeuTyrArgThrThrTyrThrAspLysAspGlyThrThrLysIleAlaAla 211
QY 731 GTAACAGATTTTGGCAACCCAGGACCGATGCGCTTCCCTTGTGTTGATGACCGTTG 790
Db 212 CysThrHisMetGluProThrAspAlaArgLeuMetValProCysPheAspGluProThr 231
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Db 931 LeuIysAsnLeuTyrLysAsn-...AspLysArgAlaArgGluTyrGlyAlaPheGlyGly 949  
Qy 2945 GTTCTGGAAACGATACCAAAAATATAAAATGGCTGGAGAGAAATCTTCCGACTCTG 3001  
Db 950 AlaIleGluArgSerGluHisArgValIleGlyTrpIleGluLysHisPheArgLysLeu 968  
RESULT 11  
US-09-129-366-22  
; Sequence 22. Application US/09129366  
; Patent No. 6534638  
; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, MARGARET  
; APPLICANT: SMITH, TREVOR STANLEY  
; APPLICANT: MUNN, EDWARD ALBERT  
; APPLICANT: KNOX, DAVID PATRICK  
; APPLICANT: OLIVER, JOANNA JANE  
; APPLICANT: NEWTON, SUSAN ELIZABETH  
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rochwell, Figg, Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/129.366  
; FILING DATE: 05-AUG-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/335,844  
; FILING DATE: 09-JAN-1995  
; PRIOR APPLICATION NUMBER: GB PCT/GB93/00943  
; APPLICATION DATE: 06-MAY-1993  
; APPLICATION DATA:  
; APPLICATION NUMBER: GB 9209936  
; FILING DATE: 08-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1181-241A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 977 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-129-366-22  
Alignment Scores:  
Pred. No.: 1.91e-110 Length: 977  
Score: 1165.00 Matches: 280  
Percent Similarity: 49.22% Conservative: 192  
Best Local Similarity: 29.20% Mismatches: 411  
Query Match: 19.71% Indels: 76  
DB: 4 Gaps: 21  
US-10-039-073-2 (1-3366) x US-09-129-366-22 (1-977)  
Qy 260 TCAGTGCCATCTAGTTATCACTTCACT-----CAGGAT 292

Db 41 SerIleGlyLeuThrTyrTyrPheThrArgLysAlaPheAspThrThrGlyGlyAsnGly 60  
Qy 293 CTTGGGGCTTTCCAGTAGCCACTAATGGGAAACGATTTCCTTGGCAGGAGTAAAGGCTC 352  
Db 61 LysGlyAspGlnProIleValAspAspAsnSerProSerAla---GluGluLeuArgGlu 79  
Qy 353 CCCAGTGTGGTCATTCCTCTCCATTATGACCTCTTTGTCTCCAC-----CCCAATCTC 403  
Db 80 ProThrThrIleLysProLeuThrTyrAspLeuValIleLysThrTyrLeuProAsnTyr 99  
Qy 404 ACCTCTCTG-----GACTTT-----GTTGCATCTGAG 430  
Db 100 ValAsnTyrProProGluLysAspPheAlaIleAspGlyThrValValIleAlaMetGlu 119  
Qy 431 AAGATCGAAGCTCTTGGTCACCAATGCTACCCAGTTTATCATCTTGACACACAAAGATCTT 490  
Db 120 ValValGlu-----ProThrThrSerIleValLeuAsnSerLysAsnIle 134  
Qy 491 GAAATCACGAATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAAACCCAGGAAAA 550  
Db 135 ProVal-----IleAlaAspGlnCysGluLeuPheSerAsnAsnGlnLysLeuAspIle 152  
Qy 551 GAACGTGAAAGTTTGTAGTTACCTGCTCATGAACAAATTCGACTGCTGGTTCAGAGAAA 610  
Db 153 Glu---LysValValAspGlnProArgLeuGluLysValGluPheValLeuLysLys 171  
Qy 611 CTTACGCTCACCTGAAATACTATGTGCTATGCATTCACAGCTTCCAGCCAAAGTAGGTGGC 670  
Db 172 LeuGluLysAsnGlnLysIleThrLeuLysIleValTyrIleGlyLeuIleAsnAspMet 191  
Qy 671 TTTGAAGGGTTTATATAAGCACATACAGAACTCTTGGTGGTGAACAAGAAATCTTTGCA 730  
Db 192 LeuGlyGlyLeuTyrArgThrThrTyrThrAspLysAspGlyThrThrLysIleAla 211  
Qy 731 GTAACAGATTTTGAGCCAAACCCAGGACCGATGCTTCCCTTGTGTTGTATGAACCGTTG 790  
Db 212 CysThrHisMetGluProThrAspAlaArgLeuMetValProCysPheAspGluProThr 231  
Qy 791 TTCAAAGCCCAACTTTTCAATCAAGATACGAAGAGAGAGAGGCATATATGCATATCAAC 850  
Db 232 PheLysAlaAsnTrpThrValThrValIleHisProLysGlyThrSerAlaValSerAsn 251  
Qy 851 ATGCCAAAGGTTAAGACAATTGAACCTTGAAGAGAGGCTCTTTTGAAGATCACTTTGAA 910  
Db 252 GlyIleGluLysGlyGluGlyGluValSerGlyAspTrpValThrThrArgPheAspPro 271  
Qy 911 ACTGTAAATAGTAGTACATACCTTTGTAGCTCATAGTTGTGATTTCCACTCTCTAGT 970  
Db 272 ThrProArgMetProSerTyrLeuIleAlaLeuValIleSerGluPheLysTyrIleGlu 291  
Qy 971 GGCTTCACTTCATCAGGGGTCAAGGTGTCATTCATGCATCCCGACCAACAAACGGAATCA 1030  
Db 292 AsnTyrThrLysSerGlyValArgPheArgIleProAlaArgProGluAlaMetLysMet 311  
Qy 1031 ACACATTATGCTTTGAGGATCATCAAGCTACTTGGTATTTATGAAAAAGTACTTTGAT 1090  
Db 312 ThrGluTyrAlaMetIleAlaGlyIleLysCysLeuAspTyrTyrGluAspPheGly 331  
Qy 1091 ATCTACTATCCACTCTCCAAACTGGATTTAATGCTATTCTGCTTCTGCTTTGCTGGAGCC 1150  
Db 332 IleLysPheProLeuProLysGlnAspMetValAlaLeuProAspPheSerSerGlyAla 351  
Qy 1151 ATGGAATAATGGGGCTCATTACATATAGGAGAGGTCACCTGCTTTTGTAGCCCCAAGACC 1210  
Db 352 MetGluAsnTrpGlyLeuIleThrTyrArgGluGlySerValLeuTyrAspGluAsnLeu 371  
Qy 1211 TCTTCTCTTCCGATAAACTGTGGGTCAACAGAGTCATAGCCCATGAACCTGCGCACCCAG 1270  
Db 372 TyrGlyProMetAsnLysGluArgValAlaGluValIleAlaHisGluLeuAlaHisGln 391  
Qy 1271 TGGTTTGGCACTCTGGTCAACATGGAATGTGGAATGATATTTGGCTTAAAGGAGGTTT 1330

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Db 392 TrpPheGlyAsnLeuValThrMetLysTrpTrpAspAsnLeuTrpLeuAsnGluGlyPhe 411
QY 1331 GCAAAATACATGAACTTATCCTGTTAAATGCTACATATCCAGAGCTG---CAATTGAT 1387
Db 412 AlaSerPheValGluTyrIleGlyAlaAspPheIleSerAspGlyLeuTrpGluMetLys 431
QY 1388 GACTATTTTGAATGTGTTT---GAAGTAATTTAGAAAAGATTCATTGAATTCATCC 1444
Db 432 AspPheLeuLeuAlaProTyrThrSerGlyIleThrAlaAspAlaValAlaSerSer 451
QY 1445 CGCCCTATCTCCAAACCGGCAACCCCGACTCAAAATACAGAAATGTTTTCATGAAGTT 1504
Db 452 HisProLeuSerPheArgIleAspLysAlaAlaAspValSerGluAlaPheAspIle 471
QY 1505 TCCTATAACAGGAGCTGTTATTTTGAATATGCTCAAGGATTTTTCGGTGAGGAGAA 1564
Db 472 ThrTyrArgLysGlyAlaSerValLeuGlnMetLeuLeuAsnLeuValGlyAspGluAsn 491
QY 1565 TTCCAGAAAGGAATATTCAGTACTTAAGAATGTTTCAGCTATAGAAATGCTAAGATGAT 1624
Db 492 PheLysGlnSerValSerArgTyrLeuLysLysPheSerTyrAspAsnAlaAlaGlu 511
QY 1625 GACTTGTGAGCAGCTGTGCAATAGTTGTTTAGAAAGTGATTTTACATCTCGTGAGTT 1684
Db 512 AspLeuTrpAlaAlaPhe-----AspGluThrValGlnGlyIle 524
QY 1685 TGTCAATTCGGATCCCAAGATGACAAGTAAATGCTCGCTTCTCGGGGAAAATCCAGAG 1744
Db 525 -----TrpGlyProAsn-----GlyGlyProLeuLys 533
QY 1745 GTCAAGAGATGATGACTACATGAGTCTCCAGAAAGGATCCCTGCTGCTGTTAA 1804
Db 534 MetSerGluPheAlaProGlnTrpThrGlnMetGlyPheProValLeuThrValGlu 553
QY 1805 CAA---GAGCGGTGTCTACTCGACTGCAACAGGAGCGTCTCTCCAGGGGTTTTCCAG 1861
Db 554 SerValAsnAlaThrThrLeuLysValThrGlnLysArgTyrArgGlnAsnLysAspAla 573
QY 1862 GAAGACCTTGAA---TGGAGGCGCTCGCAGGAGAGGTACTGTCGATATCCCATGACC 1918
Db 574 LysGluProGluLysTyrArgHisProThrTyrGlyPheLysTrpAspValProLeuTrp 593
QY 1919 TACTCCAGAGTCTTCTAATGTGATCCACAGACATCTTAATTAATCAAGACAGATACT 1978
Db 594 TyrGlnGluAspGluGlnValLysArgThrTrpLeuLysArgGluGluProLeuTyr 613
QY 1979 CTGGATCTACCTGAAAGACCACTTGGGTGAATTTAATGTGGACTCAATGTTACTTAC 2038
Db 614 PheHisValSerAsnSerAspSerSerValValAsnAlaGluArgAlaPheCys 633
QY 2039 ATCGTTCTACTATGAGGCTCATGGATGGGACCACTCATACACAGCTGAATCAGAACCA 2098
Db 634 ArgSerAsnTyrAspAlaAsnGlyTrpArgAsnIleMetArgArgLysGlnAsnHis 653
QY 2099 ACATCTTCCAGACCTTAAGACAGAGTAGTCTGATTCATGATGTGTTTCAGCTAGTTGGT 2159
Db 654 LysValTyrGlyProArgThrArgAsnAlaLeuIleSerAspAlaPheAlaAlaAla 673
QY 2159 GCAGGGAGAGTACCTCGACAAAGCTCTTGACATGACTTACTACTCCACATCAACA 2218
Db 674 ValGluGluMetAsnTyrGlnThrValPheGluMetLeuLysTyrThrValLysGlu 693
QY 2219 AGCAGCCCGCCTTCTCGAAGCTGTGAGTACTTGGAAATCCTTTTACCACATGATGAC 2278
Db 694 AspTyrLeuProTrpLysGluAlaIleSer-----GlyPheAsnThrIleLeuAsp 710
QY 2279 AGAAGGAATATTTACAGATATCTTGAAACCTCAAGCGTTACTTCTTCAGTATTTTAA 2338
Db 711 PhePheGlySerGluProGluSerGlnTrpAlaSerGluTyrMetArgLysLeuMetLys 730
QY 2339 CCAGTGATTTGACAGGCAAGC-----TGGAGTGACAGAGGCTCA 2377
Db 731 ProfileTyrAspLysSerSerIleLysPheIleAlaGluAsnTyrLysAspSerLeu 750
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QY 2378 GTCGGGACAGATGCTCCGCTCGCTCTCTTGAAGCTGGCTGTGACCTGAACCATGCT 2437
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QY 2438 CCTTGCTCCAGAAAGCTGCTGAACCTCTTCTCCAG-----TGG 2476
Db 771 GluCysLeuGluGluMetLysLeuPheAspLysGluValMetLysCysGlnProGly 790
QY 2477 ATGGAATCCAGTGAAATTAATATATACCAACAGATGTTTAAAGATTTGTATTCTGTG 2536
Db 791 GlnGlnAlaThrAspCysValLysValThrAlaProLeuArgLysThrValTyrCysTyr 810
QY 2537 GGTGCTCAGACA-----ACAGCAGGATGGAATACCTTTTAGACAAATATGAATGTCA 2590
Db 811 GlyValGlnGluGlyGlyAspGluAlaPheAspLysValMetGluLeuTyrAsnAlaGlu 830
QY 2591 ATGTCNAGTGTGCAACAAACAAAATTCGTATCTGCTTGTCAACGACGACGATCAGGAA 2650
Db 831 GlnValGlnLeuGluLysAspSerLeuArgGluAlaLeuGlyCysHisLysAspValThr 850
QY 2651 AAGTTACTGAAGTTAAATTTGAATAGGAATGAA-----GGAAAGGTTATCAAGACACAG 2704
Db 851 AlaLeuLysGlyLeuLeuMetLeuAlaLeuAspArgAsnSerSerPheValArgLeuGln 870
QY 2705 AACTTGGCAGCTCTCTTCATGCGATTGCCAGAGCTCCAAAGGGGCGACAACTAGCATGG 2764
Db 871 AspAlaHisAspValPheAsnIleValSerArgAsnProValGlyAsnGluLeuLeuPhe 890
QY 2765 GATTTGTAGAGAAATTTGACCCATCTTCTGAAAAAATTTTGACTTGGGCTCATATGAC 2824
Db 891 AsnPheLeuThrGluLysArgTrpGluGluIleLeuGluSerLeuSerIleArgHisArgSer 910
QY 2825 ATAAGGATGATCATCTCTGGCAACACAGCTCACTTTCTTCCAAGGATAAGTTGCAAGAG 2884
Db 911 ValAspArgValIleLysAlaCysThrArgGlyLeuArgSerArgGluGlnValGlnGln 930
QY 2885 GTGAAACTATTTTGAATCTCTTGAGCTCAAGGATCAGATCTGTGATATTTTCAAACT 2944
Db 931 LeuLysAsnLeuTyrLysAsn---AspLysArgAlaArgGluTyrGlyAlaPheGlyGly 949
QY 2945 GTTCTGGAAACGATAACCAAAATATATAATGCTGGAGAGAAATCTTCCGACTCTG 3001
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## RESULT 12

US-08-335-844A-24

; Sequence 24, Application US/08335844A

; Patent No. 6066503

; GENERAL INFORMATION:

; APPLICANT: GRAHAM, MARGARET

; APPLICANT: SMITH, TREVOR STANLEY

; APPLICANT: MUNN, EDWARD ALBERT

; APPLICANT: KNOX, DAVID PATRICK

; APPLICANT: OLIVER, JOANNA JANE

; APPLICANT: NEWTON, SUSAN ELIZABETH

; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING

; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF

; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst &amp; Kurz

; STREET: Suite 701-E, 555 Thirteenth St., N.W

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-335-844A-24

Alignment Scores:
Pred. No.: 1,68e-105 Length: 972
Score: 1117.00 Matches: 279
Percent Similarity: 48.93% Conservative: 199
Best Local Similarity: 28.56% Mismatches: 391
Query Match: 18.89% Indels: 108
DB: 3 Gaps: 25

US-10-039-073-2 (1-3366) x US-08-335-844A-24 (1-972)

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Qy 299 GCT-----TTCCAGTAGCCACTTAATGGGGAACGA 328
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 52 LysAspAspThrGlyLysAspLysAspAsnSerProSerAlaAa----- 67
Qy 329 TTTCCTGGCAGGAGCTAAGGCTCCCAAGTGTGTCATCTCTCCATTATGACCTCTTT 388
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 68 -----GluLeuLeuLeuProSerAsnileLysProLeuSerTyrrAspLeuThr 83
Qy 389 GTC-----CACCCCAATCTCACCTCTCGGACTTTGTT 421
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 84 IleLysThrTyrrLeuProGlyTyrrValAspPheProGluLysAsnLeuThrPheAsp 103
Qy 422 GCATCTGAGAGATCGAAGTCTGTCAGCAATGCTACCCAGTTTATCATCTTCACAGC 481
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 104 GlyArgValGluIleSerMetValIleGluProThrLysSerIleValLeuAsnSer 123
Qy 482 AAGATCTTGAATCAGCAATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAAA 541
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 124 LysLysIleSerValIle-----ProGlnGluCysGluLeuValSer 137
Qy 542 CCAGAAAGACTGAAGTTTGTAGT-----TACCTGCTCATGAACAATGGCA 592
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 138 GlyAspLysLysLeuGluIleGluSerValLysGluHisProArgLeuGluLysValGlu 157
Qy 593 CTGCTGGTTCCAGAGAACTTACGCCCTCACCTGAAATACTATGTGGCTATGGACTTCAA 652
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Qy 158 PheLeuIleLysSerGlnLeuGluLysAspGlnGlnIleLeuLeuLysValGlyTyrrile 177
Qy 653 GCCAAGTTAGTGGCTTTGAAGGGTTTATAAAGCACATACAGAACTCTTTGGTGGT 712
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Qy 178 GlyLeuIleSerAsnSerPheGlyGlyIleTyrrGlnThrTyrrThrThrProAspGly 197
Qy 713 GAACACAGAAATCTTGGAGTAACAGATTTTGAGCCCAACCCAGGACCGATGGCTTCCT 772
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Qy 198 ThrProLysIleAlaAlaValSerGlnAsnGluProIleAspAlaArgMetValPro 217
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Qy 773 TGCTTTGATGAACCGTTGTTTCAAAGCCAACCTTTTCAATCAAGATACGACGAGAGCAGG 832
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 218 CysMetAspGluProLysTyrrLysAlaAsnTrpThrValThrValIleHisProLysGly 237
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 833 CATATTGCATCTCAACATGCGCAAGGTTAAG---ACAATTGAACCTTGAAGGAGGCTTT 889
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 238 ThrLysAlaValSerAsnGlyIleGluValAsnGlyAspGlyGluIleSerGlyAspTrp 257
Qy 890 TTGGAAGATCATTGAAACTACTGTAAATAAGTACATACCTTTGTAGCTACATAGTT 949
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 258 IleThrSerLysPheLeuThrThrProArgMetSerTyrrLeuLeuAlaValMetVal 277
Qy 950 TGTGATTTCACCTCTCTGAGTGGCTTCATCAGGGGTCAAGGTGTCATCTATGCA 1009
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 278 SerGluPheGluTyrrileGluGlyGluThrLysThrGlyValArgPheArgIleTrpSer 297
Qy 1010 TCCCCAGACAAACGGAATCAACACATATTGCTTTGCAGGCATCATCTGAAGTACTTGTAT 1069
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 298 ArgProGluAlaLysLysMetThrGlnTyrrAlaLeuGlnSerGlyIleLysCysIleGlu 317
Qy 1070 TTTTATGAAAAGTACTTTGATATCTACTATCTCCACTCTCCAACTGGATTTAATGCTATT 1129
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 318 PheTyrrGluAspPhePheAspIleArgPheProLeuLysLysGlnAspMetIleAlaLeu 337
Qy 1130 CCTGACTTTGCACCTGGAGCCATGGAAATTTGGGGCTCATTAACATATAGGAGACGTCA 1189
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Qy 338 ProAspPheSerAlaGlyAlaMetGluAsnTrpGlyLeuIleThrTyrrArgGluAsnSer 357
Qy 1190 CTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGATAAACTGTGGGTACACAGAGTCATA 1249
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Qy 358 LeuLeuTyrrAspAspPheTyrrAlaProMetAsnLysGlnArgIleAlaVal 377
Qy 1250 GCCCATGAACTGGCGCACCTGCTGTCACAACTGTCACAACTGGAATGGTGAATGAT 1309
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Qy 378 AlaHisGluLeuAlaHisGlnTrpPheGlyAspLeuValThrMetLysTrpTrpAspAsn 397
Qy 1310 ATTTGGCTTAAGGAGGTTTTCGAAAATCATGCAACTTATC---GCTGTTAATGCTTACA 1366
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 398 LeuTrpLeuAsnGluGlyPheAlaArgPheThrGluPheIleGlyAlaGlyGlnIleThr 417
Qy 1367 TATCCAGAGCTGCAATTTGATGATCTATTTTGTG---AATGTGTTTTTGAAGTAATTACA 1423
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 418 GlnAspAspAlaArgMetArgAsnTyrrPheLeuIleAspValLeuGluArgAlaLeuLys 437
Qy 1424 AAGATTCATTGAATTCATCCGCCCTATCTCCAAACCCGCGGAACCCGAGCTCAATA 1483
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 438 AlaAspSerValAlaSerSerHisProLeuSerPheArgIleAspLysAlaIleGluVal 457
Qy 1484 CAGAAATGTTTGAATGATTTCTTATTAACAAGGAGCTTGTATTTTGAATATGCTCAAG 1543
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 458 GluGluAlaPheAspIleThrTyrrAlaLysGlyAlaSerValLeuThrMetLeuArg 477
Qy 1544 GATTTTCTGGTGGAGAGAAATTCGAGAAAGGAATAATTCACTATTAAAGAGTTTCAGC 1603
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 478 AlaLeuIleGlyGluLysHisLysHisAlaValSerGlnTyrrLeuLysLysPheSer 497
Qy 1604 TATAGAAATGCTAAGATGATGATCTGTCGAGCAGTCTGTCAAAATAGTTTGTAGAAAGT 1663
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 498 TyrrSerAsnAlaGluAlaThrAspLeuTrpAlaValPheAspGluValValThrAspVal 517
Qy 1664 GATTTTACATCTGCTGGAGTTTGTCTTCATTCGGATCCCAAGATGACAACTAATCATGCTCGCC 1723
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 518 GluGlyProAspGly-----LysProMetLysThr----- 528
Qy 1724 TTCTGGGGGAAAATGACAGAGGTCAAGAGATGATGATGATGATGATGATGATGATGATGAT 1783
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 529 -----GluPheAlaSerGlnTrpThrThrGlnMetGly 539
Qy 1784 ATCCCTCTGCTGGTGGTTAAACAA---GACGGGTGTTTCACTCCGACTGCAACGAGGCGC 1840
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 540 PheProValIleSerValAlaGluPheAsnSerThrThrLeuLysLeuThrGlnSerArg 559
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 1841 TTC---CTCCAGGGGTTTTCAGGAAGACCTCGAATGAGGGCCCTCGCAGAGAGGTAC 1897  
Db TyrGluAlaAsnLysAspAlaValGluLysGluLysTyrArgHisProLysTyrGlyPhe 579  
QY 1898 CTGTGGCATATCCCATTTGACCTACTCCACGAGTCTCTTAATGTGATCCACACACACATT 1957  
Db LysTrpAspIleProLeuTrpTyrGlnGluGlyAspLysLysGluLysLysArgThrTrp 599  
QY 1958 CTAAATCAAGACAGACTACTCTGGATCTACCTGAAAGACACAGTTGGTGAAATTT--- 2014  
Db LeuArg---ArgAspGluProLeuTyrLeuHisValSerAspAlaGlyAlaProPheVal 618  
QY 2015 ---AATGGGACTCAATGTGTACTACATCGTTCTACTATGAGGGTCATGGATGGACCAA 2071  
Db ValAsnAlaAspArgTyrGlyPheTyrArgGlnAsnHisAspAlaAsnGlyTrpLysLys 638  
QY 2072 CTCATTACAGCTCAATCAGAACACACACACTTCTCAGACCTTAAGCAGAGTAGTGTCTG 2131  
Db IleIleLysGlnLeuLysAspAsnHisGluValTyrSerProArgThrArgAsnValIle 658  
QY 2132 ATTCATGATGTGTTTCAGCTAGTTGGTCAGGGAGACTCACCTTAGACAAAGCTCTTGAC 2191  
Db IleSerAspAlaPheAlaAlaAlaThrAspAlaIleGluTyrGluThrValPheGlu 678  
QY 2192 ATGACTTACTCTCAACATGAACACAGCAGCCCGCAGCTT-----CTCGAAGGT 2242  
Db LeuLeuAsnTyrAlaGluLysGluThrGluTyrLeuProLeuGluIleAlaMetSerGly 698  
QY 2243 CTGAGTCTACTTGGATCGTTTACACATGATGGACAGAGGAATATTCAGATATCTCT 2302  
Db IleSerIleLeuLysTyrPheProThrGluProGlu-----Ala 712  
QY 2303 GAAACCTCAGCGTTACCTCTTCAGTATTTTAAGCCAGTGAATTCACAGGCAAGC--- 2359  
Db LysProAlaGlnThrTyrMetMetAsnIleLeuLysProMetTyrGluLysSerIle 732  
QY 2360 -----TGGAGTGACAGGGCTCAGTCTGGGACAGGATGCTCGCTCG 2401  
Db AspPheIleAlaAsnAsnTyrArgAsnAspLysLeuPhePheGlnIleAsnLeuGlnLys 752  
QY 2402 GCTCTCTTGAAGCTGGCTGACCTGAACCATGCTCTTCATCCAGAAAGCTGCTGAA 2461  
Db AspValIleAspMetPheCysAlaLeuGlySerGlnAspCysArgLysLysTyrLysLys 772  
QY 2462 TCTCTTC---TCCAGTGTGATGAATCCAGTGGGAAATTAATATACCAACAGATCTTTTA 2518  
Db LeuPheAspAspGluValMetAsnLysCysArgAspGlyGlnAlaAlaThrGluCysVal 792  
QY 2519 AAGATT-----GTGTATTCGTGGGTGCTCAGACACACAGCAGA 2557  
Db ArgIleAlaAlaProLeuArgSerSerValTyrCysTyrGlyValLys-----GluGly 810  
QY 2558 TGAATTAC-----CTTTAGACATATGAAGTCTCAATGTCAGTCTGAA 2605  
Db GlyAspTyrAlaSerAspLysValMetGluLeuTyrThrAlaGluThrLeuAlaLeuGlu 830  
QY 2606 CAAAAAATTCGTATCTGTTGTCAACGACAGCATCAGGAAAGTTA-----CTG 2659  
Db LysAspPheLeuArgLeuAlaLeuGlyCysHisLysAspValThrAlaLeuLysGlyLeu 850  
QY 2660 AAGTTAATGAAGTGAAGTGAAGAGGTTATCAAGACACAGACTTGGCAGCTCTC 2719  
Db LeuLeuArgAlaLeuAspArgAsnSerSerPheValArgMetGlnAspIleProSerAla 870  
QY 2720 CTTTCGATTCGACAGCTGCAAGGGCAGCACTAGCATGGGATTTCTAGAGAA 2779  
Db PheAsnAspValAlaAlaAsnProIleGlyGluGluPheIlePheAsnPheLeuGlu 890  
QY 2780 AATGGACCATCTCTCTGAAAAAATTTGACTTGGGCTCATATGACATGAAGGATGATCATC 2839  
Db ArgTrpProAspIleIleGluSerIleGlyThrLysHisThrTyrValGluLysValIle 910  
QY 2840 TCTGGCACACAGCTCACTTTTCTTCCAGGATGAAGTTCAGAGAGGTGAAACTATTTT 2899

Db 911 ProLysThrSerGlyIleArgSerGlnGlnGlnIleAspGlnLeuLys----- 927  
QY 2900 GAATCTCTTGAAGCTCAAGGATCACT-----CTGGATATTTTCAAACTCTTCTG 2950  
Db ---AsnLeuGlnLysAsnGlyMetAsnAlaArgGlnPheGlyAlaPheAspLysAlaIle 946  
QY 2951 GAAACGATAACCAAAATATAAATGGCTGGAGAGAAATCTTCGACTCTG 3001  
Db GluArgAlaGlnAsnArgValAspTrpIleLysHisPheGlnLysLeu 963  
RESULT 13  
US-09-129-366-24  
; Sequence 24, Application US/09129366  
; Patent No. 6534638  
; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, MARGARET  
; APPLICANT: SMITH, TREVOR STANLEY  
; APPLICANT: MUNN, EDWARD ALBERT  
; APPLICANT: KNOX, DAVID PATRICK  
; APPLICANT: OLIVER, JOANNA JANE  
; APPLICANT: NEWTON, SUSAN ELIZABETH  
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/129,366  
; FILING DATE: 05-AUG-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/335,844  
; FILING DATE: 09-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB PCT/GB93/00943  
; FILING DATE: 06-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9209936  
; FILING DATE: 08-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1181-241A  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 972 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-129-366-24  
Alignment Scores:  
Pred. No.: 1.68e-105 Length: 972  
Score: 1117.00 Matches: 279  
Percent Similarity: 48.93% Conservative: 199  
Best Local Similarity: 28.56% Mismatches: 391  
Query Match: 18.89% Indels: 108  
DB: 4 Gaps: 25



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QY 2303 GAAACCTCAAGCGTTACCTCTTCAGTATTTTAAAGCCAGTGAATGACAGGCAAGC--- 2359
Db 713 LysProAlaGlnThrTyrMetMetAsnIleLeuLysProMetTyrGluLysSerSerIle 732
QY 2360 -----TGGAGTGACAAGGGCTCAGTCTGGGACAGGATGCTCGCTCG 2401
Db 733 AspPheIleAlaAsnAsnTyrArgAsnAspLysLeuPhePheGlnIleAsnLeuGlnLys 752
QY 2402 GCTCTCTTGAAGCTGGCCCTGACCTGAACTGCTCTCTGTCATCCAGAAAGCTGCTGAA 2461
Db 753 AspValIleAspMetPheCysAlaLeuGlySerGlnAspCysArgLysIleTyrLysLys 772
QY 2462 CTCCTC---TCCAGTGGATGAATCCAGTGAAGAAATTAATATACCAACAGATGTTTA 2518
Db 773 LeuPheAspAspGluValMetAsnLysCysArgAspGlyGlnAlaAlaThrGluCysVal 792
QY 2519 AAGATT-----GTGTATTCTGTGGTGCTCAGACACACAGCAGGA 2557
Db 793 ArgIleAlaAlaProLeuArgSerSerValTyrCysTyrGlyValLys-----GluGly 810
QY 2558 TGAATTAC-----CTTTAGAGCAATATGAACCTGCAATGTCAAGTGTCTGAA 2605
Db 811 GlyAspTyrAlaSerAspLysValMetGluLeuTyrThrAlaGluThrLeuAlaLeuGlu 830
QY 2606 CAAACAAAAATCTGTATGCTTTGTCAAGCAGCAAGCATCAGGAAAGTTA-----CTG 2659
Db 831 LysAspPheLeuArgLeuAlaLeuGlyCysHisLysAspValThrAlaLeuLysGlyLeu 850
QY 2660 AAGTTAATTGAACCTAGGATGAAGAAAGTTATCAACACACAGCAACTTGGCAGCTCTC 2719
Db 851 LeuLeuArgAlaLeuAspArgAsnSerSerPheValArgMetGlnAspIleProSerAla 870
QY 2720 CTTTCATGCGATGCCAGAGCTCCAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAA 2779
Db 871 PheAsnAspValAlaAlaAsnProIleGlyGluPheIlePheAsnPheLeuIleGlu 890
QY 2780 AATTGACCCCATCTTCTGAAATAATTTGACTTGGGCTCATATGACATGAAGATGATCATC 2839
Db 891 ArgTrpProAspIleIleGluSerIleGlyThrLysHisThrTyrValGluLysValIle 910
QY 2840 TCTGGCACACAGCTCACCTTTCTTCCAGGATAAGTTCGAAGAGTGAACATATTTTT 2899
Db 911 ProAlaCysThrSerGlyIleArgSerGlnGlnIleAspGlnLys----- 927
QY 2900 GAATCTCTTGAGGCTCAAGGATCACAT-----CTGGATATTTTCAAACCTGTTCTG 2950
Db 928 ---AsnLeuGlnLysAsnGlyMetAsnAlaArgGlnPheGlyAlaPheAspLysAlaIle 946
QY 2951 GAAACGATAACCAAAATATAAAATGGCTGGAGAAAGATCTTCCGACTCTG 3001
Db 947 GluArgAlaGlnAsnArgValAspTrpIleLysLysHisPheGlnLysLeu 963

RESULT 14
US-08-335-844A-23
; Sequence 23, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
```

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; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335.844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-335-844A-23

Alignment Scores:
Pred. No.: 9,46e-104 Length: 972
Score: 1100.00 Matches: 284
Percent Similarity: 47.02% Conservative: 190
Best Local Similarity: 28.17% Mismatches: 390
Query Match: 18.61% Indels: 144
DB: 3 Gaps: 26

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QY 269 TCTAGTTTATCACTTCACCT-----GAGGAT 292
Db 35 LeuThrTyrTyrPheThrArgLysAlaPheAspThrThrGlnLysGluGlnLysAspAsp 54
QY 293 CTTGGGGCT-----TTCCAGTAGCCACTAATGGGGAACGATTTTCTTTGG 337
Db 55 SerGlyGlyLysGluLysAspAsnSerProSerAla----- 66
QY 338 CAGGAGCTAAGGCTCCCGAGTGGTCTCTCCATTTATGACCTTTTGTGTC----- 391
Db 67 GluGluLeuLeuLeuProThrAsnIleLysProValSerTyrAspLeuAsnIleLysThr 86
QY 392 -----CACCCCAATCTCACCTCTCTGGACTTTGTTGGCATCTGAG 430
Db 87 TyrLeuProGlyTyrValAsnPheProGluLysAsnLeuThrPheAspAlaHisVal 106
QY 431 AAGATCGAAGTCTTGGTGCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTT 490
Db 107 GluIleAlaMetValValGluProThrAsnSerIleValLeuAsnSerLysLysIle 126
QY 491 GAATACAGTAATGCCACCTTTCAGTCAGAGAAAGATTCAGATACATGAAACACAGGAAA 550
Db 127 ThrLeu-----AlaGlnGlyCysGluLeuPheSerGlyAsnGln 140
QY 551 GACTCTGAAGCTTTTGAGTTACCTGCTCATGAA-----CAAAATTCACACTCTGTT 601
Db 141 LysLeuAspIleGluSerValLysMetGlnGluArgLeuAspLysLeuGluIleThrLeu 160
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QY 2978 CTGGAGAGAAATCTTCCGACTCTG 3001  
Db :::::||||: |||  
956 IleLysLysHisPheHisArgLeu 963

Search completed: September 26, 2005, 07:54:48  
Job time : 188.682 secs

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Db      881 SerGluAspValaLgLyLeuTyrTrpLeuMetLysSerSerLeuAsnGlyAspAsnPhe 900
Qy      2551 AAGACACAGAACTTGGCAGCTCTCTTCATCGATTCGACAGCTCCAAAGGGGCGAGCAA 2610
Db      901 ArgThrGlnLysLeuSerPheIleileArgThrValGlyArgHisPheProGlyHisLeu 920
Qy      2611 CTAGCATGGGATTTTGTGAAGAGAAATTTGGACCCATCTCTCTGAAATAATTTGACTTGGGC 2670
Db      921 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly 940
Qy      2671 TCATATGACATAAGGATCATCTCTCGSCACACAGCTCACTTTCTTCCAAGGATTAAG 2730
Db      941 SerTyrThrIleGlnAsnIleValAlaGlySerThrTyrLeuPheSerThrLysThrHis 960
Qy      2731 TTGCAAGAGGTGCAACTATTTTGAATCTCTTTCAGGCTCAAGGATCATCATCTCGATATT 2790
Db      961 LeuSerGluValGlnAlaPheGluAsnGlnSerGluAlaThrPheArgLeuArgCys 980
Qy      2791 TTTCAAACTGTTCTGGAACGATACCAAAATATAATAATGGCTGGAGAGAACTTCCG 2850
Db      981 ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetGluLysAsnLeuLys 1000
Qy      2851 ACTCTGAGGACTTGGCTA 2868
Db      1001 SerLeuThrTrpTrpLeu 1006

RESULT 2
A59383
oxytocinase/insulin-responsive aminopeptidase, variant 1 [imported] - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A59383
R:Rasmussen, T.E.; Pedraza-Diaz, S.; Hardre, R.; Laustsen, P.G.; Carrión, A.G.; Kristensen, J. Biochem. 267, 2297-2306, 2000
A:Title: Structure of the human oxytocinase/insulin-regulated aminopeptidase gene and 1c
A:Reference number: A59383; MUID:20223264; PMID:10759854
A:Accession: A59383
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1025 <STO>
A:Cross-references: UNIPROT:O9UIQ6; GB:CA861646; NID:96468766; PIDN:CA861646.1
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:
Pred. No.: 1,25e-127 Length: 1025
Score: 1999.00 Matches: 400
Percent Similarity: 61.81% Conservative: 160
Best Local Similarity: 44.15% Mismatches: 310
Query Match: 39.49% Indels: 36
DB: 2 Gaps: 6

US-10-039-073-3 (1-2883) x A59383 (1-1025)
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Qy      220 ATTCCTCTCCATATGACCTCTTCTCCACCCCATCTCACTCTCTCGACTTGTGCA 279
Db      173 ValProLeuArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
Qy      280 TCTGAGAAGATCGAAGTCTTGGTCAGCAATGTCTACCAGTTTATCATCTTGCACAGCAA 339
Db      193 SerValThrIleSerValGlnAlaLeuGlnValThrTrpAsnIleIleLeuHisSerThr 212
Qy      340 GATCTTGAATACGGAATGCCACCTTCAGTCAGAGGAGATTCAGATACATGAACCA 399
Db      213 GlyHisAsnIleSerArgValThrPheMetSerAlaValSerSerGln----- 228
Qy      400 GGAAGAAGAACTGAAGTTTGTAGTTACCTGCTCATGAACAATTTGCACTGCTGTTCCA 459
Db      229 GluLysGlnAlaGluIleLeuGluTyrAlaTyrHisGlyGlnIleAlaIleValAlaPro 248

460 GAGAACTTAGCCTACCTGAAATACTATGTGCTATGACTTCCAAAGCCCACTAGGT 519
249 GluAlaLeuLeuAlaGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer 268
520 GATGGCTTTCAAGGGTTTTATAAAGCACATACAGAACTCTTGGTGGTGAACCAAGATT 579
269 SerSerTyrTyrGlyPheTyrGlyPheSerTyrThrAspGluSerAsnGluLysLysTyr 288
580 CTTGACGTAAACAGATTTTGAAGCAACCCAGCAGCATGGCTTTCCCTTGTCTTGTATGAA 639
289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
640 CCGTGTTCAAAGCAACTTTTCAATCAAGATACGAAGAGAGAGACGAGCATATTGCACTA 699
309 ProAlaPheLysAlaThrPheIleIleLysIleLeuArgAspGluGlnTyrThrAlaLeu 328
700 TCCAACATGCAAGGTTAAGACAATGAACTTGAAGGAGGTCTTTTGAAGATCAGCTTT 759
329 SerAsnMetProLysLysSerSerValValLeuAspAspGlyLeuValGlnAspGluPhe 348
760 GAAACTACTGTAAATAATGAGTACATACCTTGTAGCCTACATAGTTGTGTGATTTCCACTCT 819
349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetLysAsn 368
820 CTGAGTGGCTTCATTCATCAGGGTCAAGGTGCTCATCTATGCTATGCTATGCTATGCTATG 879
369 LeuSerGln---AspValAsnGlyThrLeuValSerIleTyrAlaValProGluAsnIle 387
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388 GlyGlnValHisTyrAlaLeuGluThrThrValLysLeuLeuGluPheGluAsnTyr 407
940 TTTGATATCTACTATCACTCTCCAACTGATTAATTCATTTCTGACTTTGCACT 999
408 PheGluIleGlnTyrProLeuLysLysLeuAspLeuValAlaIleProAspPheGluAla 427
1000 GGAGCCATGGAATAATGGGGCTCATTCATATATAGGAGAGCTCAGCTGCTTTTGGACCC 1059
428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspSer 447
1060 AAGACCTCTCTGCTCCGATATAACTCTGGTGCACAGAGTCATAGCCATCACTGAAGTGGCG 1119
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1120 CACGAGTGGTTTGGCAACCTGGTCACAATGGAATGGTGAATGATATTTGCTTAAAGAG 1179
468 HisGlnTrpPheGlyAsnLeuValThrMetLysTrpTrpAsnAspLeuTrpLeuAsnGlu 487
1180 GGTTCGCAAAATACATGGAACCTTATCGCTGTTAATGCTATATCCAGAGCTGCAATTT 1239
488 GlyPheAlaThrPheMetGluTyrPheSerLeuGluLysIlePheLysGluLeuSerSer 507
1240 GATGACTATTTTGAATGTGTGTTTGAAGTAAATACAAAAGATTTCATCAATTCATCC 1299
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1300 CGCCTATCTCCAAACAGCGGAAACCCCGACTCAAAATACAGGAAATGTTTGTGAACTT 1359
528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547
1360 TCCTATACAGGAGGCTTGTATTTGAATATGCTCAAGGATTTTCTGGGTGAGAGAAA 1419
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1420 TTCCAGAAAGAAATAATTCAGTACTTAAAGAAGTTCAGCTATAGAAAATGCTTAAGAATGAT 1479
568 PheGlnHisAlaValLeuTyrLeuHisAsnHisSerTyrAlaSerIleGlnSerAsp 587
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588 AspLeuTrpAspSerPheAsn----- 594
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Db      :::::::::::ValLysArgMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
Qy 1660 CAAGACGGGTGTTCACTCCGACTCCAAACAGAGGGCTTCCTCCAGGGGGTTTTCCAGGAA 1719
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Db      :::::::::::LysProGluIleGlnProSerAspThrSerTyrlLeuTrpHisIleProLeuSerTyrlVal 659
Qy 1780 ACGAGTCTCTTAATGTGATCCACAGACAC-----ATTCTAAATCAAGACAGAT 1830
Db      :::::::::::ThrGluGlyArgAsnTyrlSerLysTyrlGlnSerValSerLeuLeuAspLysLysSerGly 679
Qy 1831 ACTCTGGATCTACCTGAAAGACCAGTTGGGTGAAATTTAATGTGGACTCAATATGGTTAC 1890
Db      :::::::::::ValIleAsnLeuThrGluGluValLeuTrpValLysValAsnIleAsnMetAsnGlyTyrl 699
Qy 1891 TACATCGTTCACTATGAGGGTCATGGATGGGACCAACTCTATTACACAGCTGAATCAGAAC 1950
Db      :::::::::::TyrIleValHisTyrlAlaAspAspTrpGluAlaLeuIleHisGlnLeuLysIleAsn 719
Qy 1951 CACACACTTTCACACTAAGGACAGAGTAGGTCTGATTCATGATGTGTTTCAGCTAGTT 2010
Db      :::::::::::ProTyrlValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
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Db      :::::::::::GlyLeuGlyLysValProLeuLysArgAlaPheAspLeuIleAsnTyrlLeuGlyAsnGlu 759
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Qy 2191 AAGCAGCTGATGTACAGCGAAGCTGGAGTCAAGGCTCAGTCTGGGACAGATGCTC 2250
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Qy 2251 CGCTCGGCTCTCTTGAAGCTGGCTGTGACCTGAACCATGCTCTTCATCCAGAAAGCT 2310
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Db      :::::::::::MetThrThrValPheLysValGlyAlaLysThrAspLysGlyTyrlSerPheLeuLeuGly 879
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Db 940 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValGlnLysPheProLeuGly 959
Qy 2671 TCATATGACATAGGATGATCATCTCTGGCACACAGCTCACATTTTCTTCCCAAGGATAAG 2730
Db 960 SerTyrlThrIleGlnAsnIleValAlaGlySerThrTyrlLeuPheSerThrLysThrHis 979
Qy 2731 TTCACAGAGGTGAAACTATTTTGAATCTCTTGGAGCTCAAGGATCACAATCTGGATATT 2790
Db 980 LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrPheArgLeuArgCys 999
Qy 2791 TTTCAAACTGTTCTCGAAACGATAACCAAAAAATATAAAATGGCTGGAGAGAATCTTCCG 2850
Db 1000 ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetGluLysAsnLeuLys 1019
Qy 2851 ACTCTGAGGACTTGGCTA 2868
Db 1020 SerLeuThrTrpTrpLeu 1025
RESULT 3
155441
vp165 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I55441
R;Keller, S.R.; Scott, H.M.; Mastick, C.C.; Aebersold, R.; Lienhard, G.E.
J. Biol. Chem. 270, 23612-23618, 1995
A;Title: Cloning and characterization of a novel insulin-regulated membrane aminopeptidase
A;Reference number: I55441; MUID:96007507; PMID:7559527
A;Accession: I55441
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-916 <RES>
A;Cross-references: UNIPROT:P97629; EMBL:U32990; NID:gl041726; PIDN:AAB38021.1; PID:gl041726
C;Superfamily: membrane alanyl aminopeptidase
Alignment Scores:
Pred. No.: 3-52e-112 Length: 916
Score: 1771.00 Matches: 352
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Best Local Similarity: 44.73% Mismatches: 264
Query Match: 34.99% Indels: 36
DB: 2 Gaps: 5
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Qy 160 CAGTAGCCACTAATTCGGGAACGATTTCTTGTGCAGAGCTAAGGCTCCCGAGTGGTC 219
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Qy 220 ATTCTCTCCATATGACCTCTTGTGCCACCCCAATCTCACCTCTCTGGACTTTGTGCA 279
Db 173 IleProGlnArgTyrlGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192
Qy 280 TCTGAGAAGATCGAAGTCTTGGTCAGCAATGTACCAGTTTATCATCTTTCACAGCAAA 339
Db 193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr 212
Qy 340 GATCTTGAATACAGAAATGCCACCTTCAGTCAGAGGAAGATTCAGATACATGAAACCA 399
Db 213 GlyHisAsnIleSerValThrPheMetSerAlaValSerSerGln----- 228
Qy 400 GGAAGAAAGAACTGAAGTTTGTAGTTACCTGTCTCATGAACAAATTCACACTGCTGTCCA 459
Db 229 GluLysGlnValGluLeuGluTyrlProTyrlHisGluGlnIleAlaValAlaPro 248
Qy 460 GAGAAACTTACGCTCACCTCGAATAACTATGTGGCTATGGACTTCCAGCCAACTAGGT 519
Db 249 GluSerLeuLeuThrGlyHisAsnTyrlThrLeuLysIleGluTyrlSerAlaAsnIleSer 268
Qy 520 GATGGCTTGAAGGGTTTTATATAAAGCACATACAGAACTCTTGGTGGTGAACAGAAAT 579
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QY 580 CTTGCAGTAACAGATTTTGAGCCAAACCAGGACCCATCGCTTTCCCTTGGCTTTGATGAA 639
Db 289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
QY 640 CGGTGTTCAAAGCCAACTTTTCAATCAAGATACGACGAGAGAGCAGGCATATTGCACTA 699
Db 309 ProAlaPheLysAlaThrPheIleIleLysIleThrArgAspGluHisThrAlaLeu 328
QY 700 TCCAACTGCCAAAGGTTAAGACAATGAACCTTGAAGAGGTCTTTTGGAAAGATCACTTT 759
Db 329 SerAsnMetProLysSerSerValProThrGluGluGluLeuIleGlnAspGluPhe 348
QY 760 GAAACTACTGTAATAATGATACACTCTGTAGCTACATAGTTGTGATTTCCACTCT 819
Db 349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetArgAsn 368
QY 820 CTGAGTGGCTTCACTTCATCAGGGGTCAAGGTGTCCATCTATGCAATCCCGACAGAAACGG 879
Db 369 LeuSerGln---AspValAsnGlyThrLeuValSerValTyrAlaValProGluLysIle 387
QY 880 AATCAACACATATGCTTTGAGGCATCACTGAAGCTACTGTATTTTATGAAAAGTAC 939
Db 388 AsnGlnValTyrHisAlaLeuAspThrThrValLysLeuLeuGluPheTyrGlnAsnTyr 407
QY 940 TTGATATCTACTATCCACTCTCCAACTGGAATTAATGTCTATTTCTGACTTTGCACCT 999
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QY 1000 GGAGCCATGGAAAATTTGGGGCTCATTACATATAGGAGAGCTCACTGCTTTTGGACCC 1059
Db 428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspAsn 447
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Db 448 AlaThrSerSerValAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
QY 1120 CACAGTGGTTTGGCAACTGGTCTCAATGGAATGGTGGATGATATTTGGCTTAAGAG 1179
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QY 1180 GGTTTTGCAAAATACATGAACTTATCGCTGTATGCTACATATCCAGAGCTCAATTT 1239
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QY 1240 GATGACTATTTTGAATGTGTGTTTGAAGTAATTAACAAAGATTCATTGAATTCATCC 1299
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QY 1300 CGCCCTATCTCAAACCCAGCGAAACCCGACTCAATATACAGGAATGTTTGATGAAGTT 1359
Db 528 HisProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu 547
QY 1360 TCCTATACAGGAGGAGCTGTATTTGAATATGCTCAAGGATTTTCTGGGTGAGAGAAA 1419
Db 548 SerTyrPheLysGlyAlaSerLeuLeuLeuMetLeuLysSerTyrLeuSerGluAspVal 567
QY 1420 TTCCAGAAGGAATAATTCAGTACTTAAGAAGTTTCAGCTATAGAAAATGCTAAGAATGAT 1479
Db 568 PheGlnHisAlaIleLeuTyrLeuHisAsnHisSerTyrAlaAlaIleGlnSerAsp 587
QY 1480 GACTTGTGGAGCAGTCTCTCAAAATAGTTGTTTGTAGAAAGTGAATTTTACATCTGGTGGAGTT 1539
Db 588 AspLeuTrpAspSerPheAsnGlu-----ValThrGlyLeuLeuAsp 602
QY 1540 TGTCAATCGGATCCCAAGATGACAGTAACATGCTCGCTTCTCTGGGGGAAATGACAGAG 1599
Db 596 -----ValThrGlyLeuLeuAsp 602
QY 1600 GTCAAAGAGATGATGACTACATGAGTCTCCAGAAAGGAATCCCTGCTGCTGTTGTTAAA 1659
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QY 1720 GACCCTCAATGGAGGCGCTGACAGAGAGGTACCTGTGGCATATCCCATTCACCTACTCC 1779
Db 640 GlnProGluIleGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTyrVal 659
QY 1780 ACGAGTTCTTCAATGTGATCCACAGAC-----ATTCTAAATCAAAGACAGAT 1830
Db 660 ThrAspGlyArgAsnTyrSerGluTyrArgSerValSerLeuLeuAspLysLysSerAsp 679
QY 1831 ACTCTGATCTACCTGAAAAGACCCAGTTGGTGAATTTAATGTGGACTCAATGGTTTAC 1890
Db 680 ValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGlyTyr 699
QY 1891 TACATCGTTCACTATGAGGGTCAATGATGGACCAACTATTACACAGCTGAATCAGAAC 1950
Db 700 TyrIleValHisTyrAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArgAsn 719
QY 1951 CACACACTTCTCAGACCTAAGGACAGAGTAGGTCTGTATTCATGATGTGTTTCAGTAGTT 2010
Db 720 ProTyrValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
QY 2011 GGTCCAGGAGACTGACCCCTAGACAAAGCTCTTGACATGACTTACTCTCCACATGAA 2070
Db 740 GlyLeuGlyLysValProLeuGlnMetAlaPheAspLeuIleAspTyrLeuArgAsnGlu 759
QY 2071 ACAGACAGCCCGCACCTTCTCGAAGGTCTGAGTTACTTGGAAATGTTTACACATGATG 2130
Db 760 ThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrAsnLeuLeu 779
QY 2131 GACAGAGGAATATTTTCAGATATCTCTGAAACCTCAAGCGTTACCTTTCAGTATTTT 2190
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QY 2191 AAGCCACTGATTGACGGCAAGCTGAGTGCACAAAGGCTCAGTCTGGGACAGATGCTC 2250
Db 800 GlnAsnGlnIleGlnGlnGlnTrpThrAspGluGlyThrProSerMetArgGluLeu 819
QY 2251 CGCTCGGCTCTCTTGAAGCTGGCCTGTGACTGAACCATGCTCTCTGCATCCAGAAAGCT 2310
Db 820 ArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAsnCysThrThrMetAla 839
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Db 840 ThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
QY 2371 TTAAGATTGTGATTTCTGTGGGTGCTCAGACACAGCAGATGGAATTTACCTTTTAGAG 2430
Db 860 MetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLeuPheSer 879
QY 2431 CAATATCAACTGTCAATGTCAAGTGTGAACAAACAAATTTCTGTATGCTTTTGTCAACG 2490
Db 880 MetTyrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAlaSer 899
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RESULT 4
A:Title: cDNA cloning and expression of human glutamyl aminopeptidase (aminopeptidase A)
A:Reference number: A47531; MUID:94063909; PMID:8244382
A:Accession: A47531
A>Status: preliminary
glutamyl aminopeptidase (EC 3.4.11.7) - human
N:Alternate names: aminopeptidase A; differentiation antigen gp160
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: A47531; A48287
R:Li, L.; Wang, J.; Cooper, M.D.
Genomics 17, 657-664, 1993
A:Title: cDNA cloning and expression of human glutamyl aminopeptidase (aminopeptidase A)
A:Reference number: A47531; MUID:94063909; PMID:8244382
A:Accession: A47531
A>Status: preliminary
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Db      594  ValLeuPheAenArgSerGluLysGluGlyLeThrLeuAenSerSerAenProSerGly 613
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Qy      1912 CATGATGGGACCAACTCATTCATACAGCTGAATCAAGAACCAACACACTTCTCAGACCTAAG 1971
Db      634  AlathrTrpAepSerIleAlaThrAlaLeuSerLeuAenHisLysThrPheSerSerAla 653
Qy      1972 GACAGATAGCTTCATCATGATGTTTCAGCTAGTGTGGTCAGGAGAGACTGACCCCTA 2031
Db      654  AepArgAlaSerLeuLysAepAlaPheAlaLeuAlaArgAlaGlnLeuLeuAepTyr 673
Qy      2032 GACAAAGCTCTTGACATCTACTACTCTCAACATGAACAAGCAGC-----CCC 2082
Db      674  LysValAlaLeuAenLeuThrLysTyrLeuLysArgGluGluAenPheLeuProTrpGln 693
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Db      694  ArgValIleSerAlaValThrTyrIleIleSerMetPhe-----GluAep 708
Qy      2143 ATTCAGATATCTCTGAACAACTCAAGCGTTACCTTCTTCAGTATTTTAAAGCCAGTGATT 2202
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Qy      2203 GACAGGCAAAAGCTGGAGTGACAAAGGGCTCAGTCTGGGAGCAGGATGCTCCGCTCGGCTCTC 2262
Db      729  AepSerLeuGlyTrpAenAepAlaGlyAepHisValThrLysLeuLeuAepSerSerVal 748
Qy      2263 TTGAAGCTGGCTGTGACTGAACCATCTGCTCTGTCATCCAGAAAGCTGTGAATCTTTC 2322
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Qy      2323 TCCAGTCGATGGAATCCAGTGGAAATTTAAATATACCAACAGATGTTTTAAAGATTGTG 2382
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Db      787  TyrArgTyrGlyMetGlnAenSerGlyAenGluIleSerTrpAenTyrThrLeuGluGln 806
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Db      807  TyrGlnLysThrSerLeuAlaGlnGluLysGluLysLeuLeuTyrGlyLeuAlaSerVal 826
Qy      2494 AAGCATCAGGAAAGTTACTGAAGTTAATTGAATAGGAATGGAAGGAAGTTATCAAG 2553
Db      827  LysAenValThrLeuLeuSerArgTyrLeuAepLeuLysAepThrAenLeuIleLys 846
Qy      2554 ACACAGAACTTGGCAGCTCTCTTCATCGCATTTGCCAGCTCCAAAGGGGCGACCACTA 2613
Db      847  ThrGlnAepValPheThrValIleArgTyrIleSerTyrAenSerTyrGlyLysAenMet 866
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Db      946  IleArgGluTrp 949
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S30398
aminopeptidase N homolog BP-1/6C3 - mouse
N:Alternate names: surface antigen BP-1/6C3
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30398
R:Wu, Q.; Lahti, J.M.; Air, G.M.; Burrows, P.D.; Cooper, M.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 993-997, 1990
A:Title: Molecular cloning of the murine BP-1/6C3 antigen: a member of the zinc-dependen
A:Reference numbers: S30398; MUID:90139003; PMID:1689065
A:Accession: S30398
A:Molecule type: mRNA
A:Residues: 1-945 <WUQ>
A:Cross-references: UNIPROT:P16406; EMBL:M29961; NID:g191947; PIDN:AAB47732.1; PID:g3091
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: disulfide bond; glycoprotein; homodimer; membrane protein; phosphoprotein; s
Alignment Scores:
Pred. No.: 2,23e-86 Length: 945
Score: 1390.50 Matches: 322
Percent Similarity: 51.69% Conservative: 168
Best Local Similarity: 33.97% Mismatches: 373
Query Match: 27.47% Indels: 85
DB: 2 Gaps: 20
US-10-039-073-3 (1-2883) x S30398 (1-945)
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Qy      136  TTCACCTCAGGATCTGGGGCTTTCAGTAGTACCTAATGGGAACGATTCCTTCTGGCAG 195
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Qy      196  GAGCTAAGGCTCCCGAGTGTGTCATTCCTCTCCATATGACCTCTTTGTCCACCCCAAT 255
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Qy      424  TACCTGCTCATGAACAAATGCACTGCTGTTCCAGAGAACTT-----ACGCCT 474
Db      155  TyrLysLysGlnGluTyrValValIleGlnAlaGluAepLeuAlaIleThrSerGly 174
Qy      475  CACCTGAAATACTATGTGGCTATGCGACTTCCCAAGCCAAAGTTAGGTGATGGCTTTGAAGGG 534
Db      175  AspSerValTyrArgLeuThrMetGluPheLysGlyTrpLeuAenGlySerLeuValGly 194
Qy      535  TTTTATAAAGCACATACAGAACTCTTTGGTGGTGAACAAAGAAATTTCTTGCAGTACAGAT 594
Db      195  PheTyrLysThrThrTyrMetGlu---AspGlyGlnIleArgSerIleAlaAlaThrAep 213
Qy      595  TTTGAGGCAACCCGAGCAGCGCTTCCCTTGTCTTGTATGATGACCGTGTTCCTCAAGCC 654
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Qy      655  AACTTTTCAATCAAGATCAAGAGCAGGAGCATATTCACACTATCCACTATCCAAATGCCAAG 714
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[illegible]

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Db      675 AspLysGlySerTrpIleLeuGlyAsnIleasnGlnThrGlyTyrPheArgValAsnTyr 694
Qy      1906 GAGGGTCATGATGGGACCAACTCATTCATACAGCTGAATCAGAACCCACACATCTCTCAGA 1965
Db      695 AspLeuArgAsnTrpArgLeuLeuIleAspGlnLeuIleArgAsnHisGluValLeuSer 714
Qy      1966 CCTAAGCACAGTAGCTCTGATTCATGATCTGTTTCAGCTAGTGTGGTCAGGAGACTG 2025
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Qy      2026 ACCCTAGACAAAGCTCTTGACATGACTTACTACCTCCAACATGAACAAACAGCAGC- 2079
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Qy      2137 AGGAATATTCAGATATCTCTGAAACCTCAAGCGTTACCTCTTCAGTATTTTAAGCCA 2196
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Qy      2233 GTCGGGACAGGATGTCGCGCTCGCTCTCTTGAAGCTGCGCTGTGACCTGAACACCGCT 2292
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Qy      2353 AATATACCAACAGATGTTTAAAGATTGTGTATTCTGTGGTGTCTCAGACACAGCAGGA 2412
Db      848 ArgIleProLeuAsnValArgAspIleValTyrCysThrGlyValSerLeuLeuAspGlu 867
Qy      2413 -----TGGAAATACCTTTTAGCAATATGAATGCTGCAATGCAAGTCTGAACCAAAAC 2466
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Qy      2467 AAAATTCGTATGCTGTCTCAACGACCAAGCATCAGAAAAGTTACTGAAGTTAATGAA 2526
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Qy      2527 CTAGGAATGGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATGCGATT 2586
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Qy      2587 GCCAGACGTCAAAGGGCGACCAACTAGCATGGGATTTGTAAAGAGAAATTTGACCCCAT 2646
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Qy      2767 GCTCAAGGATACATCTGGATATTTTCAAACTGTTCTGGAACGATTAACCAAAATATA 2826
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Qy      2827 AATGGCTGGAGAGAATCTCCGACTCTGAGGACTTGGCTA 2868
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RESULT 7

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A32852
M:membrane alanyl aminopeptidase (EC 3.4.11.2) - rat
N:Alternate names: aminopeptidase N; microsomal aminopeptidase
C:Species: Rattus norvegicus (Norway rat)
C:date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text_change 09-Jul-2004
C:Accession: A32852; A32448; A61250
R:Watt, V.M.; Yip, C.C.
J: Biol. Chem. 264, 5480-5487, 1989
A:title: Amino acid sequence deduced from a rat kidney cDNA suggests it encodes the Zn-peptidase
A:Reference number: A32852; MUID:89174587; PMID:2564389
A:Accession: A32852
A:Molecule type: mRNA
A:Residues: 1-965 <WAT>
A:Cross-references: UNIPROT:P15684; GB:M25073; NID:G205108; PIDN:AAA41502.1; PID:G205109
R:Malfoy, B.; Kado-Pong, H.; Gros, C.; Giron, B.; Schwartz, J.C.; Hellmich, R.
Biochem. Biophys. Res. Commun. 161, 236-241, 1989
A:title: Molecular cloning and amino acid sequence of rat kidney aminopeptidase M: a mem
A:Reference number: A32448; MUID:89273642; PMID:2567164
A:Accession: A32448
A:Molecule type: mRNA
A:Residues: 1-801, 'SC', 805-806, 'A', 808-812, 'ATVPER', 819-830, 'VGR', 834-965 <MAL>
A:Cross-references: GB:M26710; NID:G601864; PIDN:AAA57129.1; PID:G601865
R:Funkhouser, J.D.; Tangada, S.D.; Jones, M.; O, S.J.; Peterson, R.D.A.
Am. J. Physiol. 260, L274-L279, 1991
A:title: p146 type II alveolar epithelial cell antigen is identical to aminopeptidase N.
A:Reference number: A61250; MUID:91206591; PMID:1673322
A:Accession: A61250
A:Molecule type: protein
A:Residues: 2-19; 68-84; 206-212, 'X', 214-215; 286-289, 291-299; 364-371 <FUN>
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; glycoprotein; membrane protein
F:114,128,234,242,264,555,606,624,780/Binding site: carbohydrate (Asn) (covalent) #status
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Pred. No.: 4,71e-81 Length: 965
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Query Match: 25.92% Indels: 96
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Db 23 ValCysThrIleIleAlaLeuSerValValTyrAlaGlnGluLysAsnArgAsnAlaGlu 42
Qy 148 -----CCTGGGGCTTCCAGTAGCCACTAAT----- 174
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Db 886 LeuPheGluAspTyrGlyGlySerPheSerPheAlaAsnLeuIleGlnGlyValThr 905  
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N;Alternate names: aminopeptidase N; microsomal aminopeptidase N; surface glycoprotein C  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 09-Oct-1994 #sequence revision 15-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: A53984; S24020; S05040; S13177  
R;Delmas, B.; Gelfi, J.; Kut, E.; Sjoestrom, H.; Noren, O.; Laude, H.  
J. Virol. 68, 5216-5224, 1994  
A;Title: Determinants essential for the transmissible gastroenteritis virus-receptor int  
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R;Delmas, B.; Gelfi, J.; L'Hardion, R.; Vogel, L.K.; Sjoestrom, H.; Noren, O.; Laude, H.  
Nature 357, 417-420, 1992  
A;Title: Aminopeptidase N is a major receptor for the entero-pathogenic coronavirus TGEV  
A;Reference number: S24020; MUID:92278435; PMID:1350661  
A;Accession: S24020  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 2-31 <DE2>  
R;Olisen, J.; Sjoestrom, H.; Noren, O.  
FEBS Lett. 251, 275-281, 1989  
A;Title: Cloning of the pig aminopeptidase N gene. Identification of possible regulatory  
A;Reference number: S05040; MUID:89325681; PMID:2568950  
A;Accession: S05040  
A;Molecule type: DNA  
A;Residues: 1-294 <OLS>  
A;Cross-references: EMBL:X16088  
R;See, H.; Reithmeier, R.A.F.  
Biochem. J. 271, 147-155, 1990  
A;Title: Identification and characterization of the major stilbene- disulphonate- and co  
A;Reference number: S13177; MUID:91024918; PMID:1977382  
A;Accession: S13177  
A;Status: preliminary  
A;Molecule type: protein  
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A;Introns: 200/2; 248/1  
A;Note: the list of introns may be incomplete  
C;Superfamily: membrane alanyl aminopeptidase  
C;Keywords: aminopeptidase; glycoprotein; transmembrane protein  
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F;33-963/Domain: extracellular #status predicted <EXT>

Alignment Scores:  
Pred. No.: 3-88e-78 Length: 963  
Score: 1269.00 Matches: 323  
Percent Similarity: 49.06% Conservative: 174  
Best Local Similarity: 31.89% Mismatches: 386  
Query Match: 25.07% Indels: 130  
DB: 2 Gaps: 28  
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Qy 133 CACTTCAGCTGAGGATCTGGGGCTTTCCAGTAGCCCACTAATGGG----- 177  
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Qy 238 CTCCTTTGTCCACCCTCACTCTCACC---TCTCTGGAC-----TTTGTTCATCT 282  
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Qy 448 CTGCTGGTTCCAGAGAACTTACGCTCACCTACCTGAAATACTATGTGCTATGGACTTCCAA 507  
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A30325  
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922	QY	GATTTTTATGAAAGTACTTTTGATATCTACTATCCACTCTCCAACTGGATTTTAATTGCT	981
326	Db	AsnPhePheAlaGlyHisTyrAspThrProTyrProLeuProLysSerAspGlnIleGly	345
982	QY	ATTCTCTGACTTTGCACCTCGAGCGCATGGAAAAATTGGCGCTCATTTACATATAGGGAGACG	1041
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1102	QY	ATAGCCCATGAAGTGGCGCACAGTGGTTGGCAACTGCTGCTCACTGGAATGGTGGAAAT	1161
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Db 542 ArgTrpThrLeuGlnMetGlyPheProValIleThrVal-----AspThrSerThrGly 559
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 1678 CGACTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCTCGAA----- 1728
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 560 ThrLeuSerGlnGluHisPheLeuLeu-----AspProAspSerAsnVal 574
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 1729 TGGAGGGCCCTGCAGGAGAGTACTGTGGGCATATCCCATTTGACC----- 1773
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 575 ThrArgProSerGluPheAsnTyrValTrpIleValProIleThrSerIleArgAspGly 594
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 1774 -----TACTCCACG 1782
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 595 ArgGlnGlnAspTyrTrpLeuIleAspValArgAlaGlnAsnAspLeuPheSerThr 614
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 1783 AGTTCTTCTAATGTGATCCACAGACACATTTCTAAATCAAAAGACAGATCTCTGGATCTA 1842
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 615 SerGlyAen----- 617
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 1843 CCTGAAAAGACCAGTTGGGTGAATTTAATGTGACTCAATGCTTACTACATCGTTTAC 1902
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 618 -----GluTrpValLeuLeuAsnLeuAsnValThrGlyTyrTyrArgValAen 633
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 1903 TATGAGGCTATGATGGGACCACTCATTAACAGCTGTAATCAGAACCAACACACTTCTC 1962
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 634 TyrAspGluGluAsnTrpArgLysIleGlnThrGlnLeuGlnArgAspHisSerAlaIle 653
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 1963 AGACCTAAGGACAGTAGTGGTCTGATTCATGATGTGTTTCAGCTAGTTGGTGCAGGAGA 2022
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 654 ProValIleAsnArgAlaGlnIleAlaIleAsnAspAlaPheAsnLeuLeuAlaSerAlaHisLys 673
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2023 CTGACCCCTAGACAAGCTCTTGACATGACTTACTCTCCACATCAAGCAAGCAGCCCC 2082
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 674 ValProValThrLeuAlaLeuAsnThrLeuPheLeuIleGluGluArgGlnTyrMet 693
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2083 GCACCTTCGAAGGCTCAGTACTTGTGAATCGTTTTACCACATGATGCAGCAGAGGAAT 2142
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 694 ProTrpGluAlaAlaLeuSerSerLeuSerTyrPheLysLeuMetPheAspArg----- 711
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
```

```
2143 ATTTCAATATCTCTGAAAACCTCAAGCGTTACTCTTCTCAGTATTTTAAAGCCAGTGATT 2202
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 712 ---SerGluValTyrGlyProMetLysAsnTyrLeuLysGlnValThrProLysPhe 730
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2203 -----GACAGGCAAGCTGGAGTGAC---AAGGGCTCAGTCTGGGACAGG 2244
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 731 IleHisPheArgAsnAsnThrAsnAsnTrpArgGluIleProGluAsnLeuMetAspGln 750
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2245 ATGCTCGCGCTCTCTTGAAGCTGGCTGTGACCTGAACCATGCTCTTGTGATCCAG 2304
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 751 TyrSerGluValAsnAlaIleSerThrAlaCysSerAsnGlyValProGluCysGluGlu 770
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2305 AAAGCTCTGAACTCTCTCCAGTGGATCCAGTGGAAAATTAATATATACCAACA 2364
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 771 MetValSerGlyLeuPheLysGlnTrpMetGluAsnProAsnAsnProIleHisPro 790
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2365 GATGTTTTAAAGATTGTGTAT-----TCTGTGGTGCTCAGACACAGCAGGATGGAAT 2418
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 791 AsnLeuArgSerThrValTyrCysAsnAlaIleAlaGlnGlyGluGluTrpAsp 810
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2419 TACCTTTTAGAGCAATATGAATGTCTCAATGTCTCAAGTCTGCAACAAACAAATTTCTGTAT 2478
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 811 PheAlaTrpGluGlnPheArgAsnAlaThrLeuValAsnGluAlaAspLysLeuArgAla 830
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2479 GCTTTGTCAACGACGACATCAGAAAAGCTTACTGAAGTTAATTAAGTAACTAGGATCGAA 2538
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 831 AlaLeuAlaCysSerLysGluLeuTrpIleLeuAsnArgTyrLeuSerTyrThrLeuAsn 850
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2539 GGAAGGTTTATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATTGCCAGACGCTCA 2598
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 851 ProAspLeuIleArgLysGlnAspAlaThrSerThrIleIleSerIleThrAsnAsnVal 870
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2599 AAGGGCAGCAACTAGCATCGGATTTTGTAAAGAAAATTTGGACCCATCTTCTGAAAAA 2658
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 871 IleGlyGlnGlyLeuValTrpAspPheValGlnSerAsnTrpLysLysLeuPheAsnAsp 890
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2659 TTTGACTTGGCGTCATATGACATAAGATCATCTCTCGGCACACAGCTCAGCTTTTCT 2718
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 891 TyrGlyGlySerPheSerPheSerAsnLeuIleGlnAlaValThrArgArgPheSer 910
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2719 TCAAGGATAAGTTGCAAGAGGTGAACATATTTTGAATCTCTTGAGGCTCAA----- 2772
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 911 ThrGluTyrGluLeuGlnGlnLeuGlnPheLysLysAspAsnGluGluThrGlyPhe 930
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2773 GGATCATCATCTGGATATTTTTCAAACTGTTCTGGAACGATAACCAAAAATATATAATGG 2832
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 931 GlySerGlyThrArgAlaLeuGlnAlaLeuGluLysThrLysAlaAsnIleLysTrp 950
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 2833 CTGGAGAGAATCTTCGACTCTGAGGACTTGGCTAATGTTTAACTACT 2880
|||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 951 ValLysGluAsnLysGluValValLeuGlnTrpPheThrGluAsnSer 966
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RESULT 10
T10052
aminopeptidase (EC 3.4.11.-) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10052
R:Constam, D.B.; Tobler, A.R.; Rensing-Ehl, A.; Kemler, I.; Herbh, L.B.; Fontana, A.
J. Biol. Chem. 270, 26931-26939, 1995
A:Title: Puromycin-sensitive aminopeptidase sequence analysis, expression, and functions
A>Note: puromycin-sensitive
C:Superfamily: membrane alanyl aminopeptidase
C:Keywords: aminopeptidase; metalloprotein; zinc
Alignment Scores: 2.06e-74 Length: 920
Pred. No.:
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Score:	1214.00	Matches:	305
Percent Similarity:	49.84%	Conservative:	167
Best Local Similarity:	32.21%	Mismatches:	353
Query Match:	23.98%	Indels:	122
DB:	2	Gaps:	26
US-10-039-073-3 (1-2883) x T10052 (1-920)			
QY	163	GTAGCCTAATGGGGAACGATTTCTTGGCAGGAGCTAAGGCTCCCGAGTGTGGTCATT	222
Db	43	LeuAlaMetProGluLysArgProPheGlu-----ArgLeuProAlaGluValSer	60
QY	223	CTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTTCATCT	282
Db	61	ProIleAsnTyrSerLeuLysProAspLeu-----LeuAspPheThrPheGlu	78
QY	283	GAGNAGATCGAAGTCTTG-----GTGCAAGTCTTACCCAGTTTATCATCTTGGCAGC	336
Db	79	GlyLysLeuGluAlaAlaGlnValArgGlnAlaThrAsnGlnIleValMetAsnCys	98
QY	337	AAAGATCTTGAATCAGCAATGCCACCTTTCAGTCTCAGGAGCAAGATTCAGATACATCAAA	396
Db	99	AlaAspIleAspIleThrAlaSerTyrAlaProGluGlyAspGluGluIleHisAla	118
QY	397	CCAGGA-----AAAGAACTGAAAGTTTGTAGTTTACCTCGCTCATGAA	438
Db	119	ThrGlyPheAsnTyrGlnAsnGluAspGluLysValThrLeuSerPheProSerThrLeu	138
QY	439	CAAAATGCACCTGTGGTTCAGAGAACTTACCGCTCACCTGAAATCTATGTGGCTATG	498
Db	139	GlnThrGly-----ThrGlyThrLeuLys-----Ile	147
QY	499	GACTTCCAAGCAAGTTAGGTAGTGGCTTTGAAGGGTTTTTATAAAGCAGATACAGAACT	558
Db	148	AspPheValGlyGluLeuAsnAspLysMetCylGlyPheTyrArgSerArgTyrThr	167
QY	559	CTTGGTGTGAAACAAGAAATCTTGCAGTAACAGATTTTGAGCCAAACCCAGGCAGCATG	618
Db	168	ProAlaGlyGluValArgTyrAlaAlaValThrGlnPheGluAlaThrAspProArgArg	187
QY	619	GCCTTCCCTGCTTGTGATGAACCGTGTTCGAAAGCCCACTTTTCAATCAAGATACGAAGA	678
Db	188	AlaPheProCysTrpAspGluProAlaIleLysAlaThrPheAspIleSerLeuValVal	207
QY	679	GAGAGCAGGCATATTGACCTATCCACATCCCAAGGTT-----AAGACAATTGAACCT	732
Db	208	ProLysAspArgValAlaLeuSerAsnMetAsnValIleAspArgLysProTyrProAsp	227
QY	733	GAAGGAGGCTCTTTGGAAGATCACTTTGAAACTACTGTAAATAGTACATACCTTTGTA	792
Db	228	AspGluAsnLeuValGluValLysPheAlaArgThrProValMetSerThrTyrLeuVal	247
QY	793	GCCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGTG	852
Db	248	AlaPheValValGlyGluTyrAspPheValGluThrArgSerLysAspGlyValCysVal	267
QY	853	TCCATCTATGCATCCCCAGACAAAGCAATCAACACATTTATGCTTTGAGGGATCACTG	912
Db	268	ArgValTyrThrProValGlyLysAlaGluGlnGlyLysPheAlaLeuValAlaAla	287
QY	913	AAGCTACTTGAATTTTATGAAAGTACTTTGATATCTTACTATCTCACTCTCCAAACTGGAT	972
Db	288	LysThrLeuProPheTyrLysAspTyrPheAsnValProTyrProLeuProLysIleAsp	307
QY	973	TTAATGTCTATCTGACTTTCACCTTGCAGGCATCGAAATTTGGGCGCTCATATAT	1032
Db	308	LeuIleAlaIleAlaAspPheAlaAlaGlyAlaMetGluAsnTrpGlyLeuValThrTyr	327
QY	1033	AGGAGACGTCACCTGCTTTTGGACCCCAAGACCTCTCTGCTTCCGATAACTGGCGTC	1092
Db	328	ArgGluThrAlaLeuIleAspProLysAsnSerCysSerSerArgGlnTrpVal	347
QY	1093	ACCAGAGTCATAGCCCATGAACCTGGCGCACCGAGTGGTGTGGCAACCTGGTCACAAATGGAA	1152
Db	348	AlaLeuValValGlyHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThrMetGlu	367
QY	1153	TGGTGAATGATATTTGGCTTAAAGAGGGTTTGGCAAAATACATGAGAACTTATCGCTGT	1212
Db	368	TrpTrpThrHisLeuTrpLeuAsnGluGlyPheAlaSerTrpIleGluTyrLeuCysVal	387
QY	1213	AATGTCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTGAATGTGTGTTGAAGTA	1272
Db	388	AspHisCysPheProGluTyrAspIleTrpThrGlnPheValSerAlaAspTyrThrArg	407
QY	1273	ATTACAAA---GATTCAATTGAATTCATCCCGCTTATCCAAACCCAGCGAAACCCCG	1329
Db	408	AlaGlnGluLeuAspAlaLeuAspAsnSerHisProIleGluValSerValGlyHisPro	427
QY	1330	ACTCAAAATACAGAAATGTTTGATGAAGTTTCTTATACAGAGGAGCTGTATTTGAAT	1389
Db	428	SerGluValAspGluIlePheAspAlaIleSerTyrSerLysGlyAlaSerValIleArg	447
QY	1390	ATGCTCAAGGATTTTCTGGTGCAGGAGAAATTCAGAAAGGAATAATTCAGTACTTAAAG	1449
Db	448	MetLeuHisAspTyrIleGlyAspLysAspPheLysGlyMetAsnMetTyrLeuThr	467
QY	1450	AAGTTCAGCTATAGAAATGCTAAGATGATGACTTGTGGAGCAGCTCTGTCAAAATAGTTGT	1509
Db	468	LysPheGlnGlnLysAsnAlaAlaThrGluAspLeuTrpGluSerLeuGluSerAla---	486
QY	1510	TTAGAAAGTGATTTTACATCTCGTGAGGTTTGTTCATCTCGATCCCAAGATGACNAGTAAC	1569
Db	486	-----	486
QY	1570	ATGCTCGCTTCTGGGGGAAAATGCAGAGGTCAAGAGATGATGACTACATGAGCTCTC	1629
Db	487	-----SerGlyLysProIleAlaValMetAsnThrTrpThrLys	500
QY	1630	CAGAAAGGAATCCCTCTGCTGGTGGTTAAA-----CAAGCAGGGTGTTCACCTC	1677
Db	501	GlnMetGlyPheProLeuIleTyrValGluAlaGluGlnValGluAspArgValLeu	520
QY	1678	CGACTGCAACAGGAGCGCTTC---CTCCAGGGGGTTTTTC-----CAGAAAGCCCTGAA	1728
Db	521	LysLeuSerGlnLysLysPheCysAlaSerGlyProTyrGlyGlyLysAspCysProGln	540
QY	1729	TGGAGGGCCCTCGCAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACAGTTCT	1788
Db	541	TrpMet-----ValProIleThrIleSerThrSerGlu	551
QY	1789	TCT---AATGTGATCCACAGACACATTTCTAAAATCAAAGACAGAT-----ACTCTG	1836
Db	552	AspProAsnGlnAlaLysLeuLysIleLeuMetAspLysProGluMetSerValValLeu	571
QY	1837	GATCTACTGAAAGACAGCTGGTGGTGAATTTATGTGGACTCAATGGTTACTATCATC	1896
Db	572	LysAsnValLysProAspGlnTrpValLysLeuAsnLeuGlyThrValGlyPheTyrArg	591
QY	1897	GTTCACTATGAGGGTTCATGGATGGGACCAACTCATTACACAGCTGAATCAGAACCCACA	1956
Db	592	ThrGlnTyrSerSerAlaMetLeuGluSerLeuLeuProGlyIleArgAsp-----Leu	609
QY	1957	CTTCTCAGACCTTAAGACAGAGTAGTGTGATTCATGATGTGTTTCAGCTAGTTGGTGCA	2016
Db	610	SerLeuProProValAspArgLeuGlyLeuGlnAsnAspLeuPheSerLeuAlaArgAla	629
QY	2017	GGGAGACTGACCTTAGACAAAGCTCTTGACATGACTTACTACTCCAAATGAAACACAGC	2076
Db	630	GlyIleIle-----	632
QY	2077	AGCCCGCAGCTTCTCGAAGGCTGTAGTTACTTGGAAATCGTTTACCACATGATGGACAGA	2136
Db	633	-----SerThrValGluValLeuLysValMetGluAlaPheValAsnGluProAsnTyr	650
QY	2137	AGGAATATTTCAGATATCTCT-----	2157

Db 651 ThrValTrpSerAspLeuSerCysAsnLeuGlyIleLeuSerThrLeuLeuSerHisThr 670  
Qy 2158 -----GAAACCTCAAGGTTACCTTCTCAGTATTTTAAAGCCAGTGTACACAGG 2208  
Db 671 AspPheTyrGluGluIleGlnPheValIysAspValPheSerProIleGlyGluArg 690  
Qy 2209 CAAGCTCGAGTGAACG-----CGCTCAGTCTGGGACAGATCTCGCTCGGCT 2259  
Db 691 LeuGlyTrpAspProIysProGlyGluGlyHisLeu---AspAlaLeuLeuArgGlyLeu 709  
Qy 2260 CTCTTGAAGCTGGCGCTGTGACCTGAACATGCTCTTGCATCCAGAAAGCTGTCAAGCTC 2319  
Db 710 ValLeuGlyIysLeuGlyIysAlaGlyHisIysAlaThrLeuGluGluAlaArgArg 729  
Qy 2320 TTCTCCAGTGGATGGAATCCAGTGGAAATTAATAATATACCAACAGATGTTTAAAGATT 2379  
Db 730 PheIysGluHisValGlu-----GlyIysGlnIleLeuSerAlaAspLeuArgSerPro 747  
Qy 2380 GTGTATTCTGTGGGTCTCAGACACAGCAGCA-----TGGATTACCTTTTAGAGCAA 2433  
Db 748 ValTyrLeuThrValLeuIysHisGlyAspGlyAlaThrLeuAspIleMetLeuIysLeu 767  
Qy 2434 TATGAACGTCAAATGTCAGTGTCAACAAACAAATTCGTATGCTTTGTCAACGAGC 2493  
Db 768 HisIysGlnAlaAspMetGlnGluIysAsnArgIleGluArgValLeuGlyAlaThr 787  
Qy 2494 AAGCATCAGGAAAGTTACTGAAGTTAATTGAACCTAGGAATGGAAGGAAAGTTATCAAG 2553  
Db 788 LeuSerProGluLeuIleGlnIysValLeuThrPheAlaLeuSerGluGluVal---Arg 806  
Qy 2554 ACACAGAACTGGCGACTCTCTTCATCGGATGTCAGACAGCTCCAAAG---GGGACAGCA 2610  
Db 807 ProGlnAspThrValSerValIleGlyValAlaGlyIysSerLysHisGlyArgIys 826  
Qy 2611 CTAGCATCGGATTTTGAAGAAATTTGAGACCACTCTCTGAAATAATTTGACTTGGCG 2670  
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Qy 2671 TCATATGATCAAGGATGATCATCTCTGGCACACACAGCTCATCTTTCTTCCAAGGATAAG 2730  
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Qy 2851 ACTCTGAGGACTTGGCTAATG 2871  
Db 905 SerIleHisGlnTyrLeuLeu 911  
RESULT 11  
S07099  
membrane alanyl aminopeptidase (EC 3.4.11.2) - rabbit (fragments)  
N:Alternate names: leukemia antigen CD13; microsomal aminopeptidase N  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Sep-1991 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
C:Accession: S07099; B25985  
R:Noren, O.; Dabelsteen, E.; Hoyer, P.E.; Olsen, J.; Sjoestrom, H.; Hansen, G.H.  
PDBS Lett. 259, 107-112, 1989  
A:Title: Onset of transcription of the aminopeptidase N (leukemia antigen CD 13) gene at  
A:Reference number: S07099; PMID:90092508; PMID:2574692  
A:Accession: S07099  
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A:Cross-references: UNIPROT:P15541; EMBL:X51508; NID:g1447; PID:CAA35873.1; PID:g1448  
R:Peracchi, H.; Maroux, S.; Bonicel, J.; Desmuelle, P.  
Biochim. Biophys. Acta 684, 133-136, 1982  
A:Title: The amino acid sequence of the hydrophobic anchor of rabbit intestinal brush bo

A:Accession: B25985  
A:Molecule type: protein  
A:Residues: 1-14 <PER>  
A:Note: this sequence represents the detergent-released form; a proteinase-released form  
C:Superfamily: membrane alanyl aminopeptidase  
C:Keywords: aminopeptidase; glycoprotein; membrane protein; surface antigen; zinc  
F:70,98,391,409,463,487,573,656/Binding site: carboxydrate (asn) (covalent) #status pred  
F:223,234,227/Binding site: zinc (His, Glu, His) #status predicted  
Alignment Scores:  
Pred. No.: 7,54e-72 Length: 805  
Score: 1176.00 Matches: 279  
Percent Similarity: 51.33% Conservative: 147  
Best Local Similarity: 33.61% Mismatches: 326  
Query Match: 23.23% Indels: 78  
DB: 2 Gaps: 22  
US-10-039-073-3 (1-2883) x S07099 (1-805)  
Qy 502 TTCCAAGCCAAAGTTAGTGATGGCTTTGAAGGGTTTATATAAGCACATACAGAACTCTT 561  
Db 16 PheGlnGlyGluLeuAlaAspAspLeuAlaGlyPheTyrArgSerGluTyrMetGlu--- 34  
Qy 562 GGTGGTGAACAACAATCTTGCAGTAACA-----GATTTTGAGCCAAACCCAGGCACGC 615  
Db 35 GlyAsnValArgIysValValAlaThrThrGlnMetGlnMetGlnAlaAlaAspAlaArg 54  
Qy 616 ATGGCTTTCCCTTCCTTTGATGAACCGTTGTTCAAAGCCAACTTTTCAATCAAGATACGA 675  
Db 55 LysSerPheProCysPheAspGluProAlaSerIysAlaThrPheAsnIleThrLeuIle 74  
Qy 676 AGAGAGACGAGCATATTCACATATCAACATG---CCAAAGGTTAAGACAAATTCGAAT 732  
Db 75 HisProArgAspTyrThrAlaLeuSerAsnMetLeuProArgSerSerThr----- 91  
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Qy 835 TCATCAGGGTCAAGGTGTCCTATCATGCCATCCAGACAAACCGAATCAACACAT--- 891  
Db 130 ProAsnValGlnIleArgIleTrpAlaArgProSerAlaIleSerGluGlyHisGly 149  
Qy 892 ---TATGCTTTGAGGATCCTCACTGAGTCTTCTGATTTTATGAAAGTACTTTGATATC 948  
Db 150 GlnTyrAlaLeuAsnValThrGlyProIleLeuAsnPhePheAlaAsnHisTyrAsnThr 169  
Qy 949 TACTATCCTCTCCAAACTGGATTAAATTGCTATTCTGCTATTTGCACTTTGCACTGGAGCCATG 1008  
Db 170 ProTyrProLeuGluIysSerAspGlnIleGlyLeuProAspPheAsnAlaGlyAlaMet 189  
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Db 210 SerIleSerAsnIysGluArgValThrValValAlaHisGluLeuAlaHisGlnTrp 229  
Qy 1129 TTTGGCAACCTGGTCAACAATGGAAATGGTGAATCATATTGGCTTTAAGGAGGGTTTGGCA 1188  
Db 230 PheGlyAsnLeuValThrValAspTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAla 249  
Qy 1189 AAATACATGGAACCTATTCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTAT 1248  
Db 250 SerTyrValGluTyrLeuGlyAlaAspTyrAlaGluProThrTrpAsnLeuIysAspLeu 269  
Qy 1249 TTT---TTGATGTGTGTTTGAAGTAATTACAAAGATTCATTAATTCATCCCGCCT 1305



QY 202 AGGCTCCCGAGTGGTCACTTCTCCATTATGACCTCTTGTGTCACCCCAATCTCACC 261  
Db 15 ArgLeuProThrPheAlaGluProThrHisTyrAsnValArgLeuSerProCysLeuAsn 34  
QY 262 TCTCGGACTTTGGTGCATCTCAGAGAATCGAAGTCTGGTCAGCAATGCTACCCAGTTT 321  
Db 35 GlnPheSerPheAspGlyHisAlaThrIleAspValThrIleGluAlaThrAspVal 54  
QY 322 ATCATCTTGCACAGCAAGATCTTGAATACGAATGCCAATCCCTTCAGTCAGAGAAT 381  
Db 55 LeuIleValHisAlaGlnSerLeuLeuIleGlnSerValSerLeuIleThrGln----- 72  
QY 382 TCAAGATACATGAACCGAAGAAAGCACTGAAGTTTTCAGTTACCTGCTCATGAACAA 441  
Db 73 -----ProGlyAspAlaSerIleSerLeuGluThrSerTyrAspAspLys 87  
QY 442 ATTGCACCTGCTG-----GTTCCAGAGAAACTTACGCCTCCACCTGAATACTATG 492  
Db 88 LeuAsnIleLeuThrIleIleLysLeuProThrThrMetGlnProGln--LysValGlnLeu 106  
QY 493 GCTATGGACTTCCAGCCCAAGTTAGTGATGGCTTTGAAGGTTTATAAAGCAATAC 552  
Db 107 AspPheLysPheValGlyGluLeuAsnAspLysMetArgGlyPheTyrArgSerGlnTyr 126  
QY 553 AGAACTCTTGGTGGTGAACACAGAATCTTGCAGTAACAGATTTTGAGCCCAACCCAGCA 612  
Db 127 LysAspLysAsnGlyThrGluLysPheLeuAlaSerThrGlnPheGluSerThrTyrAla 146  
QY 613 CCGATGGCTTCCCTTGTCTTTCATCAACCGTTGTTCAAGCCCAACTTTTCAATCAAGATA 672  
Db 147 ArgTyrAlaPheProCysPheAspGluProIleTyrLysAlaThrPheAspValThrLeu 166  
QY 673 CGAAGAGAGAGCGGCATATTGCATATCCAAATGCCAAAGGTT--AAGCAATTTGAA 729  
Db 167 GluValGluAsnHisLeuThrAlaLeuSerAsnMetAsnValIleSerGluThrProThr 186  
QY 730 CTTGAAGGAGGCTTTTGGAGATCACCTTGAACACTACTGTAAATACAGTACATACCTT 789  
Db 187 AlaAspGlyLysArgLysAlaValThrPheAlaThrSerProLysMetSerSerTyrLeu 206  
QY 790 GTAGCTACATAGTTTGTGATTCTCCACTCTCTGAGTGGCTTCACATTCATCAGGGTCAAG 849  
Db 207 ValAlaPheAlaValGlyGluLeuGluTyrIleSerAlaGlnThrLysSerGlyValGlu 226  
QY 850 GTGTCCATCTATGCATCCCGACAGCAACCGAATCAACACATATATGCTTTTCAGCGCATCA 909  
Db 227 MetArgValTyrThrValProGlyLysLysGluGlnGlyGlnTyrSerLeuAspLeuSer 246  
QY 910 CTGAAGCTACTGATTTTATGAAAGTACTTTGTATCTACTATCCTCCTCCAACTG 969  
Db 247 ValLysCysIleAspTrpTyrAsnGluTrpPheAspIleLysTyrProLeuProLysCys 266  
QY 970 GATTAAATTCCTTCTGACTTTTCACCTCGAGCCATGGAAATTTGGGGCTCATTACA 1029  
Db 267 AspLeuIleAlaIleProAspPheSerMetGlyAlaMetGluAsnTrpGlyLeuValThr 286  
QY 1030 TATAGGAGAGCGTCACTGCTTTTGGACCCCAAGACCTCTTCTGCTTCGATAAATCTGG 1089  
Db 287 TyrArgGluIleAlaLeuLeuValAspProGlyValThrSerThrArgGlnLysSerArg 306  
QY 1090 GTCACCAAGCATAGCCCATGAACCTGGCGCACCGAGTGGTTTGGCACTCGTCACAAATG 1149  
Db 307 ValAlaLeuValAlaHisGluLeuAlaHisLeuTrpPheGlyAsnLeuValThrMet 326  
QY 1150 GAATGGTGGAAATGATATTGGCTTAAGAGGGTTTTCGAAATACATGGAACTTATCGCT 1209  
Db 327 LysIleTrpThrAspLeuTrpLeuLysGluGlyPheAlaSerPheMetGluTyrMetPhe 346  
QY 1210 GTTAATGTCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTGAAT---GTGTGTTT 1266  
Db 347 ValGlyAlaAsnCysProGluPheLysIleTrpLeuHisPheLeuAsnAspGluLeuAla 366  
QY 1267 GAAGTAATTACAAAGATTCATTGANTTCATCCCGCCCTATCTCTCCAAACCAAGCGGAAC 1326

Db 367 SerGlyMetGlyLeuAspAlaLeuArgAsnSerHisProIleGluValGluIleAspAsn 386  
QY 1327 CCGACTCAAAATACAGGAAATGTTTCTCAAGAGTCTTCTATATAACAAGGGAGCTTGTATTG 1386  
Db 387 ProAsnGluLeuAspGluIleTyrAspSerIleThrTyrAlaLysSerAsnSerValAsn 406  
QY 1387 AATATGCTCAAGGATTTTCTGGGTGAGGAGAAAATTCAGAAAGGAATAATTCAGTACTTA 1446  
Db 407 ArgMetLeuCysTyrTyrLeuSerGluProValPheGlnLysGlyLeuArgLeuTyrLeu 426  
QY 1447 AAGAAGTTACGATATAGAAATGCTAAGATGATGACTTGTGAGCAGCTCTCTCAATAGT 1506  
Db 427 LysArgPheGlnTyrSerAsnAlaValThrGlnAspLeuTrpThrAlaLeuSerGluAla 446  
QY 1507 TGTTTAGAAAGTGAATTTTACATCTGGTGGAGTTGTTCATTCGGATCCCAAGATGACAA 1566  
Db 447 Ser----- 447  
QY 1567 AACATGCTCGCTTCTTGGGGGAAAATGCGAGAGTCAAAGAGATGATGACTACTATGGA 1626  
Db 448 -----GlyGlnAsn-----ValAsnGluLeuMetSerGlyTyrThr 459  
QY 1627 CTCCAGAAAGAAATCCCTCTGCTGCTGTT-----AAACAAGACGGGTGTCTCA----- 1674  
Db 460 GlnGlnMetGlyPheProValLeuLysValSerGlnArgGlnAspGlyAsnAsnArgIle 479  
QY 1675 CTCCGACTGCAACAGGAGCGCTTCTCAGGGGGTTTTCCAGGAAGACCCCTGAATGGAGG 1734  
Db 480 LeuThrValGluGlnArgArgPheIleSerAsp---GlyGlyGluAspPro----- 495  
QY 1735 GCCCTGCAGGAGGATACCTGTGGCATATCCATGTGACCTACTCTC-----ACGAGTTCT 1788  
Db 496 -----LysAsnSerGlnTrpGlnValProIleThrValAlaValGlySerSerPro 512  
QY 1789 TCTAATGTGATCCACACACACATTTCTAAATCAAGACAGAT-----ACTCTGGATCTA 1842  
Db 513 SerAspValLysAlaArgPheLeuLeuLysGluLysGlnGlnGluPheThrIleGluGly 532  
QY 1843 CCTGAAAGACCACTGGGTGAAATTTAATGTGACTCAAAATGCTTACTACATCGTTCAC 1902  
Db 533 ValAlaProGlyGluTrpValLysLeuAsnSerGlyThrThrGlyPheTyrArgValGlu 552  
QY 1903 TATGAGGTCATGATGGGACCAACTCATTCACAGCTGAATACAGAACACACACTTCTC 1962  
Db 553 TyrSer-----AspGluMetLeuThrAlaMetLeuProAspIleAlaSerArg 568  
QY 1963 AGACCTAAG-----GACAGAGTAGTCTGATTCATGATGTGTTTACAGTGTGTTGCTGCA 2016  
Db 569 ArgMetProValLeuAspArgPheGlyLeuIleAsnAspLeuSerAlaLeuLeuAsnThr 588  
QY 2017 GGGAGACTGACCTTAGACAAAGCTCTTGACATGACTTACTACCTCCCAACATGAACAAC 2076  
Db 589 GlyArgValSerIle-----AlaGlnPheValGlnValAlaAlaSer 602  
QY 2077 AGCCCC-----GCATCTCTCGAAGTCTGAGTACTTGT 2109  
Db 603 SerAlaLysGluAspGluTyrValValTrpGlyAlaIleAspGluGlyMetSerLysLeu 622  
QY 2110 GAATCGTTTACCACATGATGGACAGGAGGAATATTTTCAGATATCTCTGAAAACTCAAG 2169  
Db 623 LeuAlaCysAlaArgGluMetSer-----GluAspThrLeuLysSerAlaLys 638  
QY 2170 CGTTACCTCTTCTGATTTTAAAGCCAGTG-----ATTGACAGCGTCAAGC 2214  
Db 639 GlnLeuValValLysMetPheGluGlnThrGlyAlaGluLeuGlyPheAlaGluGlnAla 658  
QY 2215 TGGAGTGACAAGGGCTCAGTCTGGGACAGGATGCTCGCTCGGCTCTCTTTGAAGCTGGCC 2274  
Db 659 GlyGluAspSerGlnLysMet-----MetLeuArgSerLeuValGlnAlaArgLeu 675  
QY 2275 TGTGACCTGAACCACTGCTCTTTCGATCCAGAAAGCTGCTCAACTCTCTCCAGTGATG 2334

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Db 714 AlaargTyrglyGlyLysGluGlyPheAspLysLeuMetAsnLeuArgGluThrThr 733  
Qy 2449 TCAAGTCTGACAAAACAATAATCTGTATGCTTTTGTCAAGCAGCAAGCATCAGAAAAG 2508  
Db 734 PheGlnGluIleGluArgGlnThrMetValAlaMetSerGlnThrProGluGluSerLeu 753  
Qy 2509 TTACTGAAGTTAAATGTAAGTAGGATGGAAGGAGTATCAAGACACAGAACTTGGCA 2568  
Db 754 LeuAlaGlnLeuPheGluTyrglyPheGluLysAsnLysValArgProGlnAspGlnLeu 773  
Qy 2569 GCTCTCTTCATCGATGTCGACAGCTCCAAAGGGGCGCAACTAGCATGGGATTTTGTGA 2628  
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Qy 2629 AGACAAATGGACCCATCTCTGAAAAATTT---GACTGGGCTCATATGACATAAGG 2685  
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Qy 2686 ATGATCATCTCTGCGCACACAGCTCACTTTCTTCCAAAGGATAGTTGCAAGAGGTGAAA 2745  
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Qy 2746 CTATTTTTT-----GAATCTCTTGAGGCTCAAGGATCAGATCAGATCTGGAT 2787  
Db 834 AspPhePheCysAsnCysAsnValLeuSerAspThrAspArgGlnThrLeuAlaAargPro 853  
Qy 2788 ATTTTCAAACTGTTCTGGAAACGATTAACCAAAATATAAAATCGCTGGAGAGAT 2844  
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RESULT 13  
S37794  
aminopeptidase yscII (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae)  
A;Alternate names: protein YKL157w; protein YKL611  
C;Species: Saccharomyces cerevisiae  
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: S37794; S37987; S44571; S19642  
R;Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the EMBL Data Library, September 1993  
A;Description: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci of yeast 10, 35-40, 1994  
A;Reference number: S37786  
A;Accession: S37794  
A;Molecule type: DNA  
A;Residues: 1-844 <VAN>  
A;Cross-references: UNIPROT:P32454; EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g407482  
A;Experimental source: strain S288C  
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the Protein Sequence Database, March 1994  
A;Reference number: S37976  
A;Accession: S37987  
A;Molecule type: DNA  
A;Residues: 1-844 <VA2>  
A;Cross-references: EMBL:Z28157; NID:g486272; PIDN:CAA81999.1; PID:g486273; MIPS:YKL157w  
A;Experimental source: strain S288C  
R;Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
Yeast 10, 35-40, 1994  
A;Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci of yeast 10, 35-40, 1994  
A;Accession: S44571  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-844 <VA3>  
A;Cross-references: EMBL:Z26877; NID:g407482; PIDN:CAA81497.1; PID:g407491  
A;Experimental source: strain S288C  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993

R;Garcia-Alvarez, N.; Cueva, R.; Suarez-Rendueles, P.  
Eur. J. Biochem. 202, 993-1002, 1991  
A;Title: Molecular cloning of soluble aminopeptidases from Saccharomyces cerevisiae. Seq  
A;Reference number: S19642; MUID:92111552; PMID:1765107  
A;Accession: S19642  
A;Molecule type: DNA  
A;Residues: 1-163,'V',165-441,'E',443-843,'VNRDRDVVNKYLKNGYY', <GAR>  
A;Cross-references: EMBL:X63998; NID:g3367; PIDN:CAA45403.1; PID:g3368  
C;Genetics:  
A;Gene: SGD:APE2; LAP1  
A;Cross-references: SGD:S0001640; MIPS:YKL157w  
A;Map position: 11L  
C;Superfamily: membrane alanyl aminopeptidase  
C;Keywords: aminopeptidase; glycoprotein; metalloprotein; zinc  
F;250,622/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;305,309/Binding site: zinc (His) #status predicted  
F;306/Active site: Glu #status predicted

Alignment Scores:  
Pred. No.: 8,92e-68 Length: 844  
Score: 1116.00 Matches: 281  
Percent Similarity: 50.45% Conservative: 171  
Best Local Similarity: 31.36% Mismatches: 372  
Query Match: 22.05% Indels: 72  
DB: 2 Gaps: 24

US-10-039-073-3 (1-2883) x S37794 (1-844)

Qy 187 CTTGGCAGAGAGTAAGGCTCCAGTGGTGTGTCATCTCTCCATATGACCTTTGTGTC 246  
Db 6 ProAsnArgGluIle---LeuProAspAsnValProLeuHisTyrAspLeuThrVal 24  
Qy 247 CACCCCAACTCTCCTCTCGGACTTTTGTGCATCTGAGAAGATCGAAGCTTTGGTCAGC 306  
Db 25 GluProAspPheLysThrPheLysPheGluGlySerValLysIleGluLeuLysIleAsn 44  
Qy 307 AAT---GCTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAAATCAGATGCCACC 363  
Db 45 AsnProAlaIleAspThrValThrLeuAsnThrValAspThrAspIleHisSerAlaLys 64  
Qy 364 CTTCACTCAGAGGAGATTCACAGATACATGAAACAGGAAAGAACTGAAGTTTGAGT 423  
Db 65 IleGlyAspValThrSerSer-----GlutIleSer 75  
Qy 424 TACCTGCTCATCAACAAATGTCAGTGTGTTCCAGAGAAACTTACGCCTCACCTGAAA 483  
Db 76 GluGluGluGlnGlnValThrPheAlaPheProLysGlyThrMetSerSerPheLys 95  
Qy 484 TACTATGTGGCTATGGAC-----TTCCAAGCCCAAGTTAGGTGATGGCTTTGAAGGGTTT 537  
Db 96 GlyAsnAlaPheLeuAspIleLysPheThrGlyIleLeuAsnAspAsnMetAlaGlyPhe 115  
Qy 538 TATAAAGACACATACAGA---ACTCTGTGTGTGAACAACAAGATTTCTGCAGTAACAGAT 594  
Db 116 TyrArgAlaLysTyrGluAspLysLeuThrGlyLysTyrMetAlaThrThrGln 135  
Qy 595 TTTGAGCCCAACCCAGCAGCATGGCTTTCCCTTGTCTTTGTGATGAACCGTTGTTCAAAGCC 654  
Db 136 MetGluProThrAspAlaArgAlaPheProCysPheAspGluProAsnLeuLysAla 155  
Qy 655 AACTTTTCAATCAAGATACGAAGAGAGAGCAGGCATATTGCACTATCCCAACATGCCAAAG 714  
Db 156 SerPheAlaIleThrLeuValSerAspProSerLeuThrHisLeuSerAsnMet---Asp 174  
Qy 715 GTTAAACAACTGAACCTTGAAGAGGCTCTTTGGAGAGATCAGCTTTGAAACTACTGTAAA 774  
Db 175 ValLysAsnGluTyrValLysAspGlyLysValThrLeuPheAsnThrThrProLys 194  
Qy 775 ATGAGTACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTAGTGGCTTCACT 834  
Db 195 MetSerThrTyrLeuValAlaPheIleValAlaGluLeuLysTyrValGluSer---Lys 213  
Qy 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACGGAATCAACACATTAT 894



Qy	826	GGCTTCAC	TTTCATCAGGGG	TCAGAGTGTGTCATCTATGTCATCCCGACAGACAAACCGAATCAA	895
Db	207	Ser---	AsnAanPheArgIleProValaIsgValTyrSerThrProGlyAspGluLysPhe	225	
Qy	886	ACACATAT	GCCTTTGCAGGCATCAGCTGAAGCTACTTCATTTTATCAAAAGTACTTTGAT	945	
Db	226	GlyGlnPheAla	alaAanLeuAlaAlaArgThrLeuArgPheGluAspThrPheAsn	245	
Qy	946	ATCTACTAT	CCATCTCCAAACTGGAGTTAAATGGCTATTCTCTGACTTGCACCTCGAGCC	1005	
Db	246	IleGluTyrPro	leuPheMetAspMetValaValHisGluPheSerAlaGlyAla	265	
Qy	1006	ATCGAAAT	TGGGGCTCATTACATATAGGAGACGTCACCTGCTTTTGACCCCAAGACC	1065	
Db	266	MetGluAsnTrp	GlyLeuValThrTyrArgValIleAspLeuLeuAspIleGluAsn	285	
Qy	1066	TCCTTCGCT	TCCGATAAATCTGGGTCCAGAGGTCATAGCCCATGAACTGGGGCCACGAG	1125	
Db	286	SerSerLeuAsp	ArgIleGlnArgValAlaGluValIleGlnHisGluLeuAlaHisGln	305	
Qy	1126	TGGTTTGG	CAACTCGTCAATGGAAATGGTGGAAATGATATTGGCTTAAAGGAGGGTTTT	1185	
Db	306	TrpPheGlyAsn	LeuValThrMetAspTrpTrpGluGlyLeuTrpLeuAsnGluGlyPhe	325	
Qy	1186	GCAAAATAC	ATGAACTTATCGCTGTTTAATGCTACATATCCAGAGCTGCACAA---	1242	
Db	326	AlaThrTrpMet	SerTrpTyrSerCysAsnLysPheGlnProGluTrpLysValTrpGlu	345	
Qy	1243	GACTATTT	TGTAATGTGTGTTTTGAAAGTAATTAACAAAGATTCATTGAATTCATCCCGC	1302	
Db	346	GlnTyrValThr	AspAsnLeuGlnArgAlaLeuAsnLeuAspSerLeuArgSerSerHis	365	
Qy	1303	CTTATCTC	CAAAACCGCGGAAACCCGAGCTCAAAATACAGAAATGTTTCATGAAGTTTCC	1362	
Db	366	ProIleGluVal	ProValAsnAsnAlaAspGluIleAsnGlnIlePheAspAlaIleSer	385	
Qy	1363	TATAACAAG	GAGCTGTGATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTC	1422	
Db	386	TyrSerLysGly	SerSerLeuArgMetIleSerLysTrpLeuGlyGluGluThrPhe	405	
Qy	1423	CAGAAAGGA	ATAATTCAGTACTTAAAGAGTTCAGCTATAGAAATGCTAAGAATGATGAC	1482	
Db	406	IleLysGlyVal	SerGlnTyrLeuAsnLysPheLysTyrGlyAsnAlaLysThrGlyAsp	425	
Qy	1483	TTGTGAGAG	AGCTGTGCAAAATAGTTGTTTAGAAGTGATTTTATCATCTGTGGAGTTGT	1542	
Db	426	LeuTrpAspAla	leu-----AlaAspAlaSerGlyLysAspValCys	439	
Qy	1543	CATTTCGGAT	CCCCAAGATGACAAGTAAACATGCTCGCCTTTCTGGGGGAAAATGCAGAGGTC	1602	
Db	439	-----	-----	439	
Qy	1603	AAGAGATGAT	GACTACATGGACTCTCCAGAAGGAATCCCTCGTGTGGTTAAACAA	1662	
Db	440	---SerValMet	AsnIleTrpThrLysArgValGlyPheProValLeuSerValLysGlu	458	
Qy	1663	GACGGGTGT	CACTCCGAGTCGCAACAGGAGCGTCTCTCCAG---GGGGTTTCCAGGA	1719	
Db	459	HisLysAsnLys	IleThrLeuThrGlnHisArgTyrLeuSerThrGlyAspValLysGlu	478	
Qy	1720	GACCTCGAAT	TGGAGGCCCTGCGAGGAGGTACTCTGGCATATCCATTCGACTACTCC	1779	
Db	479	GluGluAspThr	ThrIle-----TyrProIleLeuLeuAlaLeuLysAspSer	494	
Qy	1780	ACGAGTTC	TCTTAATGTGATCCACAGACACATCTTAAATCAAAAGACAGATACCTGGAT	1839	
Db	495	ThrGlyIleAsp	AsnThrLeu-----ValLeuAsnGluLysSerAlaThrPheGlu	511	
Qy	1840	CTACCTGAAA	GACCACTGGGTGGAATTTAATGTGGACTCAATGTGTTTACTATACATCGTT	1899	
Db	512	Leu---LysAsn	GluGluPheLysIleAsnGlyAspGlnSerGlyIlePheIleThr	530	
Qy	1900	CACTATGAG	GGGTCACTGGATGGGACCAACTCATTTACACAGCTGAATCAGAACACACACTT	1959	

Db	531	SerTyrSerAspGluArgTrpAlaLysLeuSerLysGlnAlaAsn-----Leu	546
Qy	1960	CTCAGACCTAAGGACAGACAGTAGGTCTCATTTTCATCATGTGTTTCAGCTAGTTGGTCGAGGG	2019
Db	547	LeuSerValGluAspArgValGlyLeuValAlaAspAlaLysAlaSerGly	566
Qy	2020	AGACTGACCTAGACAAAGCTCTTGACATGACTTACTCTCCACATGAAACAGCAGC	2079
Db	567	TyrThrSerThrAsnPheLeuAsnLeuIleSerAsnTrpLysAsnGluAspSerPhe	586
Qy	2080	-----CCCGCACCTTCTCGAAGGCTCGAGTTACTTGAATCGTTTTACCACATGATG	2130
Db	587	ValValTrpGluGlnIleIleAsnSerLeuSerAlaLeuLysSerThrTrpValPhe---	605
Qy	2131	GACAGAGGAATATTCCAGATATCTCTGAAACACTCAAGGCTTACCTTCTTCAGTATTTT	2190
Db	606	-----GluProGluAspIleLeuAsnAlaLeuAspLysPheThrLeuAspLeuVal	622
Qy	2191	AAGCCAGTGTATGACAGCGAAAGCTGCAGT-----CACAAAGGCTCAGTCTGGACAGG	2244
Db	623	LeuAsnLysLeuSerGluLeuGlyTrpAsnIleGlyGluAspSerPheAlaIleGln	642
Qy	2245	ATGCTCCGCTCGGCTCTCTTCAAGCTCGCCTGTGCACCTGAACCATGCTCCTTCATCCAG	2304
Db	643	ArgLeuLysValThrLeuPheSerAlaAlaCysThrSerGlyAsnGluLysMetGlnSer	662
Qy	2305	AAAGCTGCTGAACCTTCTCCAGTGTGATCGAATCCAGTGGAAATTAATATACCAACA	2364
Db	663	IleAlaValGluMetPheGluGluTyr--AlaAsnGlyAsnLysGlnAlaIleProAla	681
Qy	2365	GATGTTTTAAAGATTTGTGTATTTCTGGGTGCTCCAGACACAGCAGCATGGAAATTAC---	2421
Db	682	LeuPheLysAlaValValPheAsnThrValAlaArgLeuGlyGlyGluAsnAsnTyrGlu	701
Qy	2422	---CTTTTAGACAAATATGAACCTGCTCAATGTCAAGTCTGCTGAACAAACAAAATTCGTAT	2478
Db	702	LysIlePheAsnIleTyrGlnAsnProValSerSerGluGluLysIleIleAlaLeuArg	721
Qy	2479	GCTTTTGTCACAGCAGCATCAGAAAAGTTACTGAAGTTTAATTGAATAGCAATGGAA	2538
Db	722	AlaLeuGlyArgPheGluAspLysGlyLeuLeuGluArgThrLeuSerTyrLeuLeuAsp	741
Qy	2539	GGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATCGGATTCGCACACGTCCA	2598
Db	742	GlyThrValLeu--AsnGlnAspPheTyrIleProMetGlnGlyIleArgValHisLys	760
Qy	2599	AAGGGGAGCAACTAGCATCGGATTTTGTAAAGAGAAAATTTGGACCCATCTTCGAAAAA	2658
Db	761	LysGlyIleGluArgLeuTrpAlaTrpMetGlnGluHisTrpAspGluIleAlaLysArg	780
Qy	2659	TTTGACTTGGCTCATATGATCAATGAAGTATCATCTCTGGCACACAGCTCACTTTCT	2718
Db	781	LeuGlnProGlySerProValLeuGlyValLeuThrLeuGlyLeuThrAsnPheThr	800
Qy	2719	TCCMAGGATTAAGTTTGAAGAGGTGAACACTATTTTTTGAATCTCTTGAGGCTCAGGATCA	2778
Db	801	SerPheGluAlaLeuGluLysIleSerAlaPheTyrSerArgLysValThrLysGlyPhe	820
Qy	2779	CATCTGATATTTTTTCAACTGTTCTCGAAACGATAACCAAAAATAATAAAATGGCTGGAG	2838
Db	821	AspGlnThrLeuAlaGln--AlaLeuAspThrIleArgSerLysAlaGlnTrpValSer	839
Qy	2839	AAGAAATCTTCGACTCTGAGCACTTGCGTA	2868
Db	840	ArgAspArgGluIleValAlaThrTyrLeu	849

RESULT 15  
T39789  
aminopeptidase - fission yeast (*Schizosaccharomyces pombe*)  
C/Species: *Schizosaccharomyces pombe*  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T39789

R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21816  
A:Accession: T39789  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-882 <SEE>  
A:Cross-references: UNIPROT:Q9USX1; EMBL:AL122033; PIDN:CAB58971.1; GSPDB:GN00067; SPDB:  
A:Experimental source: strain 972h-; cosmid c1921  
C:Genetics:  
A:Gene: SPDB:SPBC1921.05  
A:Map position: 2  
C:Superfamily: membrane alanyl aminopeptidase

Alignment Scores:		
Pred. No.:	3.97e-63	882
Score:	1047.50	277
Percent Similarity:	47.67%	Conservative: 162
Best Local Similarity:	30.08%	Mismatches: 391
Query Match:	20.69%	Indels: 91
DB:	2	Gaps: 24

US-10-039-073-3 (1-2883) x T39789 (1-882)

Qy	205	CTCCCCAGTGTGGTCATTCCTCTCCATTATGACATCTCTTTGTCCACCCCAATCTCACTCT	264
Db	20	LeuProLysAsnValLysProIleHisTyrAspLeuSerLeuTyrProAspLeuGluThr	39
Qy	265	CTGACATTTTGTGATCTGAGAGACATCGAAGTCCTTGGTCACAGATCTCTACCCAGTTTATC	324
Db	40	PheThrTyrGlyGlyLysValValValThrLeuAspValLeuGluAspSerAsnSerIle	59
Qy	325	ATCTTCACAGCAAAAGATCTTGAATACGAAATGCCACCTTCAGTCTCAGAGGAGATTC	384
Db	60	ThrLeuHisGlyIleAsnLeuArgIleLeuThrAlaLeuGluThrPglySerGlnThr	79
Qy	385	AGATACATGAAACACGAGGAAAAGAACTGAAAGTTTGGAGTTTACCTGCTCATGAACAAAT	444
Db	80	ValTrpAlaSerGlu-----ValSerTyr--GlyAspGluArgIle	92
Qy	445	GCATCTGTGTTTCAGAGAAACTTACGCCTCACCTGGAATACTATGTGGCTATGACATTC	504
Db	93	ValLeuGlnPheProSerThrValProAlaAsnSerValAlaValLeuThrLeuProPhe	112
Qy	505	CAAGCCAAATTTAGGTGATGGCTTGAAGGGTTTTATAAAGCACATCAAGAACTCTTGGT	564
Db	113	ThrAlaArgIleSerSerGlyMetGluGlyPheIleYrArgSerSerTyrValAspSerAsp	132
Qy	565	GGTGAACAACAAGAAATCTTTGTCAGTAACAGATTTTGGAGCCAAACCCAGGCGCATGGCTTTC	624
Db	133	GlyAsnThrLysTyrLeuAlaThrThrGlnMetGluProThrSerAlaArgAlaPhe	152
Qy	625	CTTTGCTTTGATGAACCGTGTCTCAAAGCCAACTTTTCAATCAAGATACGAAGACAGAGC	684
Db	153	ProCysTrpAspGluProAlaLeuLysAlaThrPheThrIleAspIleThrAlaLysGlu	172
Qy	685	AGGCATATTGCACATATCAACATCCCAAGGTTTAAGCAATTGAATCTGAAGAGGTCTT	744
Db	173	AsnTyrThrIleLeuSerAsnMetAsnAlaValGluGlu---ThrValLysAspGlyLeu	191
Qy	745	TTGGAAGATCACTTTGAAACTACTGTAAAAATAGTACATACCTTGTGTACCTACATAGTT	804
Db	192	LysThrAlaArgPheAlaGluThrCysArgMetSerThrTyrLeuLeuAlaTrpIleVal	211
Qy	805	TGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA-----GGGGTCAAGGTG	852
Db	212	AlaGluLeuGluTyrValGluTyrPheThrProGlyLysHisCysProArgLeuProVal	231
Qy	853	TCCATCTATGCATCCCGACAGACAAACGGAAATCAACACATATTATGTTTTCGCATCACTG	912
Db	232	ArgValTyrThrThrProGlyPheSerGluGlnGlyLysPheAlaAlaGluLeuGlyAla	251
Qy	913	AAGCTACTGATTTTTATGAAAAGTACTTTGATATCTACTATCCACTCTCCAAACTGGAT	972



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 26, 2005, 06:07:35 ; Search time 451.896 Seconds  
(without alignments)  
6533.911 Million cell updates/sec

Title: US-10-039-073-3  
Perfect score: 5062  
Sequence: 1 atgttcattcttcttgcatt.....ggctaatggtaataactaa 2883

o

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cgn2\_1/USPTO\_0pool\_p/US10035073/runat\_26092005\_070409\_21306/app\_query.fasta\_1.6606  
-DB=UniProt -QFMT=fastcan -SUFFIX=rup -MINMATCH=0.1 -LOOPCT=0 -LOOPTXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HRAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10035073 @CNC 1 1 1214 @runat\_26092005\_070409\_21306 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5052	99.8	960	2 Q9HBX2	Q9hb22 homo sapien
2	5047	99.7	960	2 Q725K1	Q725k1 homo sapien
3	4789.5	94.6	915	2 Q6P179	Q6p179 homo sapien
4	2768	54.7	532	2 Q8TD32	Q8td32 homo sapien
5	2516.5	49.7	929	1 ART1 HUMAN	Q9nz08 h adipocyte
6	2512.5	49.6	941	2 Q6UWY6	Q6uw66 homo sapien
7	2480	49.0	930	1 ART1 MOUSE	Q9sqh2 mus musculus
8	2430	48.0	930	1 ART1 RAT	Q9jj22 rattus norv
9	2034	40.2	1003	2 Q6PE23	Q6pe23 brachydanio
10	2027	40.0	1025	1 LCAP RAT	P97629 r leucyl-cy
11	2022	39.9	1025	2 Q8C129	Q8c129 mus musculus
12	1999	39.5	1025	1 LCAP HUMAN	Q9uig6 homo sapien
13	1883	37.2	694	2 Q8C9W5	Q8c9w5 mus musculus
14	1847	36.5	997	2 Q6PCG5	Q6pcg5 xenopus lae
15	1690	33.4	350	2 Q8WVJ4	Q8wvj4 homo sapien
16	1564	30.9	549	2 Q8C4S7	Q8c4s7 mus musculus

17	1455.5	28.8	942	1	AMPE_PIG	Q95334 eus afroa
18	1444	28.5	957	1	AMPE_HUMAN	Q07075 homo sapien
19	1391.5	27.5	1012	2	Q9VFW7	Q9vfw7 drosophila
20	1391	27.5	945	1	AMPE RAT	P50123 rattus norv
21	1390.5	27.5	945	1	AMPE MOUSE	P16406 mus musculu
22	1389.5	27.4	1036	2	Q86P55	Q86p55 drosophila
23	1373.5	27.1	994	2	Q86NQ5	Q86ng5 drosophila
24	1371.5	27.1	991	2	Q7PQR3	Q7pq3 anopheles g
25	1367	27.0	903	2	Q8INH5	Q8inh5 drosophila
26	1367	27.0	1025	2	Q8INH6	Q8inh6 drosophila
27	1361.5	26.9	988	2	Q9VFX0	Q9vfx0 drosophila
28	1343	26.5	885	2	Q8IHC5	Q8ihc5 drosophila
29	1340	26.5	942	2	Q9VFW9	Q9vfw9 drosophila
30	1339	26.5	885	2	Q9VFW8	Q9vfw8 drosophila
31	1329.5	26.3	691	2	Q8BZ14	Q8bz14 mus musculu
32	1329.5	26.3	862	2	Q8IGR1	Q8igr1 drosophila
33	1327	26.2	1025	1	THDE RAT	Q10836 rattus norv
34	1322	26.1	1024	2	Q6UWJ4	Q6uwj4 homo sapien
35	1320	26.1	1024	1	THDE HUMAN	Q8uk6 homo sapien
36	1312	25.9	964	1	AMPN_RAT	P15684 rattus norv
37	1310	25.9	1025	1	THDE MOUSE	Q8K093 mus musculu
38	1298	25.6	966	1	AMPN_FELCA	P79171 felis silve
39	1290.5	25.5	1007	2	Q9U0D1	Q9u0d1 aplysia cal
40	1280.5	25.3	866	2	Q9W0E4	Q9w0e4 drosophila
41	1280.5	25.3	1053	2	Q8IRH0	Q8irho drosophila
42	1280.5	25.3	1075	2	Q8IRH1	Q8irh1 drosophila
43	1275	25.2	997	2	Q7QAH5	Q7qah5 anopheles g
44	1274	25.2	965	1	AMPN_RABIT	P15541 oryctolagus
45	1272.5	25.1	866	2	Q9GPG3	Q9gpg3 drosophila

ALIGNMENTS

RESULT 1

Q9HBX2	Q9HBX2	PRELIMINARY;		
ID	Q9HBX2	PRT;	960	AA.
AC	Q9HBX2;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 15, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Amino-peptidase.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Schomburg L.			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF191545; AAG28383.1; -			
DR	MEROPS; M01.024; -			
DR	GO; GO:0004177; F:amino-peptidase activity; IEA.			
DR	GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR001930; Peptidase_M1.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	Pfam; PF01433; Peptidase_M1; 1.			
DR	PRINTS; PR00756; ALADIPTASE.			
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.			
KW	Amino-peptidase.			
SQ	SEQUENCE 960 AA; 110461 MW; 261EFC06870D644E CRC64;			

Alignment Scores:  
Pred. No.: 0 Length: 960  
Score: 5052.00 Matches: 960  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.80% Indels: 0  
DB: 2 Gaps: 0

US-10-039-073-3 (1-2883) x Q9HBX2 (1-960)

Qy 1 ATGTTCCATTCTTCTGCAATGGTTAATTCACAGAAAACCAATGTTTAACATTCACAGA 60

Db	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
Qy	61GGATTTTACTGCTTAACAGAGCCATCTGCCCCAAATATGCAATTGTCTCTCAGTCTCAGTG	120
Db	21GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
Qy	121CCATCTAGTTATCACTTCACTAGGATCCTGGGCTTTCCAGTAGCAGTAAATGGGGAA	180
Db	41ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
Qy	181CGATTTCTTGGCAGGAGCTTAAGCTCCCAAGTGTGTCATCTCTCCATTAATGACCTC	240
Db	61ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu	80
Qy	241TTTGTCCACCCCAATCTCACTCTCTGCACTTGTCTGCATCTCAGAGAGATCGAAGTCTTG	300
Db	81PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
Qy	301GTCAGCAATGCTACCCAGTTTATCATCTTCACAGCAAGATCTTGAATCACGAATGCC	360
Db	101ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
Qy	361ACCCTTCAGTCAGGAGAGATTCAAGATACATGAACACGAGAAAGAACTGAAAGTTTG	420
Db	121ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140
Qy	421AGTTACCTGCTCATGAACAAATTCGACCTGCTGCTCCAGAGAACTTACGCTCACCTG	480
Db	141SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160
Qy	481AAATACTATGTGGCTATGGACTTCCAAAGCCAAAGTTAGTGATGGCTTTGAAGGTTTAT	540
Db	161LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
Qy	541AAAGCAATACAGAACTCTTGGTGGTGAACACAGAAATCTTCGAGTAAACAGATTTTGAG	600
Db	181LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
Qy	601CCAAACCAGCAGCATGGCTTTCCCTGCTTGTGATGAACCGTGTTCAAAGCCCACTTT	660
Db	201ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220
Qy	661TCATCAAGATACAAGAGAGAGCAGGCATATTGCATCTCAACATGCCAAAGGTTAAG	720
Db	221SerIleLysIleArgAlaArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
Qy	721ACAAATTGAACCTTGAGAGGTCTTTTGGAGATCACTTTGAAACTACTGTAAAAATGAGT	780
Db	241ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260
Qy	781ACATACCTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA	840
Db	261ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
Qy	841GGGTCAAGTGTCCATCTATGATCCCCCAGACAAACGGAAATCAACACATTAATGCTTTG	900
Db	281GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
Qy	901CAGGCATCATGAAGCTACTTGATTTTATGAAAGPACTTTTGATATCTACTATCCACTC	960
Db	301GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
Qy	961TCCAAATCGATTTAATTGCTATTCCTGACTTTGCACTGGAGCCATGGAAATTCGGGC	1020
Db	321SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
Qy	1021CTCATTAATATATGGGAGAGCTCACTGCTTTTGGACCCCAAGACCTCTCTGCTCCGAT	1080
Db	341LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
Qy	1081AACTGTGGTCCACGAGTCATAGCCCATGAATCGCGCACAGTGGTTTGGCAACCTG	1140
Db		
Db	361LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
Qy	1141GTCACAATGGAATGGTGAATGATATTTGGCTTAAGGAGGTTTTCAAAAATACATGGAA	1200
Db	381ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
Qy	1201CTTATCGCTGTTTAATGCTACATATCCAGAGCTGCCAATTTGATGACTATTTTGAATGTG	1260
Db	401LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
Qy	1261TGTGTTTGAAGTAAATACAAAGATTCATTGAATTCATCCGGCCCTATCTCCAAACCCAGG	1320
Db	421CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla	440
Qy	1321GAAACCCCGACTCAAAATACAGAGAAATGTTTGAATTTCCATATAACAGGAGGCTGTGT	1380
Db	441GluThrProThrGlnIleGlnMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
Qy	1381ATTTTGAATATGCTCAAGGATTTCTGGGTGAGGAGAAATCCAGAAAGGAATAAATCAG	1440
Db	461IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln	480
Qy	1441TACTTAAAGAACTTCAGCTATAGAAATGCTAAGATGATGACTTGTGGAGCAGCTCTGTC	1500
Db	481TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerLeuSer	500
Qy	1501AATAGTTGTTTAAAGATGATTTTACATCTGGTGGAGTTTGTTCATTCCGATCCCAAGATG	1560
Db	501AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet	520
Qy	1561ACAAGTAAACATGCTCGCTTCTGGGGGAAATGCAGAGGTCAAAGAGATGATGACTACA	1620
Db	521ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetThrThr	540
Qy	1621TGGACTCTCCAGAAAGGAATCCCCCTGCTGGTGGTAAACAAGACGGGTTCACCTCGA	1680
Db	541TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg	560
Qy	1681CTGCAACAGGAGCGCTTCTCCAGGGGGTTCAGAGAGACCTCGAATGGAGGGCCCTG	1740
Db	561LeuGlnGlnLysArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	580
Qy	1741CAGGAGAGGTACCTGTGGCATATCCATTCGACTACTCCACGAGTTCTTCTAATGTGATC	1800
Db	581GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle	600
Qy	1801CACAGACATTTCTAAATCAAAGACAGATACTCGGATCTACCTGAAAGACCAAGTTCG	1860
Db	601HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp	620
Qy	1861GTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTTCACTATGAGGTCATGGATGG	1920
Db	621ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp	640
Qy	1921GACCAACTCATTAACAGCTGAATCAGAACCAACACACTTCTCAGACCTTAAGACAGAGTA	1980
Db	641AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal	660
Qy	1981GGTCTGATTCATGATGTGTTTCAGTAGTTGGTCAGGGAGACTGACCTTAGACAAAGCT	2040
Db	661GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla	680
Qy	2041CTTTGACATCACTTACTTACCTCCAAATGAAACAAGCAGCCCCGCACTTCTCGAAGTCTG	2100
Db	681LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu	700
Qy	2101AGTTACTTGGAAATCGTTTTACCACATGATGGACAGAGGAATATTTTCAGATATCTCTGAA	2160
Db	701SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu	720
Qy	2161AACCTCAAGCGTTACCTTCTTCAGTATTTTAAAGCCAGTGAATTCACAGGCAAGCTGAGT	2220
Db	721AsnLeuLysArgTyrTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer	740

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QY 2221 GACAAAGGCGCTAGTCTGGGACAGGATGCTCGGCTCTCTTGAAAGCTGGCTGTGAC 2280
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Db 741 AsplysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
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|
QY 2281 CTGACACCATGCTCCCTGGCATCCAGAAAGCTGCTGAACCTCTTCCAGTGGATGGAATCC 2340
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Db 761 LeuAsnHisAlaProCysGileGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
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QY 2341 AGTGAAATATAATATACCAACACAGATGTTTTAAAGATTGTGTATCTTCTGTGGGTCTCAG 2400
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Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800
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QY 2401 ACAACAGCAGGATGGAATACCTTTTGTAGCAATATGAACCTGTCATGTCGAAGTCTGAA 2460
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|
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820
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QY 2461 CAACAACAAATCTGTATGCTTGTTCACAGCAGCAGCATCAGGAAAGCTTACTGAAGTTA 2520
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Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu 840
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QY 2521 ATTGAACTAGGAATCGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
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Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
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QY 2581 GCGATTGCCAGCGTCCAAAGGGCAGCAACTAGCATGGATTTTGTGAAGAGAAATGG 2640
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Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
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QY 2641 ACCCATCTTCGAAAAATTTGACTTGGCTCATATGACATGAAGATCATCTCTGGC 2700
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QY 2701 ACAACAGCTCACCTTTCTTCCAAGGATAAGTTGCAAGAGTGAAACTATTTTGAATCT 2760
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Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPheGluSer 920
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QY 2761 CTTGAGGCTCAAGGATCATCTGGATATTTTCAAACTGTTCTGGAAACGATAACCAA 2820
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|
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
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|
QY 2821 AATATAAATGGCTGAGAGNAGTCTCCGACTCTGAGACTTGGCTTAATGGTTAATCT 2880
|
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Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
|
|
|
RESULT 2
Q7Z5K1 PRELIMINARY; PRT; 960 AA.
ID Q7Z5K1;
AC Q7Z5K1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase long form variant.
GN Name=l-rap;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12799365; DOI=10.1074/jbc.M305076200;
RA Tanlaka T., Hattori A., Maeda S., Nomura Y., Nakayama H.,
RA Mizutani S., Tsujimoto M.;
RT "Human leukocyte-derived arginine aminopeptidase:The third member of
RT the oxytocinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 278:32275-32283(2003).
DR EMBL; AB109031; BAC78818.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
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DR Pfam; PF01433; Peptidase_M1; 1.
KW PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 960 AA; 110447 MW; 27898FE2107E814E CRC64;
Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5047.00 Matches: 959
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QY 361 ACCCTTCAGTCACAGGAAGATTCAAGATACATGAACCAAGCAAGAAAGAACTGAAAGTTTG 420
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AC Q6P179; 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
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 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
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 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
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 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
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QY 2761 CTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCTGGAAACGATAACCAA 2820
DB 876 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 895
QY 2821 AATATAAATGGCTGAGAGAAATCTTCCGACTCTGAGACTTGGCTAATGGTTAATACT 2880
DB 896 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 915
RESULT 4
Q8TD32 PRELIMINARY; PRT; 532 AA.
ID Q8TD32 AC
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte-derived arginine aminopeptidase short form.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21374137; PubMed=11481040;
RA Hattori A., Matsumoto K., Mizutani S., Teujimoto M.;
RA Mizutani S., Teujimoto M.;
RT "Human leukocyte-derived arginine aminopeptidase: The third member of
RT the oxytocinase subfamily of aminopeptidases.";
RL J. Biol. Chem. 0:0-0(2003).
DR EMBL; AY028805; AAK37776.1; -.
DR MEROPS; M01.024; -.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase M1; 1.
DR PRINTS; PR00756; ALADIP7ASE.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Aminopeptidase.
SQ SEQUENCE 532 AA; 60937 MW; DA0F4F00AD9E0D71 CRC64;
Alignment Scores:
Pred. No.: 2,19e-178 Length: 532
Score: 2768.00 Matches: 523
Percent Similarity: 99.81% Conservative: 1
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 54.68% Indels: 0
DB: 2 Gaps: 0
US-10-039-073-3 (1-2883) x Q8TD32 (1-532)
QY 1 ATGTTCCATCTTCTCAATGGTTAATTCACAGAAAACCAATGTTTAACATTCACAGA 60
DB 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20
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QY 61 GGAATTTTACTGCTTAACAGCCATCTTGGCCCAAAATATGCAATTTGTTCTCAGTTCCTCAGTG 120  
 Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
 QY 121 CCATCTAGTTATCACTTCACTGAGGATCTCTGGGGCTTTCCAGTAGTACGACCAATCGGGAA 180  
 Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
 QY 181 CGATTTCCCTGGCAGGAGCTAAGGCTCCCCAGTGTGGTCATTCCTCTCCATATGACCTC 240  
 Db 61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
 QY 241 TTGTGCCACCAATCTCACTCTCTGCACTTGTGTCATCTGAGAACATCGAAGTCTTG 300  
 Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGlyIleGluValLeu 100  
 QY 301 GTCAGCAATGCTPACCCAGTTTATCATCTTGCACACCAAGATCTTGAATCAGCAATGCC 360  
 Db 101 ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
 QY 361 ACCCTTCAGTCAGAGAAATTCAGATACATGAACACGAGAAAGAACTGAAAGTTTG 420  
 Db 121 ThrLeuGlnSerGluAspSerArgTyrMetLysProGlyLysGluLeuValLeu 140  
 QY 421 AGTTACCTGCTCATGAACAAATTCGACTGCTGTTCCAGAGAACTTACGCTCACCTG 480  
 Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
 QY 481 AAATACTATGGCTATGCACTTCCAGCACTTCCAGCAAGTGTAGGTGCTTGAAGGTTTAT 540  
 Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
 QY 541 AAAACACATACAGAACTCTTGGTGTGAAACAGAACTTCTGCACTAACAGATTTTCAG 600  
 Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200  
 QY 601 CAACCCAGCGCATGGCTTTCCTTGTGATGAACCGTGTTCCTCAAGCCCACTT 660  
 Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
 QY 661 TCNATCAGATACGAGAGAGAGAGAGGATGATTCACCTATCCACATGCCAAGGTTAAG 720  
 Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
 QY 721 ACAATTGAACCTGAAGGAGGCTTTTGAAGATCACTTTGAACTACTGTAATAATGAGT 780  
 Db 241 ThrIleGluLeuGlyGlyLeuLeuGluAspHisPheGluThrValLysMetSer 260  
 QY 781 ACATACCTTTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCA 840  
 Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
 QY 841 GGGGTCAAGGTGTCATCTATGATCCCGACAGAAACGGAATCAACACATATGCTTTG 900  
 Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
 QY 901 CAGGCATCACTGAAGCTACTGATTTTATGAAAAGTACTTTGATATCTACTATCCACTC 960  
 Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
 QY 961 TCCAACTGGATTAATTTGCTATTCTCCTGACTTTTGCACTGGAGCCATCGAAAATTTGGGC 1020  
 Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
 QY 1021 CTCATTACATATAGGAGACGTCATGCTTTTGTACCCCAAGACCTCTTCTGCTTCGAT 1080  
 Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
 QY 1081 AAACCTGGGTCCACAGATCATAGCCCATGACTGGCGCCAGGAGTGGTTGGCACTTG 1140  
 Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380

QY 1141 GTCACAATGGAATGGTGAATGATATTTGGCTTAAGGAGGGTTTTTGCAAAATACATGAA 1200  
 Db 381 ValThrMetGluTyrTrpAsnAspIleTrpLeuAsnGluGlyPheAlaLysTyrMetGlu 400  
 QY 1201 CTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG 1260  
 Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420  
 QY 1261 TGTTTGAAGTAAATTAACAAAAGATTCAATTGATTCATCCGCCCTATCTCCAAACACGCG 1320  
 Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerArgProIleSerLysProAla 440  
 QY 1321 GAAACCCCGACTCAATACAGAGAAATGTTTCATGAACTTCTTATTAACAAGGAGCTTGT 1380  
 Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
 QY 1381 ATTTTGAATATGCTCAAGGATTTTCTGGTCAGAGAGAAATTCAGAAAGGAAATTAATTCAG 1440  
 Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleIleGln 480  
 QY 1441 TACTTAAAGAAAGTTCAAGTATAGAAATGCTTAAGAAATGATGATCTTGTGGAGCAGTCTGTCA 1500  
 Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500  
 QY 1501 AATAGTTGTTTGAAGAGTATTTTACATCTCGTGGAGTTTGTCTCCGATCCCAAGATG 1560  
 Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520  
 QY 1561 ACNAGTAACATGCTC 1575  
 Db 521 ThrSerAsnMetVal 525

RESULT 5  
 ART1\_HUMAN STANDARD; PRT; 929 AA.  
 AC Q9NZ08; Q60278; Q8NEL4; Q8TAD0; Q9UHF8; Q9UKY2;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-LAP) (ARNS-1) (aminopeptidase PILS) (Puromycin-insensitive leucyl-specific aminopeptidase) (PILS-AP) (Type 1 tumor necrosis factor receptor shedding aminopeptidase regulator).  
 GN Name=ARTS1; Synonyms=APPILS, KIAA0525;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=White adipose tissue;  
 RX MEDLINE=992338715; PubMed=10220586;  
 RA Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;  
 RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly related to placental leucine aminopeptidase/oxytocinase.";  
 RL J. Biochem. 125:931-938(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=21374137; PubMed=11481040;  
 RA Hattori A., Matsumoto K., Mizutani S., Tsujimoto M.;  
 RT "Genomic organization of the human adipocyte-derived leucine aminopeptidase gene and its relationship to the placental leucine aminopeptidase/oxytocinase gene.";  
 RL J. Biochem. 130:235-241(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC Schomburg L.;  
 RT "Molecular characterization of human aminopeptidase PILS.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Cui X., Alsaaty S., Lawrence M., Combs C.A., Rouhani F.N.,

RA Levine S.J.;  
RT "Identification of an aminopeptidase regulator of type I tumor  
RT necrosis factor receptor shedding";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND REVISION TO 718.  
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
RA Nomura N., Ohara O.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 62-929 FROM N.A. (ISOFORM 2).  
RC TISSUE=Brain;  
RX MEDLINE=98290545; PubMed=9628581;  
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
RA Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. IX.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res. 5:31-39(1998).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Butlerfield Y.S.N., Krywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8]  
RP SEQUENCE OF 25-37, AND CHARACTERIZATION.  
RX MEDLINE=20512052; PubMed=11056387;  
RA Hattori A., Kitatani K., Matsumoto H., Miyazawa S., Rogi T.,  
RA Tsuruoka N., Mizutani S., Natori Y., Tsujimoto M.;  
RT "Characterization of recombinant human adipocyte-derived leucine  
RT aminopeptidase expressed in Chinese hamster ovary cells.";  
RL J. Biochem. 128:755-762(2000).  
CC -1- FUNCTION: May play a role in the inactivation of peptide hormones.  
CC May be involved in the regulation of blood pressure through the  
CC inactivation of angiotensin II and/or the generation of bradykinin  
CC in the kidney.  
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-1-  
CC Xbb-, in which Xaa is preferably Leu, but may be other amino acids  
CC including Met, Cys and Phe.  
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -1- SUBUNIT: Monomer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- EVENT-Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9NZ08-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9NZ08-2; Sequence=VSP\_005450;  
CC -1- TISSUE SPECIFICITY: Ubiquitous.  
CC -1- PTM: N-glycosylated.  
CC -1- SIMILARITY: Belongs to the peptidase M1 family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; AF106037; AAF07395.1; ALT\_INIT.  
DR EMBL; AY028806; AAK37777.1; ALT\_INIT.  
DR EMBL; AY028807; AAK37778.1; ALT\_INIT.  
DR EMBL; AF183569; AAF20384.1; ALT\_INIT.  
DR EMBL; AF222340; AAF34664.1; ALT\_INIT.  
DR EMBL; AB011097; BAA25451.2; ALT\_INIT.  
DR EMBL; BC030775; AAH30775.1; ALT\_INIT.  
DR IntAct; Q9NZ08;  
DR MEROPS; M01.018;  
DR H-InvDB; HIX0005052;  
DR MiM; 606832;  
DR GO; GO:0005829; C:cytosol; NAS.  
DR GO; GO:0005783; C:endoplasmic reticulum; NAS.  
DR GO; GO:0005766; C:extracellular; IDA.  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR GO; GO:0005138; F:interleukin-6 receptor binding; IPI.  
DR GO; GO:0004178; F:leucyl aminopeptidase activity; IDA.  
DR GO; GO:0004239; F:methionyl aminopeptidase activity; NAS.  
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IPI.  
DR GO; GO:0008270; F:zinc ion binding; NAS.  
DR GO; GO:0045444; P:adipocyte differentiation; NAS.  
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; NAS.  
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; IDA.  
DR GO; GO:0005714; P:positive regulation of protein secretion; IDA.  
DR GO; GO:0008217; P:regulation of blood pressure; NAS.  
DR GO; GO:0045088; P:regulation of innate immune response; NAS.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR001930; PeptIdase\_M1.  
DR Pfam; PF01433; Peptidase\_M1;  
DR PRINTS; PS00756; ALADIPITASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
DR Alternative splicing; Aminopeptidase; Direct protein sequencing;  
DR Glycoprotein; Hydrolase; Metalloprotease; Polymorphism; Protease;  
DR Signal; Zinc.  
FT SIGNAL 1 24 Adipocyte-derived leucine aminopeptidase.  
FT CHAIN 25 929 Zinc (catalytic) (By similarity).  
FT METAL 341 341 By similarity.  
FT ACT\_SITE 342 342 Zinc (catalytic) (By similarity).  
FT METAL 345 345 Zinc (catalytic) (By similarity).  
FT METAL 464 464 Zinc (catalytic) (By similarity).  
FT ACT\_SITE 426 426 Proton donor (Potential).  
FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 402 402 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 748 748 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 889 889 N-linked (GlcNAc...) (Potential).  
FT VARSPLIC 928 929 RM -> HDPEADATG (in isoform 2).  
FT VARIANT 115 115 /FTId=VSP\_005450.  
FT R -> P (in dBSNP:26653).  
FT /FTId=VAR\_012779.  
FT I -> M (in dBSNP:26618).  
FT /FTId=VAR\_012780.  
FT G -> D (in dBSNP:27895).  
FT /FTId=VAR\_012781.  
FT M -> V (in dBSNP:2287987).  
FT /FTId=VAR\_012782.  
FT K -> R (in dBSNP:27434).  
FT /FTId=VAR\_012783.  
FT Q -> E (in dBSNP:27044).  
FT /FTId=VAR\_012784.  
FT G -> R (in Ref. 3).  
FT CONFLICT 502 502 D -> N (in Ref. 2, 5 and 6).  
FT CONFLICT 563 563 R -> Q (in Ref. 2, 5 and 6).  
FT CONFLICT 713 713  
SQ SEQUENCE 929 AA; 105846 MW; 75C6AD58D0D70D51 CRC64;  
Alignment Scores: 2.39e-161 Length: 929  
Pred. No.:

Score: 2516.50 Matches: 478  
Percent Similarity: 69.34% Conservative: 171  
Best Local Similarity: 51.07% Mismatches: 268  
Query Match: 49.71% Indels: 19  
DB: 1 Gaps: 7

US-10-039-073-3 (1-2883) x ART1\_HUMAN (1-929)

QY 67 TACTGCTTAACAGCCATCTTGCCCAATATGCAATTTGTTCTCAAGTTCTCAAGTGCATCT 126  
Db 3 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 18  
QY 127 AGTTATCACTTCACTGAGATCCTGGGCTTCCAGTAGCCACTAAATGGGGAACGATT 186  
Db 19 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 35  
QY 187 CTTGGCAGGAGTAAGGCTCCCAAGTGTGGTCAATCTCTCCATATGACCTCTTTGTC 246  
Db 36 ProTyrAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeu 55  
QY 247 CACCCCAATCTCACTCTGAGACTTTGTCATCTGAGAGATCGAAGTCTTGGTCAGC 306  
Db 56 HisAlaAsnLeuThrThrLeuThrPheTyrGlyThrThrLysValGluIleThrAlaSer 75  
QY 307 AATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACCAGATGCCACCTT 366  
Db 76 GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 95  
QY 367 CAGTCAGAGGAAGATTCAAGATACATGAACCCAGGAAAGAACTGAAAGTTTGTGTTAC 426  
Db 96 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 113  
QY 427 CTGCTCATGAACAAATTCGCTGCTTCCAGAGAAATCTTACGCCCTCACCTGGAATPAC 486  
Db 114 ProArgGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 133  
QY 487 TATGTCCTATGGACTTCCAGCCCAAGTTAGTGTAGTCTTGAAGGTTTATTAAGC 546  
Db 134 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 153  
QY 547 ACATACAGAACTCTTGGTGGTGAACAAGAAATCTTGCAGTAACAGATTTTGAGCCACC 606  
Db 154 ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 173  
QY 607 CAGGCACGATCGCTTCCCTTGTGATGAAACCGTTGTTCAAAGCCAACTTTTCAATC 666  
Db 174 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerile 193  
QY 667 AAGATACCAAGAGAGAGGAGCATATTCGATATCCAAACATGCCAAAGGTTAAGCAATT 726  
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QY 727 GAACCTGAAGGAGGCTTTTGAAGATCACATTTTGAACACTGTGTAATAATCAGTACATAC 786  
Db 214 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 233  
QY 787 CTTGAGCCTACATATTTGTTGATTTCCACTCTCTGAGTGGCTTCATCTCATCAGGGGTC 846  
Db 234 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 253  
QY 847 AAGGTGTCATCTATGCATCCCGACAGCAAAAGGAATCAACACATATGCTTTGCAGGCA 906  
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QY 907 TCACCTGAAGCTACTGATTTTATCAAAAGTACTTTGATATCTACTATCCACTCTCCAAA 966  
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QY 967 CTGGAATTAATTTGCTTATCTGACCTTTCGACCTCGAGCCATCGGAAATTTGGGGCTCAT 1026  
Db 294 GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTyrGlyLeuThr 313  
QY 1027 ACATATAGGAGACGCTACTGCTTTTGGACCCCAAGACCTCTTCTGCTTCCGATAAAGCTG 1086

Db 314 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 333  
QY 1087 TGGGTCCACAGCATCATAGCCCATCACTGCGCAGCAGTGGTGTGGCAACCTCGTCTACA 1146  
Db 334 GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTyrPheGlyAsnLeuValThr 353  
QY 1147 ATGAATGGTGGATGATATTTGGCTTAAGAGGGTTTTGCAAAATACATCATGAATATC 1206  
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QY 1207 GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTGTGTTT 1266  
Db 374 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 393  
QY 1267 GAAGTAATTAACAAGATTTCAATGAATTCATCCCGCCCTATCTCCAAACCCAGCGAAACC 1326  
Db 394 AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 413  
QY 1327 CCGACTCAATACAGGAAATGTTTGTAGTGAAGTTCCTATACAGAGGAGCTTGTATTTG 1386  
Db 414 ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 433  
QY 1387 AATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTA 1446  
Db 434 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 453  
QY 1447 AAGAAGTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTGTCAAATAGT 1506  
Db 454 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerile 473  
QY 1507 TGTTTAGAAAGTGAATTTTACATCTGGT-----GGAGTTTGTTCATTCGGATCCCAAGATG 1560  
Db 474 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 491  
QY 1561 ACAAGTAACATGCTCGCTTCTCGGGGAAATTCAGAGAGTCAAGAGATGATGACTACA 1620  
Db 492 SerSerSerSerHisTyrHisGlnGluGlyValAspValLysThrMetMetAsnThr 511  
QY 1621 TGGACTCTCCAGAAAGGAATCCCTCTGCTGGGTGTTAAACAAGACGGGTGTTCCCGA 1680  
Db 512 TrpThrLeuGlnLysGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 531  
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCCAGGAAGACCTCGAATGAGGGGCCCTG 1740  
Db 532 MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 545  
QY 1741 CAGGAGAGGTACCTGTCGCATATCCCATTCAGCTACTCCAGAGTCTTCTTAATGTGATC 1800  
Db 546 AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal 565  
QY 1801 CACAGACACATTTCTAAATCAAAGACAGATACTCTGGATCTTACCTGAAAGACCCAGTTGG 1860  
Db 566 HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp 585  
QY 1861 GTGAATTTAATGGGACTCAAATGGTTACTACATCGTTTCACTATGAGGGTCAATGATGG 1920  
Db 586 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspGlyTrp 605  
QY 1921 GACCAACTCATACAGCTGAATCAGAACACACACTTCTCAGACCTTAAGAGCAGAGCTA 1980  
Db 606 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 625  
QY 1981 GGTCTGATTCATGATGTGTTTCAGTAGTTGGTGCAGGAGACTGACCCCTAGACAAAGCT 2040  
Db 626 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 645  
QY 2041 CTTGACATGATCTTACTCTCAACATGAACAGAGAGCCCGCCACTTCTCGAAGGCTG 2100  
Db 646 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 665  
QY 2101 AGTTACTTGGAAATCGTTTTCACCATGATGACAGAGGAATATTTTCAGATATCTCGAA 2160  
Db 2101 AGTTACTTGGAAATCGTTTTCACCATGATGACAGAGGAATATTTTCAGATATCTCGAA 2160



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QY 787 CTTGTAGCCTACATAGTTGTGATTTTCACTCTCTGAGTGGCTTCACTTTCATCAGGGTC 846
Db 246 LeuValAlaPheIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265
QY 847 AAGGTGTCATCTATGCATCCCGACAGAAACGGAATCAACACATATATGCTTTGCAGCA 906
Db 266 LysValSerValAlaValProAspLysIleAenGlnAlaAepTyAlaLeuAspAla 285
QY 907 TCACCTGAAGCTACTGATTTTATGAAAGTACTTTGTATATCTATATCCACTCTCCAAA 966
Db 286 AlaValThrLeuLeuGluPheTyGluAepTyPheSerIleProTyProLeuProllys 305
QY 967 CTGGATTTAATGCTATCTGACCTTTCGACCTGGAGCATGGAAAAATGGGGCTCATTT 1026
Db 306 GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAenTrpGlyLeuThr 325
QY 1027 ACATATAGGGAGAGCTGCTCTCTTTTTCACCCCAAGAGCTCTCTGCTCCGATAAAGCTG 1086
Db 326 ThrTyArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 345
QY 1087 TGGGTCCACAGAGTCATAGCCCATCACTGGCGCACCAAGTGGTTTGGCAACTGTGCACA 1146
Db 346 GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365
QY 1147 ATGGAATCGTGGAATGATTTTGGCTTAAGGAGGTTTTCGAAATACATGCAACTATTC 1206
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAenGluGlyPheAlaLysPheMetGluPheVal 385
QY 1207 GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTCAATGTGTGTTT 1266
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyPhePheGlyLysCysPhe 405
QY 1267 GAAATAATTACAAAGATTCAATTGAATTCATCCCGCCCTCTCTCCAAACACAGCGGAACC 1326
Db 406 AspAlaMetGluValAspAlaLeuAenSerSerHisProValSerThrProValGluAen 425
QY 1327 CCGACTCAAAATACAGAAATGTTTGATGAAGTTTCTTAATAACAAGGAGCTGTGATTTTG 1386
Db 426 ProAlaGlnIleArgGluMetPheAspAspValSerTyAspLysGlyAlaCysIleLeu 445
QY 1387 AATATGCTCAAGGATTTCTGGTCAGGAGAAATTCAGAAAGGATTAATTCAGTACTTA 1446
Db 446 AsnMetLeuArgGluTyLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyLeu 465
QY 1447 AAGAAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTGCAAAATAGT 1506
Db 466 GlnLysHisSerTyLysAsnThrLysAsnGluAepLeuTrpAspSerMetAlaSerIle 485
QY 1507 TGTTTAGAAAGTGATTTTACATCTGGT-----GGAGTTTGTCTCATTCGGATCCCAAGATG 1560
Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503
QY 1561 ACAAGTAACATGCTCGCTTCTGGGGGAAAATGACAGAGGTCAAGAGATGATGACTACA 1620
Db 504 SerSerSerSerSerHisThrPheIleGlnGluGlyValAspValLysThrMetMetAsnThr 523
QY 1621 TGGACTCTCCAGAAGGAATCCCTGCTGGTGTGTTAAACAAGCGGTGTTCTACTCGA 1680
Db 524 TrpThrLeuGlnArgGlyPheProleuIleThrIleThrValArgGlyArgAsnValHis 543
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCAGGAGAAGCCCTGAAATGGAGGGCCCTG 1740
Db 544 MetLysGlnGluHisTyMetLysGly-----SerAspGlyAlaPro 557
QY 1741 CAGGAGAGGTACCTGTGGCATATCCCATGACTTCTCCAGAGTCTTCTTAATGTGATC 1800
Db 558 AspThrGlyTyLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal 577
QY 1801 CACAGACATTTCTAAAATCAAAGACAGATCTCTGGATCTACCTGAAAGACCAAGTTGG 1860
Db 578 HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp 597
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QY 1861 GTGAATTTAATGTGGACTCAATGGTTACTACATCGTTCACTATGAGGTCATGGATGG 1920
Db 598 IleLysPheAsnValGlyMetAsnGlyTyTyIleValHisTyIleGluAspAspGlyTrp 617
QY 1921 GACCAACTCATTCACACAGCTGAATCAGAAACACACACTTCTCAGACCTTAAGACAGAGTA 1980
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637
QY 1981 GGTCGTGATTCATGATGTGTTTTCAGCTAGTTGGTCGAGAGACTGACCTTAGACAAAGCT 2040
Db 638 SerLeuIleAenAenAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657
QY 2041 CTTGACATGACTTACTACTCCCAACATGAAACAGACAGCCCGCAGCTTCTCGAAGTCTG 2100
Db 658 LeuAspLeuSerLeuTyIleLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677
QY 2101 AGTTACTTGGAAATCGTTTACCACATGATGACAGAGAAGGAATATTTTCAGATATCTCTGAA 2160
Db 678 AsnGluLeuIleProMetTyLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
QY 2161 AACCTCAAGCGTTTACCTTCTTTCAGTATTTTAAAGCCAGTATTGACAGCAAGCTGGAGT 2220
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717
QY 2221 GACAAGGCTCAGTCTGGACAGGATCTCGCTCGCTCTCTTGAAGCTGGCCTGTGAC 2280
Db 718 AspGluGlySerValSerGlnMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal 737
QY 2281 CTGAACCATGCTCTCTCCAGCAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCC 2340
Db 738 HisAsnTyArgGlnProCysValGlnArgAlaGluGlyTyPheArgLysTrpLysGluSer 757
QY 2341 AGTGGAAAAATTAATATATACCAACAGATGTTTAAAGATTTGTGATTTCTGTCGGTCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
QY 2401 ACAACACAGAGTGAATTAACCTTTTAGACATATGAACGTCAATGTCAGTCAAGTCTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTySerLysTyArgPheSerLeuSerSerThrGlu 797
QY 2461 CAAACAAAAATCTGTATGCTTCTTCAACGAGCAAGCATCAGGAAAGTACTTGAAGTTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
QY 2521 ATTGAATCTAGGAATGGAAGGAAGTTTATCAAGACACAGAACTTTGGCAGCTCTCTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
QY 2581 GCGATTCACAGACCTCAAGGGGACAGCACTAGCATGGGATTTTGTAAAGAGAAATGG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
QY 2641 ACCCATCTCTGAAAAATTTGACTTGGCTCATATGACATAAGGATGATCATCTCTGCG 2700
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
QY 2701 ACAACAGCTCACTTTTCTTCCAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2760
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
QY 2761 CTTGAGGCTCAGGATCAGATCAGATCGGATTTTTCAACTGTTCTGGAACCATACCAA 2820
Db 898 LeuLysGluAenGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
QY 2821 AATATAAATGGCTGGAGAAGAACTTCTCCGACTCTGAGGACTTCGCTA 2868
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

RESULT 7
ART1_MOUSE
ID -ART1_MOUSE STANDARD; PRT; 930 AA.
AC Q9EQH2; Q9EF63;
DT 28-FEB-2003 (Rel. 41, Created)
```

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Adipocyte-derived leucine aminopeptidase precursor (EC 3.4.11.-) (A-  
 LAP) (ARNS-1) (Aminopeptidase PILS) (Puromycin-insensitive leucyl-  
 specific aminopeptidase) (PILS-AP) (VEGF induced aminopeptidase).  
 DE Name=Artei; Synonyms=Appilis;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hattori A., Kitatani K., Matsumoto H., Mizutani S., Tsujimoto M.;  
 RT "Molecular cloning of murine adipocyte-derived leucine aminopeptidase  
 and its expression in adipocyte cell line, 3T3-L1 cells.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21961541; PubMed=11964289; DOI=10.1182/blood.V99.9.3241;  
 RA Miyashita H., Yamazaki T., Akada T., Niizeki O., Ogawa M.,  
 RA Nishikawa S., Sato Y.;  
 RT "A mouse orthologue of puromycin-insensitive leucyl-specific  
 aminopeptidase is expressed in endothelial cells and plays an  
 important role in angiogenesis.";  
 RL Blood 99:3241-3249(2002).  
 CC -1- FUNCTION: May play a role in the inactivation of peptide hormones.  
 CC May be involved in the regulation of blood pressure through the  
 CC inactivation of angiotensin II and/or the generation of bradykinin  
 CC in the kidney (By similarity).  
 CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-  
 CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- SIMILARITY: Belongs to the peptidase M1 family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 DR EMBL; AF227511; AAG44260.1; -;  
 DR EMBL; AB047552; BAB11982.1; -;  
 DR MEROPS; M01.018; -;  
 DR MGD; MGI:1933403; Artsl.  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0005783; C:endoplasmic reticulum; ISS.  
 DR GO; GO:0005576; C:extracellular; ISS.  
 DR GO; GO:0016021; C:integral to membrane; ISS.  
 DR GO; GO:0005138; F:interleukin-6 receptor binding; ISS.  
 DR GO; GO:004178; F:leucyl aminopeptidase activity; ISS.  
 DR GO; GO:004239; F:methionyl aminopeptidase activity; ISS.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; ISS.  
 DR GO; GO:0008270; F:zinc ion binding; ISS.  
 DR GO; GO:0045444; F:adipocyte differentiation; ISS.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; ISS.  
 DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.  
 DR GO; GO:0050714; P:positive regulation of protein secretion; ISS.  
 DR GO; GO:0008217; P:regulation of blood pressure; ISS.  
 DR GO; GO:0045088; P:regulation of innate immune response; ISS.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR001930; Peptidase\_M1.  
 DR InterPro; IPR003163; Yeast\_DNA\_bind.  
 DR Pfam; PF01433; Peptidase\_M1; 1.  
 DR PRINTS; PR00756; ALADIPTASE.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Aminopeptidase; Glycoprotein; Hydrolase; Metalloprotease; Protease;  
 KW Signal; Zinc.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 930 Adipocyte-derived leucine aminopeptidase.

FT	METAL	342	342	342	Zinc (catalytic) (By similarity)
FT	ACT SITE	343	343	343	By similarity.
FT	METAL	346	346	346	Zinc (catalytic) (By similarity).
FT	METAL	465	465	465	Zinc (catalytic) (By similarity).
FT	ACT SITE	427	427	427	Proton donor (Potential).
FT	CARBOHYD	59	59	59	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	143	143	143	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	403	403	403	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	540	540	540	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	655	655	655	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	749	749	749	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	890	890	890	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	540	541	541	NA -> KG (in Ref. 2).
SQ	SEQUENCE	930 AA;	106598 MW;	17430DBE5EAD7668 CRC64;	

  

Alignment Scores:	Pred. No.:	Length:	Matches:	Score:
		6,97e-159	2480.00	462
		Percent Similarity:	69.73%	Conservative:
		Best Local Similarity:	51.22%	Mismatches:
		Query Match:	48.99%	Indels:
		DB:	1	Gaps:
				4

  

US-10-039-073-3 (1-2883) x ART1\_MOUSE (1-930)

Qy	166	GCACCTAATGGGGAACGATTTCTTGGCAGGAGCTAAGCTCCCGAGTGGTGCATTCCT	225
Db <td>30 <td>AlaserAsnGlyAspSerPheProTrpAsnAsnMetArgLeuProGluTrpMetThrPro <td>49</td> </td></td>	30 <td>AlaserAsnGlyAspSerPheProTrpAsnAsnMetArgLeuProGluTrpMetThrPro <td>49</td> </td>	AlaserAsnGlyAspSerPheProTrpAsnAsnMetArgLeuProGluTrpMetThrPro <td>49</td>	49
Qy <td>226 <td>CTCCATNTAGACCTCTTTGTCACCCCAATCTACCTCTCTGCGATTTGTTGGCATCTGAG <td>285</td> </td></td>	226 <td>CTCCATNTAGACCTCTTTGTCACCCCAATCTACCTCTCTGCGATTTGTTGGCATCTGAG <td>285</td> </td>	CTCCATNTAGACCTCTTTGTCACCCCAATCTACCTCTCTGCGATTTGTTGGCATCTGAG <td>285</td>	285
Db <td>50 <td>IleHisTyrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPheTrpGlyLysThr <td>69</td> </td></td>	50 <td>IleHisTyrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPheTrpGlyLysThr <td>69</td> </td>	IleHisTyrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPheTrpGlyLysThr <td>69</td>	69
Qy <td>286 <td>AGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTCATCATCTTTCACACGACCAAGATCTT <td>345</td> </td></td>	286 <td>AGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTCATCATCTTTCACACGACCAAGATCTT <td>345</td> </td>	AGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTCATCATCTTTCACACGACCAAGATCTT <td>345</td>	345
Db <td>70 <td>GluValGluIleIleAlaSerArgProThrSerThrIleIleMetHisSerHisLeu <td>89</td> </td></td>	70 <td>GluValGluIleIleAlaSerArgProThrSerThrIleIleMetHisSerHisLeu <td>89</td> </td>	GluValGluIleIleAlaSerArgProThrSerThrIleIleMetHisSerHisLeu <td>89</td>	89
Qy <td>346 <td>GAAATCAGCAATGCCACCTTTCAGTCAGAGGAAGATACAGATACATGAAACACGAGAAA <td>405</td> </td></td>	346 <td>GAAATCAGCAATGCCACCTTTCAGTCAGAGGAAGATACAGATACATGAAACACGAGAAA <td>405</td> </td>	GAAATCAGCAATGCCACCTTTCAGTCAGAGGAAGATACAGATACATGAAACACGAGAAA <td>405</td>	405
Db <td>90 <td>GlnIleSerLysAlaThrLeuArg-----ArgGlyAlaGlyGluMetLeuSerGluGlu <td>107</td> </td></td>	90 <td>GlnIleSerLysAlaThrLeuArg-----ArgGlyAlaGlyGluMetLeuSerGluGlu <td>107</td> </td>	GlnIleSerLysAlaThrLeuArg-----ArgGlyAlaGlyGluMetLeuSerGluGlu <td>107</td>	107
Qy <td>406 <td>GAACTGAAAGTTTGGATTTACCTGTCATGACAAATTCGACTGCTGGTTCAGAGAAA <td>465</td> </td></td>	406 <td>GAACTGAAAGTTTGGATTTACCTGTCATGACAAATTCGACTGCTGGTTCAGAGAAA <td>465</td> </td>	GAACTGAAAGTTTGGATTTACCTGTCATGACAAATTCGACTGCTGGTTCAGAGAAA <td>465</td>	465
Db <td>108 <td>ProLeuLysValLeuGluTrpProIleHisGluGlnValAlaLeuLeuAlaGlnPro <td>127</td> </td></td>	108 <td>ProLeuLysValLeuGluTrpProIleHisGluGlnValAlaLeuLeuAlaGlnPro <td>127</td> </td>	ProLeuLysValLeuGluTrpProIleHisGluGlnValAlaLeuLeuAlaGlnPro <td>127</td>	127
Qy <td>466 <td>CTTACGCCTCACGAAATACTATGCGCTATGCGCTTCCAGCTTCCAGCAAGTTAGTGTGGC <td>525</td> </td></td>	466 <td>CTTACGCCTCACGAAATACTATGCGCTATGCGCTTCCAGCTTCCAGCAAGTTAGTGTGGC <td>525</td> </td>	CTTACGCCTCACGAAATACTATGCGCTATGCGCTTCCAGCTTCCAGCAAGTTAGTGTGGC <td>525</td>	525
Db <td>128 <td>LeuLeuAlaGlySerLeuTrpValIleIleAspTyrAlaAlaAsnLeuSerGluSer <td>147</td> </td></td>	128 <td>LeuLeuAlaGlySerLeuTrpValIleIleAspTyrAlaAlaAsnLeuSerGluSer <td>147</td> </td>	LeuLeuAlaGlySerLeuTrpValIleIleAspTyrAlaAlaAsnLeuSerGluSer <td>147</td>	147
Qy <td>526 <td>TTTGAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGTGAACAAAGAAATCTTGTGA <td>585</td> </td></td>	526 <td>TTTGAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGTGAACAAAGAAATCTTGTGA <td>585</td> </td>	TTTGAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGTGAACAAAGAAATCTTGTGA <td>585</td>	585
Db <td>148 <td>PheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGlyGluMetArgIleLeuAla <td>167</td> </td></td>	148 <td>PheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGlyGluMetArgIleLeuAla <td>167</td> </td>	PheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGlyGluMetArgIleLeuAla <td>167</td>	167
Qy <td>586 <td>GTAACAGATTTTGGCCCAAGCCAGGACGCTTCCCTTGGTGGTGAACCAAGCCCTTG <td>645</td> </td></td>	586 <td>GTAACAGATTTTGGCCCAAGCCAGGACGCTTCCCTTGGTGGTGAACCAAGCCCTTG <td>645</td> </td>	GTAACAGATTTTGGCCCAAGCCAGGACGCTTCCCTTGGTGGTGAACCAAGCCCTTG <td>645</td>	645
Db <td>168 <td>AlaThrGlnPheGluProThrAlaAlaArgMetAlaPheProCysPheAspGluProAla <td>187</td> </td></td>	168 <td>AlaThrGlnPheGluProThrAlaAlaArgMetAlaPheProCysPheAspGluProAla <td>187</td> </td>	AlaThrGlnPheGluProThrAlaAlaArgMetAlaPheProCysPheAspGluProAla <td>187</td>	187
Qy <td>646 <td>TTCAAAGCCAACTTTTCAATCAAGATACGAAGAGAGAGAGGAGCATATATGCACTATCAAC <td>705</td> </td></td>	646 <td>TTCAAAGCCAACTTTTCAATCAAGATACGAAGAGAGAGAGGAGCATATATGCACTATCAAC <td>705</td> </td>	TTCAAAGCCAACTTTTCAATCAAGATACGAAGAGAGAGAGGAGCATATATGCACTATCAAC <td>705</td>	705
Db <td>188 <td>LeuLysAlaSerPheSerIleLysIleLysArgAspProArgHisLeuAlaIleSerAsn <td>207</td> </td></td>	188 <td>LeuLysAlaSerPheSerIleLysIleLysArgAspProArgHisLeuAlaIleSerAsn <td>207</td> </td>	LeuLysAlaSerPheSerIleLysIleLysArgAspProArgHisLeuAlaIleSerAsn <td>207</td>	207
Qy <td>706 <td>ATCCCAAGGTTAAGACAATTTGAACCTTGAAGAGGCTCTTTTGGAGAGATCATCTTTGAAC <td>765</td> </td></td>	706 <td>ATCCCAAGGTTAAGACAATTTGAACCTTGAAGAGGCTCTTTTGGAGAGATCATCTTTGAAC <td>765</td> </td>	ATCCCAAGGTTAAGACAATTTGAACCTTGAAGAGGCTCTTTTGGAGAGATCATCTTTGAAC <td>765</td>	765
Db <td>208 <td>MetProLeuValLysSerValAsnValAlaGluGlyLeuIleGluAspHisPheAspIle <td>227</td> </td></td>	208 <td>MetProLeuValLysSerValAsnValAlaGluGlyLeuIleGluAspHisPheAspIle <td>227</td> </td>	MetProLeuValLysSerValAsnValAlaGluGlyLeuIleGluAspHisPheAspIle <td>227</td>	227
Qy <td>766 <td>ACTGTAAATGAGTACATACCTTGTAGCCGTACATAGTTTGTGTATTTCCATCTCTCAGT <td>825</td> </td></td>	766 <td>ACTGTAAATGAGTACATACCTTGTAGCCGTACATAGTTTGTGTATTTCCATCTCTCAGT <td>825</td> </td>	ACTGTAAATGAGTACATACCTTGTAGCCGTACATAGTTTGTGTATTTCCATCTCTCAGT <td>825</td>	825
Db <td>228 <td>ThrValLysMetSerThrTyrLeuValAlaPheIleIleSerAspPheLysSerValSer <td>247</td> </td></td>	228 <td>ThrValLysMetSerThrTyrLeuValAlaPheIleIleSerAspPheLysSerValSer <td>247</td> </td>	ThrValLysMetSerThrTyrLeuValAlaPheIleIleSerAspPheLysSerValSer <td>247</td>	247
Qy <td>826 <td>GGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCTATGATCATCCCGACAGCAACCGAAATCAA <td>885</td> </td></td>	826 <td>GGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCTATGATCATCCCGACAGCAACCGAAATCAA <td>885</td> </td>	GGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCTATGATCATCCCGACAGCAACCGAAATCAA <td>885</td>	885
Db <td>248 <td>LysMetThrLysSerGlyValLysValSerValTyrAlaValProAspLysIleAsnGln <td>267</td> </td></td>	248 <td>LysMetThrLysSerGlyValLysValSerValTyrAlaValProAspLysIleAsnGln <td>267</td> </td>	LysMetThrLysSerGlyValLysValSerValTyrAlaValProAspLysIleAsnGln <td>267</td>	267



GN Name=Arts1; Synonyms=App1s;  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN=Sprague-Dawley; TISSUE=Pineal gland;  
 RX MEDLINE=20285344; PubMed=10824104;  
 RA Schomburg L., Kollmus H., Friedrichsen S., Bauer K.;  
 RT "Molecular characterization of a puromycin-insensitive leucyl-specific  
 RL Eur. J. Biochem. 267:3198-3207(2000).  
 CC -1- FUNCTION: May play a role in the inactivation of peptide hormones.  
 CC May be involved in the regulation of blood pressure through the  
 CC inactivation of angiotensin II and/or the generation of bradykinin  
 CC in the kidney (By similarity).  
 CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-  
 CC Xbb-, in which Xaa is preferably Leu, but Met is also acceptable.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9J22-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9J22-2; Sequence=VSP\_005451, VSP\_005452;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous.  
 CC -1- SIMILARITY: Belongs to the peptidase M1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF148323; AAF73106.1; -;  
 DR EMBL: AF148324; AAF73107.1; -;  
 DR MEROPS: M01.018; -;  
 DR GO: GO:0005829; C:cytosol; ISS.  
 DR GO: GO:0005783; C:endoplasmic reticulum; ISS.  
 DR GO: GO:0005576; C:extracellular; ISS.  
 DR GO: GO:0016021; C:integral to membrane; ISS.  
 DR GO: GO:0005138; F:interleukin-6 receptor binding; ISS.  
 DR GO: GO:0004178; F:leucyl aminopeptidase activity; ISS.  
 DR GO: GO:0004239; F:methionyl aminopeptidase activity; ISS.  
 DR GO: GO:0005164; F:tumor necrosis factor receptor binding; ISS.  
 DR GO: GO:0008270; F:zinc ion binding; ISS.  
 DR GO: GO:0045444; P:adipocyte differentiation; ISS.  
 DR GO: GO:0019885; P:antigen processing, endogenous antigen via . . ; ISS.  
 DR GO: GO:0006509; P:membrane protein ectodomain proteolysis; ISS.  
 DR GO: GO:0050714; P:positive regulation of protein secretion; ISS.  
 DR GO: GO:0008217; P:regulation of blood pressure; ISS.  
 DR GO: GO:0045088; P:regulation of innate immune response; ISS.  
 DR InterPro: IPR006025; Rept\_M\_Zn\_BS.  
 DR InterPro: IPR001930; Peptidase\_M1.  
 DR Pfam: PF01433; Peptidase\_M1; 1.  
 DR PRINTS: PR00756; ALADIP7ASE.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Alternative splicing; Aminopeptidase; Glycoprotein; Hydrolase;  
 KW Metalloprotease; Protease; Signal; Zinc.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 930 Adipocyte-derived leucine aminopeptidase.  
 FT METAL 342 342 Zinc (catalytic) (By similarity).  
 FT ACT\_SITE 343 343 By similarity.  
 FT METAL 346 346 Zinc (catalytic) (By similarity).  
 FT METAL 465 465 Zinc (catalytic) (By similarity).  
 FT ACT\_SITE 427 427 Proton donor (Potential).  
 FT CARBOHYD 59 59 N-linked (GlcNAc.. ) (Potential).  
 FT 143 143 N-linked (GlcNAc.. ) (Potential).

FT	CARBOHYD	403	403	N-linked (GlcNAc.. ) (Potential).
FT	CARBOHYD	655	655	N-linked (GlcNAc.. ) (Potential).
FT	CARBOHYD	749	749	N-linked (GlcNAc.. ) (Potential).
FT	CARBOHYD	890	890	N-linked (GlcNAc.. ) (Potential).
FT	VARSPLIC	883	884	FP -> CM (in isoform 2).
FT	VARSPLIC	885	884	/FTID=VSP_005451.
FT	VARSPLIC	885	930	Missing (in isoform 2).
FT	VARSPLIC	885	930	/FTID=VSP_005452.
SQ	SEQUENCE	930 AA;	106418 MW;	928E7143CBD0BE7F CRG64;

  

Alignment Scores:				
Pred. No.:	1.66e-155	Length:	930	
Score:	2430.00	Matches:	456	
Percent Similarity:	68.90%	Conservative:	171	
Best Local Similarity:	50.11%	Mismatches:	265	
Query Match:	48.00%	Indels:	18	
DB:	1	Gaps:	6	

  

US-10-039-073-3 (1-2883) x ARTI_RAT (1-930)				
QY	154	GCTTTCCAGTAGCCTAATGGGAAACGATTTCCTTGGCAGGAGCTAAGGCTCCCGAGT	213	
DB	26	AlaSerProlyAlaSerAsnGlyAlaSerPheProTyrAsnMetArgLeuProGlu	45	
QY	214	GTGTCATTCTCTCCATTATGACCTCTTTGTCACCCCAATCTACCTCTCTGGACTTT	273	
DB	46	TyrIleThrProIleHisTyrAspLeuMetIleHisAlaAsnLeuSerThrLeuThrPhe	65	
QY	274	GTGTCATCTGAGAGATCGAAGTCITGTGTCACCAATGCTACCCAGTTTATCATCTTGCAC	333	
DB	66	TyrGlyLysThrGluValGluIleThrValSerGlnProThrSerThrIleIleMetHis	85	
QY	334	AGCAAGATCTTGAATCACGAATGCCCTTCAG-----TCAGAGGAAGATTCAAGA	387	
DB	86	SerHisGlnLeuGlnIleSerLysAlaThrLeuArgArgGlyAlaGluGlu	102	
QY	388	TGATGAAACCGAGAAAGAAAGCTGAAAGTTTGAGTTTACCTGCTCATGAACAATGCA	447	
DB	103	--MetLeuProGluGluProLeuLysLeuMetGluTyrSerAlaHisGluGlnValAla	121	
QY	448	CTGCTGGTTCCAGAGAAACTTACGCTCCTACCTGAATATCTATGCTGATGAGTCCCA	507	
DB	122	LeuLeuThrAlaGlnProLeuLeuAlaGlySerValTyrThrValIleIleThrTyrAla	141	
QY	508	GCCAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGCACATACAGAACTCTTGTGTGT	567	
DB	142	AlaAsnLeuSerGluAsnPheHisGlyPheTyrLysSerThrTyrArgThrGlnGluGly	161	
QY	568	GAAACAAGAAATCTTGCACTAAGATTTGAGCCAAACCCAGCAGCATGGCTTCCCT	627	
DB	162	GluArgGlyLeuAlaAlaThrGlnPheGluProThrAlaAlaArgMetAlaPhePro	181	
QY	628	TCCTTTGATGAACCGTTGTTCAAGCCAACTTTCAATCAAGATACAGAGAGAGAGAG	687	
DB	182	CysPheAspGluProAlaLeuLysAlaSerPheSerIleLysLysArgAspProArg	201	
QY	688	CATATTGCTACTATCCAACTATGCAAGGTTAAGACAACTTCAAGAGAGTCTTTTG	747	
DB	202	HisLeuAlaIleSerAsnMetProLeuValLysSerValThrValAlaGluGlyLeuIle	221	
QY	748	GAAGATCACTTTGAAACTACTGTAAATAAGTACATACCTGTGACCTACATAGTTTGT	807	
DB	222	GluAspHisPheAspIleThrValLysMetSerThrTyrLeuValAlaPheIleIleSer	241	
QY	808	GATTTCCACTCTGAGTGGCTTTCATCTCAGGGGTCAAGGTGCCATCTATGATCC	867	
DB	242	AppPheLysSerValSerLysMetThrLysSerGlyValLysValSerValTyrAlaVal	261	
QY	868	CCAGACAAACCGAAATCAACACATTTATGCTTTGGCAGGATCATCAAGCTACTTGT	927	
DB	262	ProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAlaAlaValThrLeuLeuGluPhe	281	
QY	928	TATGAAAAGTACTTTGATATCTACTATCCACTCTCCAACTGGATTTAATGCTATCTCT	987	

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Db 282 TyrGluAspTyrPheSerIleProTyrProLeuProLysGlnAspLeuAlaIlePro 301
Qy 998 GACTTTGCACCTGGAGCCATGAAATTTGGGGCTCATTTACATATAGGGAGACGCTCACTG 1047
Db 302 AspPheGlnSerGlyAlaMetGluAenTrpGlyLeuThrThrTyrArgGluSerAlaLeu 321
Qy 1048 CTTTTTGCACCAAGACCTCTTCTGCTCCGATAAACGTGGTGGTCCACAGAGTCATAGCC 1107
Db 322 LeuTyrAspLysGluSerSerAlaSerSerLysLeuGlyIleThrMetThrValSer 341
Qy 1108 CATGAATCGGCGCACAGCTGTTGGCAACTGGTCAAAATGGAATGGTGGTGAATGATATT 1167
Db 342 HisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThrMetGluTrpTrpAsnAspLeu 361
Qy 1168 TGGCTTAAGGAGGGTTTGCAAAATACATGAACTTATCGCTGTTTAATGCTACATATCCA 1227
Db 362 TrpLeuAsnGluGlyPheAlaLysPheMetGluPheValSerValThrValThrHisPro 381
Qy 1228 GAGCTGCAATTTGATGACTATTTTGAATGTGTGTTTGAAGTAATTAACAAAGATTCA 1287
Db 382 GluLeuLysValGluGluTyrPhePheGlyLysCysPheAsnAlaMetGluValAspAla 401
Qy 1288 TTGAATTCATCCCGCTATCTCAAAACACGCGGAAACCCGACTCAAAATACAGGAATG 1347
Db 402 LeuAsnSerSerHisProValSerThrProValGluAsnProAlaGlnIleArgGluMet 421
Qy 1348 TTTGATGAAGTTTCTTATAACAGGGAGCTTGTATTTTGAATATGCTCAAGGATTTTCTG 1407
Db 422 PheAspGluValSerTyrGluLysGlyAlaCysIleLeuAsnMetLeuArgAspTyrLeu 441
Qy 1408 GGTGAGGAGAAATCCAGAAAGGAATTAATCAGTACTTAAAGAGTTCAGCTATAGAAAT 1467
Db 442 SerAlaAspThrPheLysArgGlyIleValGlnTyrLeuGlnLysTyrSerTyrLysAsn 461
Qy 1468 GCTAAGATGATGCTGTGGAGCAGTCTGCAAAATAGTGTCT---TTAGAAGTGATTTT 1524
Db 462 ThrLysAsnGluAspLeuTrpAsnSerMetMetHisIleCysProThrAspGlyThrGln 481
Qy 1525 ACATCTGCTGGTGGTGTTCATTCGATCCCAAGATGACAAGTAAACATGCTCGCTCTCTG 1584
Db 482 ThrMetAspGlyPheCys---SerArgAsnGlnHisSerSerSerThrSerHisTrpArg 500
Qy 1585 GGGGAAATGCAGAGGTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1644
Db 501 GlnGluValIleAspIleLysSerMetMetAsnThrTrpThrLeuGlnLysGlyPhePro 520
Qy 1645 CTGCTGTGGTTAAACAGACGGGTGTCTCCTCGAGTCAACAGGAGCGCTTCTCTCCAG 1704
Db 521 LeuIleThrIleThrValArgGlyArgAsnValHisLysGlnGluHisTyrMetLys 540
Qy 1705 GGG-----GTTTCCAGAGAGCCCTGAATGGAGGGCCCTGCAGGAGAGTACTGTGG 1758
Db 541 GlySerGluCysPheProGluThrGlySer-----LeuTrp 552
Qy 1759 CATATCCCATGACTACTCCACGAGTCTTCTTAATGTGATGCCAGACACATCTTAAAA 1818
Db 553 HisValProLeuThrPheIleThrSerLysSerAspSerValGlnArgPheLeuLys 572
Qy 1819 TCAAGACAGATACTCTGGATCTACCTCAAAAGACCAGTGGGTGGAATTTAATGTGGAC 1878
Db 573 ThrLysThrAspValIleLeuProGluAlaValGluTrpIleLysPheAsnValGly 592
Qy 1879 TCAATGGTTACTACATCGTTTCACTATGAGGCTCATGATGGGACCAACTCATTTACACAG 1938
Db 593 MetAsnGlyTyrTyrIleValHisTyrGlyAspAspGlyTrpAlaSerLeuAsnGlyLeu 612
Qy 1939 CTGAATCAGAACCCACACATCTCTCAGACCTAAGGACAGAGTAGGTCTGATTTCATGATGTG 1998
Db 613 LeuLysGluAlaHisThrThrIleSerSerAsnAspArgAlaSerLeuIleAsnAsnAla 632
Qy 1999 TTTGAGCTAGTGTGGTGCAGGAGACTGACCTCCTAGACAAAGCTCTTGACATGACTTACTAC 2058
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Db 633 PheGlnLeuValSerIleGlyLysLeuSerIleGluLysAlaLeuAspLeuIleLeuTyr 652
Qy 2059 CTCAACATGAAACAAGACCCCGCACTTCTCGAAGTCTGAGTTACTTGGAAATCGTTT 2118
Db 653 LeuLysAsnGluThrGluIleMetProIlePheGlnGlyLeuAsnGluLeuIleProMet 672
Qy 2119 TACCACATGATGGACAGGAATATTTTCAGATATCTCTGAAAACCTCAACGGTTACCTT 2178
Db 673 TyrLysLeuMetGluLysArgAspMetValGluValGluThrGlnPheLysAspPheLeu 692
Qy 2179 CTTCAAGTATTTAAGCCAGGATGACAGGCAAGCTGGAGTGAACAAGGGCTCAGTCTGG 2238
Db 693 LeuArgLeuLeuLysAspLeuIleAsnLysGlnThrTrpThrAspGluGlySerValSer 712
Qy 2239 GACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGCGCTGTGACCTGAACACCTGCTCTTC 2298
Db 713 GluArgMetLeuArgSerGlnLeuLeuLeuAlaCysValHisArgTyrGlnLeuCys 732
Qy 2299 ATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATGGAATCCAGTGGAAAATTAATATA 2358
Db 733 ValGlnArgAlaGluArgTyrPheArgGluTrpLysAlaSerAsnGlyAsnMetSerLeu 752
Qy 2359 CCAACAGATGTTTAAAGATTGTGATTCTGTGGTCTCAGACACACAGCAGGATGCAAT 2418
Db 753 ProIleAspValThrLeuAlaValPheAlaValGlyAlaGlnAsnThrGluGlyTrpAsp 772
Qy 2419 TACCTTTTAGACCAATATGAATGCTCAATGCTCAAGTCTGAACAAACAAATAATCTGTAT 2478
Db 773 PheLeuTyrSerLysTyrGlnSerSerSerSerSerThrGluLysSerGlnIleGluPhe 792
Qy 2479 GCTTTGTCAAGCAGCATCAGGAAAGTACTGAGTAACTTGAATAGGAAATGGAA 2538
Db 793 SerLeuCysIleSerGlnAspProGluLysLeuGlnTrpLeuLeuAspGlnSerPheLys 812
Qy 2539 GGAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATTTCGCAGACGTCCA 2598
Db 813 GlyGluIleIleLysThrGlnGluPheProHisIleLeuThrLeuIleGlyArgAsnPro 832
Qy 2599 AAGGGCAGCAACTAGCATGGGATTTTGAAGAAATAATGGACCCATCTTCTGAAAATA 2658
Db 833 ValGlyTyrProLeuAlaTrpLysPheLeuLysGluAsnTrpAsnLysIleValGlnLys 852
Qy 2659 TTTGACTTGGCTCATATGACATAAGGATCATCTCTGCGACACACAGCTCATTCTTCT 2718
Db 853 PheGluLeuGlySerSerSerIleAlaHisMetValMetGlyThrThrAsnGlnPheSer 872
Qy 2719 TCAAGGATAAGTTGCAAGAGGTGAAACTATTTTCAATCTCTTGAGGCTCAAGGATCA 2778
Db 873 ThrArgAlaArgLeuGluGluValLysGlyPhePheSerSerLeuLysLysAsnGlySer 892
Qy 2779 CATCTCGATATTTTCAAACTGTTTGGAAACGATACCAACAAAATATAATAATGCTGAG 2838
Db 893 GlnLeuArgCysValGlnGlnThrIleGluThrIleGluGluAsnIleArgTrpMetAsp 912
Qy 2839 AAGAATCTCCGACTCTGAGGACTTGCTA 2868
Db 913 LysAsnPheAspLysIleArgLeuTrpLeu 922
RESULT 9
Q6PE23 PRELIMINARY; PRT; 1003 AA.
AC Q6PE23;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein zgc:66103.
GN OlfNames=zgc:66103;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1)
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QY 1534 GGAGTTTGTCTATTCGGATCCCAAGATGCAAGTAAACATGCTCGCTTCTCGGGGGAAT 1593  
Db 580 ----- 580  
QY 1594 GCAGAGGTCAAGAGATGATGACTACATGAGTCTCCAGAAAGAAATCCCTCTCGGTG 1653  
Db 581 LeuAsnValSerGluMetCysAsnThrTrpValHisLysGlyPheProLeuValThr 600  
QY 1654 GTTAAACAGACGGGTGTTCACTCCGACTGCAACAGAGAGCGCTTCTCCACAGGGGTTTC 1713  
Db 601 ValLysArgAsnGlyProGlnValThrLeuSerGlnGluHisPheLeuLeuAsnAla--- 619  
QY 1714 CAGGAAGACCTGAATGGAGGGCCCTCGACGAGAGGTACTGTCGATATCCCATTTGACC 1773  
Db 620 -----GluAsnGlyThrAspAspSerLeuTrpHisIleProLeuThr 634  
QY 1774 TACTCCACGAGTCTCTTAATGTATCCACAGA-----CACATTCTAAAA 1818  
Db 635 TyrValAsnAspSerCysSerValLeuArgSerCysLysGlnValPheHis---LeuLys 653  
QY 1819 TCAAGACAGATACCTGGATCTACCTGAAAGACCAAGTTGGGTGAAATTTAATGTGGAC 1878  
Db 654 AspLysGluAlaThrLeuGlnLeuProGlyGlnValLysTrpLeuLysPheAsnPheArg 673  
QY 1879 TCAATGTTACTACATGCTTCACTATGAGGTGATGATGGAGCAACTCATTTACACAG 1938  
Db 674 SerAspGlyPheTyrIleValHisIleTyrAspGluGlnGlyTrpSerAspLeuIleSerAla 693  
QY 1939 CTGAATCAGAACACACACTCTCAGACCTAAGACAGAGTAGTCTGATTCATGATGTG 1998  
Db 694 LeuLysValAspValAsnValLeuProSerGluAspLysAlaAlaLeuIleAsnAsnIle 713  
QY 1999 TTTCACTAGTTGGTGGCAGGAGACTGACCCCTAGACAAAGCTCTTGACACTTACTTAC 2058  
Db 714 PheAlaLeuSerArgLeuGlyLysValSerPheArgGlnValLeuAsnLeuMetAspTyr 733  
QY 2059 CTCACACATGAAACAGACGCCCCGACTCTTCGAAGCTGAGTACTTGGAAATCGTTT 2118  
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QY 2119 TACCACATGATGGACAGAGAAATATTTACATATCTCTGAAACCTCAACGGTTACCTT 2178  
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Db 774 GluSerHisPheGlySerLeuMetGluSerGlnSerTrpGluValGluThrSerValSer 793  
QY 2239 GACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGCGCTGACCTGAACCACTGCTCTTGC 2298  
Db 794 LysMetThrLeuArgSerAlaLeuLeuGluThrAlaCysAlaLeuAsnArgProAsnCys 813  
QY 2299 ATCCAGAAGCTGCTGAACCTCTTCCAGTGGATGGAATCCAGTGGAAAATTAATATA 2358  
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QY 2359 CCAACAGATGTTTAAAGATTGTATTCTCTGGTGTCTCAGACACAGCAGGAGTGAAT 2418  
Db 834 ProSerAspLeuMetArgThrValPheLysValAlaLysThrAspGluGlyTrpSer 853  
QY 2419 TACCTTTTGAAGCAATATGAATCTGCAATGCTCAAGTGTGCAACAAAAACAAATTTCTGTAT 2478  
Db 854 LysLeuLeuGlySerTyrLysHisSerIleTyrAspThrGluLysArgLysMetLeuGlu 873  
QY 2479 GCTTTGTCAAGCAGCAACATCAGAAAGTTACTGAATTAATGAAGTGAAGTGAATGGA 2538  
Db 874 AlaLeuAlaSerThrGlnAspValArgLysIleIleTrpValLeuGlnLysSerLeuAsp 893  
QY 2539 GGAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTTCATGCGATGGCAGAGTCCA 2598  
Db 894 GlySerGluIleGlnAsnGlnGluPheProLeuValIleHisThrValCysArgAspPhe 913  
QY 2599 AAGGGCAGCACTAGCATGGGATTTTGTAAAGAGAAAATTGGACCCATCTTCTGAAAAA 2658

Db 914 AlaGlyTyrLeuTyrAlaTrpAspPheMetCysGluAsnTrpGluLysIleThrGlnLys 933  
QY 2659 TTTGACTTGGGCTCATATGACATAAGGATCATCTCTGGCACAACAGCTCACTTTTCT 2718  
Db 934 PheProIleGlySerPheAlaIleGlnSerIleIleThrSerThrThrSerGlnPheSer 953  
QY 2719 TCAAGGATAAGTTCGACAGAGGTGAACATATTTTGAATCTCTTGAAGGCTCAAGGATCA 2778  
Db 954 ThrLysThrHisLeuAlaGluValGlnAsnPhePheSerSerLeuGlyAlaLysGlySer 973  
QY 2779 CATCTGGATATTTTCAAACTGTTCTGGAACGATACCAACAAAATATATAATGCTGAG 2838  
Db 974 GlnMetArgIleValGlnGluAlaIleGluThrIleLysHisAsnMetArgTrpMetGlu 993  
QY 2839 AAGAATCTCCGACTCTGAGGACTTGGCTA 2868  
Db 994 LysAsnLeuAsnThrLeuGlnSerTrpLeu 1003  
RESULT 10  
LCAP RAT ID LCAP RAT STANDARD; PRT; 1025 AA.  
AC P97629; Q11009;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Leuyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)  
DE (Oxytocinase) (Insulin-regulated membrane aminopeptidase)  
DE (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine  
DE aminopeptidase) (P-LAP) (Vesicle protein of 165 kDa) (Vp165) (GP160).  
GN Name=lrnp; Synonyms=lrnp, Otase;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
RX MEDLINE=96007507; PubMed=7559527; DOI=10.1074/jbc.270.40.23612;  
RA Keller S.R., Scott H.M., Mastick C.C., Aebersold R., Lienhard G.E.;  
RT "Cloning and characterization of a novel insulin-regulated membrane  
RT aminopeptidase from Glut4 vesicles";  
RL J. Biol. Chem. 270:23612-23618(1995).  
RN [2]  
RP SEQUENCE OF 168-176; 387-399; 731-740 AND 893-905.  
RX MEDLINE=94164972; PubMed=8119954;  
RA Mastick C.C., Aebersold R., Lienhard G.E.;  
RT "Characterization of a major protein in GLUT4 vesicles. Concentration  
RT in the vesicles and insulin-stimulated translocation to the plasma  
RT membrane.";  
RL J. Biol. Chem. 269:6089-6092(1994).  
CC -1- FUNCTION: Release of an N-terminal amino acid, cleave before  
CC cysteine, leucine as well as other amino acids. Degrades peptide  
CC hormones such as oxytocin, vasopressin and angiotensin III and  
CC plays a role in maintaining homeostasis during pregnancy. May be  
CC involved in the inactivation of neuronal peptides in the brain.  
CC Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may  
CC be the angiotensin IV receptor in the brain (By similarity).  
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-  
CC Xaa, in which the half-cysteine residue is involved in a disulfide  
CC loop, notably in oxytocin and vasopressin.  
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -1- SUBUNIT: Homodimer. Binds tankyrases 1 and 2 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Localized mainly  
CC in intracellular vesicles together with GLUT4. Relocalizes to the  
CC plasma membrane in response to insulin. The dileucine  
CC internalization motif and/or the interaction with tankyrases may  
CC be involved in intracellular sequestration.  
CC -1- TISSUE SPECIFICITY: Highly expressed in heart, brain, spleen,  
CC lung, kidney and white adipose tissue. Detected at lower levels in  
CC skeletal muscle and liver.  
CC -1- PTM: N-glycosylated.  
CC -1- SIMILARITY: Belongs to the peptidase M1 family.

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or send an email to license@isb-sib.ch).
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EMBL; U76997; AAB19066.1; --
EMBL; U32990; AAB38021.1; --
PIR; I55441; I55441.
MEROPS; M01.011; -.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01433; Peptidase_M1_1.
DR PRINTS; PR00756; ALADIP7ASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Aminopeptidase; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Metal-binding; Metalloprotease; Protease; Signal-anchor;
KW Transmembrane; Zinc.
FT DOMAIN 1 109 Cytoplasmic (Potential).
FT TRANSMEM 110 131 Signal-anchor for type II membrane
protein (Potential).
FT DOMAIN 132 1025 Extracellular (Potential).
FT SITE 53 54 Dileucine internalization motif
(Potential).
FT SITE 76 77 Dileucine internalization motif
(Potential).
FT SITE 96 101 Tankyrase binding (By similarity).
FT METAL 464 464 Zinc (catalytic) (By similarity).
FT ACT_SITE 465 465 By similarity.
FT METAL 468 468 Zinc (catalytic) (By similarity).
FT METAL 487 487 Zinc (catalytic) (By similarity).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 447 447 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 525 525 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 578 578 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 664 664 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 682 682 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 695 695 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 758 758 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 834 834 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 850 850 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 989 989 N-linked (GlcNAc...) (Potential).
FT CONFLICT 909 916 LMKSSLDG -> YGTQRAW (in Ref. 1;
AAB38021).
FT CONFLICT 916 1025 Missing (in Ref. 1; AAB38021).
SQ SEQUENCE 1025 AA; 117201 MW; 8AD3BA3A446FB5EF CRC64;

Alignment Scores:
Pred. No.: 2,8e-128 Length: 1025
Score: 2027.00 Matches: 402
Percent Similarity: 61.81% Conservative: 158
Best Local Similarity: 44.37% Mismatches: 310
Query Match: 40.04% Indels: 36
DB: 1 Gaps: 5

US-10-039-073-3 (1-2883) x LCAP_RAT (1-1025)
QY 160 CCAGTACCACTAATGGGAAACGATTTCCTTGGCAGGAGCTAAGGCTCCCGAGTGGTC 219
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
153 ProileAlaThrAsnGlyLysValPheProTrpAlaGlnIleArgLeuProThrAlaIle 172
QY 220 ATTCCTCTCATATGACCTCTTTGGTCCACCCCAATCTCACTCTCTGGACTTTGTGCA 279
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 IleProGlnArgTyrGluLeuSerLeuHisProAsnLeuThrSerMetThrPheArgGly 192

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QY 280 TCTGAGAAAGATCGAAGCTCTTGGTCAGCAATGCTTACCAGTTTATCATCTTGACACGAAA 339
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr 212
QY 340 GATCTTGAATAACAGAAATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAAACCA 399
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
213 GlyHisAsnIleSerValThrPheMetSerAlaValSerSerGln----- 228
QY 400 GGAAGAAGAACTGNAAGTTTGGATTACCTGCTCATGAACAAATTCGACTGCTGCTGCTTCCA 459
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
229 GluLysGlnValGluIleLeuGluTyrProTyrHisGluGlnIleAlaValAlaPro 248
QY 460 GAGAAACTTACGCCTCACCTGAAATATGATGTGGCTATGAGCTTCCAAAGCCAAAGTTAGGT 519
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
249 GluSerLeuLeuThrGlyHisAsnTyrThrLeuLysIleGluTyrSerAlaAsnIleSer 268
QY 520 GATGGCTTGAAGGGTTTATAAAGACACATACAGAACTCTTGGTGGTGAACAAGAAAT 579
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 AsnSerTyrTyrGlyPheTyrGlyIleThrTyrThrAspLysSerAsnGluLysLysAsn 288
QY 580 CTTCAGTAACAGATTTTGGAGCAACCCAGGACGATGGCTTCCCTTCCCTTGGTGTGA 639
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
289 PheAlaAlaThrGlnPheGluProLeuAlaAlaArgSerAlaPheProCysPheAspGlu 308
QY 640 CCGTTGTTCAAGGCCAACTTTTCAAGATACGAAGAGAGAGAGAGAGGATATTCGACTA 699
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
309 ProAlaPheLysAlaThrPheIleIleLysIleThrArgAspGluHisThrAlaLeu 328
QY 700 TCAACATGCCAAAGGTTAAGCAATTAAGAGGAGGCTTTTGGAGAGATCACTTT 759
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
329 SerAsnMetProLysLysSerValProThrGluGluGlyLeuIleGlnAspGluPhe 348
QY 760 GAACTACTGTAAATAAGTAGTACATACCTTGTAGCTACATAGTTTGTGATTCACCTCT 819
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349 SerGluSerValLysMetSerThrTyrLeuValAlaPheIleValGlyGluMetArgAsn 368
QY 820 CTGAGTGGCTTCACTTTCATCAGGGGTCAAGGTGTCCATCATGCATCCCAAGCAACGG 879
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
369 LeuSerGln---AspValAsnGlyThrLeuValSerValTyrAlaValProGluLysIle 387
QY 880 AATCAAAACATATTATGCTTTGCAGGCATCATCGAAGCTACTGATTTTATGAAAAGTAC 939
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
388 AspGlnValTyrHisAlaLeuAspThrThrValLysLeuLeuGluPheTyrGlnAsnTyr 407
QY 940 TTTGATATCTACTATCCACTCTCCAAACTGGATTAAATTGCTATTCTCTGACCTTGCACCT 999
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
408 PheGluIleGlnTyrProLysLysLysLeuAspLeuValAlaIleProAspPheGluAla 427
QY 1000 GGAGCCATGGAAAATTTGGGGCTCATTAACATATAGGAGACGCTGCTGCTTTTGGACCCC 1059
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 GlyAlaMetGluAsnTrpGlyLeuLeuThrPheArgGluGluThrLeuLeuTyrAspAsn 447
QY 1060 AAGACCTCTTCTGCTTCGATAAATGTTGGGTCCACAGAGTCATAGCCCATGAAGTGGCG 1119
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
448 AlaThrSerSerValAlaAlaAspArgLysLeuValThrLysIleIleAlaHisGluLeuAla 467
QY 1120 CACCAAGTGGTTGGCAACCTGCTCAATGGAGTGGTGAAGTATATTTGGCTTAAGGAG 1179
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
468 HisGlnTrpPheGlyAsnLeuValThrMetGlnTrpTrpAsnAspLeuTrpLeuAsnGlu 487
QY 1180 GGTTTTGGAAAATACATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTT 1239
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488 GlyPheAlaThrPheMetGluTyrPheSerValGluLysIlePheLysGluLeuAsnSer 507
QY 1240 GATGACTATTTTGAATGTGTGTTTGAAGTAATATTACAAAAGATTTCATTGAATTCATCC 1299
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
508 TyrGluAspPheLeuAspAlaArgPheLysThrMetArgLysAspSerLeuAsnSerSer 527
QY 1300 CGCCCTATCTCCAAACACGAGGAAACCCCGACTCAAAATACAGAAATGTTGATGAAGTT 1359
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 HisProIleSerSerValGlnSerSerGluGlnIleGluMetPheAspSerLeu 547

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QY 1360 TCCTATAACAGGAGCTGTATTTTGAATGCTCAAGGATTTTCTGGGTGAGGAGAA 1419
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548 SerTyrPheLysGlyAlaSerLeuLeuMetLeuLysSerTyrLeuSerGluAspVal 567
QY 1420 TTCCAGAAAGGAATAATTCAGTACTTAAGAAGTTTCAGCTATAGAAAATGCTAAGAAATGAT 1479
Db 1421 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
568 PheGlnHisAlaIleLeuTyrLeuHisSerTyrAlaAlaIleGlnSerAsp 587
QY 1480 GACTTGTGAGCAGCTCTCTCAAAATAGTTGTTTGAAGATGATTTTACATCTGGTGGAGTT 1539
Db 1481 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
588 AspLeuTyrAspSerPheAsnGlu----- 595
QY 1540 TGTCATTCCGATCCCAAGATGACAAGTAAACATGCTCGCCTTCTCGGGGGAATAATGCACAG 1599
Db 1541 -----ValThrGlyLeuThrLeuAsp 602
QY 1600 GTCAAAGAGATGATGACTACATGAGTCTCCAGAAAGGAATCCCTCTCGTGGTTAAA 1659
Db 1601 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
603 ValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrValGln 622
QY 1660 CAAGACGGGTGTTCACTCCGACTGCAACAGAGCGCTTCTCCAGGGGGTTTTCAGGAA 1719
Db 1661 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
623 ArgLysGlyThrGluLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 639
QY 1720 GACCTGAATGAGGGCCCTCAGAGAGGTACCTGCGCATATCCCATTCACCTACTCC 1779
Db 1721 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
640 GlnProGluIleGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTyrVal 659
QY 1780 ACGAGTTCTTCTAATGTGATCCACAGACAC-----ATTCTAAATCAAGACAGAT 1830
Db 1781 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
660 ThrAspGlyArgAsnTyrSerGluTyrArgSerValSerLeuLeuAspLysSerAsp 679
QY 1831 ACTCTGGATCTACCTGAAACACCAAGTTGGTGGTAAATTTAATGTGGACTCAAAATGGTTAC 1890
Db 1832 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
680 ValIleAsnLeuThrGluGlnValGlnTrpValLysValAsnThrAsnMetThrGlyTyr 699
QY 1891 TACATCGTTCACTATGAGGTCATGGATGGACCACTCATATACACAGCTGAATCAGAAC 1950
Db 1892 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
700 TyrIleValHisTyrAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArgAsn 719
QY 1951 CACACATCTTCAGACCTTAAGACAGACTAGTCTGATTTCATGATGTTTTCAGTAGTT 2010
Db 1952 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
720 ProTyrValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeuAla 739
QY 2011 GGTGAGGAGACTCACCTCAGACAAAGCTCTTGACATGACTTACTACTCTCAACATGAA 2070
Db 2012 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
740 GlyLeuGlyLysValProLeuGlnMetAlaPheAspLeuIleAspTyrLeuArgAsnGlu 759
QY 2071 ACAAGACGCGCCGACTCTCGAAGTCTGAGTTACTTGGAAATCGTTTACCACATGATG 2130
Db 2072 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
760 ThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrAsnLeuLeu 779
QY 2131 GACAGAGGAATATTTTCAGATATCTCTGAAACCTCAAGCGTTACCTTCTTCAGTATTTT 2190
Db 2132 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
780 GluLysLeuGlyHisMetAspLeuSerSerArgLeuValThrArgValHisLysLeuLeu 799
QY 2191 AAGCAGCTGATTGACAGCAAGCTGGAGTGACAGGGCTCAGTCTGGGACAGGATGCTC 2250
Db 2192 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
800 GlnAsnGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGluLeu 819
QY 2251 CGCTCGGCTCTCTGAAGCTGGCTGTGACCTGAACCATGCTCCTTGTGATCCAGAAAGCT 2310
Db 2252 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
820 ArgSerAlaLeuLeuGluPheAlaCysAlaHisSerLeuGluAsnCysThrThrMetAla 839
QY 2311 GCTGAATCTTCTCCAGTGGATGAATCCAGTGGAAAATTAATATATACCAACAGATGTT 2370
Db 2312 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
840 ThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAspVal 859
QY 2371 TTAAGAGTTGTATTTCTGGTGGTCTCAGACACAGCAGGATGGAATTACCTTTTAGAG 2430
Db 2372 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
860 MetThrThrValPheLysValGlyAlaArgThrGluLysGlyTrpLeuPheLeuPheSer 879
QY 2431 CAATATGAATGTCTAATGTCAAGTCTGAAACAAAACAAATTTCTGTATGTCTTGTCAACG 2490
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Db 880 MetTyrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAlaSer 899
QY 2491 AGCAAGCATCAGGAAAAAGTTACTGCAAGTTAATTCGAACTAGGAATGGAAGAAAGTTATC 2550
Db 2492 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
900 SerAlaAspAlaHisLysLeuTyrTrpLeuMetLysSerSerLeuAspGlyAspIleIle 919
QY 2551 AAGACACAGAACTGGGAGCTCTCTTCATGCGGATTCGACAGACGTCCTCAAGGGGAGCAA 2610
Db 2552 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
920 ArgThrGlnLysLeuSerLeuIleArgThrValGlyArgGlnPheProGlyHisLeu 939
QY 2611 CTACATGGGATTTTGAAGAGAAATTTGGACCCATCTTCTGAAAAAATTTGACTTGGGC 2670
Db 2612 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
940 LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeuGly 959
QY 2671 TCATATGACATAAGATGATCATCTCTGGCACACAGCTCACATTTTCTTCCAAGGATAAG 2730
Db 2672 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
960 SerTyrThrIleGlnSerIleValAlaGlySerThrHisLeuPheSerThrLysThrHis 979
QY 2731 TTGCAAGAGGTGAACATATTTTGAATCTCTTCAGGCTCAAGGATCACATCTCGATATT 2790
Db 2732 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
980 LeuSerGluValGlnGluPhePheGluAsnGlnSerGluAlaThrLeuGlnLeuArgCys 999
QY 2791 TTTCAAACTGTTCTGGAACGATAACCAAAAATATAAAATGGCTGGAGAAATCTTCCG 2850
Db 2792 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1000 ValGlnGluAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeuLys 1019
QY 2851 ACTCTGAGGACTTGGCTA 2868
Db 1020 ThrLeuThrLeuTrpLeu 1025
PRELIMINARY; PRT; 1025 AA.
RESULT 11
ID Q8C129 PRELIMINARY; PRT; 1025 AA.
AC Q8C129;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732490P18 product:INSULIN-REGULATED MEMBRANE
DE AMINOPEPTIDASE IRAP homolog.
GN Name=Lnpep;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RC The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
```



Qy	1480	GAC	TTG	TGG	AGC	AGT	CTG	TCA	AA	TAG	TTG	TTG	TTA	AAA	AGT	GAT	TTT	TCA	TCT	G	TG	G	AG	T	1539
Db	588	Asp	Leu	Trp	Asp	Ser	Phe	Asn	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	594	
Qy	1540	TGT	CAT	TCG	GAT	CCCA	AGAT	GCAC	AA	GTGA	CA	CA	TG	CT	CG	CC	T	T	T	CG	G	G	G	1599	
Db	595	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	602		
Qy	1600	GT	CAA	GAG	AGAT	GAT	GAT	CTA	CA	TG	AG	CT	CTC	CA	GAA	AGAA	T	CC	CC	T	G	T	G	1659	
Db	603	Val	lys	Met	Met	lys	Thr	Trp	Thr	Leu	Gln	lys	Gly	Phe	Pro	Leu	Val	Thr	Val	Gln	----	----	----	622	
Qy	1660	CAA	GAC	GGT	GT	TCA	CT	CCG	ACT	GCA	AC	GAG	AGC	GT	TCT	CC	GAG	GGG	T	TT	T	CC	CA	1719	
Db	623	Arg	lys	Gly	Thr	Glu	Leu	Leu	Gln	Gln	Arg	Phe	----	----	----	----	----	----	----	----	----	----	639		
Qy	1720	GAC	CT	GAA	TGG	AGG	CC	CTG	CAG	GAG	AGT	ACT	G	TG	G	CAT	AT	CC	CA	T	T	G	1779		
Db	640	Gln	Pro	Glu	Ser	Gln	Pro	Ser	Asp	Thr	Ser	His	Leu	Trp	His	Leu	Trp	His	Leu	Ser	Trp	Val	659		
Qy	1780	ACG	AGT	TCT	TCT	TA	TG	TG	AT	CC	AC	GAC	----	----	----	----	----	----	----	----	----	----	1830		
Db	660	Thr	Asp	Gly	Arg	Asn	Thr	Ser	Glu	Tyr	Arg	Ser	Val	Ser	Leu	Leu	Asp	Leu	Ser	Asp	----	----	679		
Qy	1831	ACT	CT	G	GAT	CT	CA	CT	G	A	A	A	A	C	C	A	G	T	T	G	A	A	T	1890	
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Qy	1891	TAC	AT	CT	T	CA	T	AT	G	AG	G	T	CA	T	G	G	CA	CA	T	AT	T	CA	CA	1950	
Db	700	Tyr	Ile	Val	His	Tyr	Ala	His	Asp	Asp	Trp	Thr	Ala	Leu	Ile	Asn	Gln	Leu	ys	Arg	Asn	----	719		
Qy	1951	CAC	ACA	CT	CT	CAG	AC	CT	TA	G	G	CAG	AGT	AG	T	CT	GAT	CA	T	G	T	T	2010		
Db	720	Pro	Tyr	Val	Leu	Ser	Asp	lys	Asp	Arg	Ala	Asn	Leu	Ile	Asn	Leu	Ile	Phe	Glu	Leu	Ala	739			
Qy	2011	GGT	CG	AGG	AG	AT	GA	CC	T	AG	CA	AA	G	CT	T	CT	G	AT	CA	T	T	CA	2070		
Db	740	Gly	Leu	Gly	lys	Val	Pro	Leu	Arg	Met	Ala	Phe	Asp	Leu	Ile	Asp	Tyr	Leu	ys	Asn	Glu	759			
Qy	2071	ACA	AG	CAG	CCCC	G	CA	CT	T	CT	G	CA	AG	G	T	CA	T	T	G	GA	T	T	2130		
Db	760	Thr	His	Thr	Ala	Pro	Ile	Thr	Glu	Ala	Leu	Phe	Gln	Thr	Asn	Leu	Ile	Tyr	Asn	Leu	Leu	779			
Qy	2131	GAC	AGA	AG	GA	TAT	T	T	CAG	AT	AT	CT	CT	G	AAA	C	T	C	A	G	G	T	2190		
Db	780	Glu	lys	Leu	Gly	His	Met	Asp	Leu	Ser	Arg	Leu	Val	Ala	Arg	Val	His	lys	Leu	Leu	----	799			
Qy	2191	AAG	CCA	G	T	G	T	T	G	AC	G	CA	AA	G	CT	G	AG	T	GA	CA	AGG	CT	2250		
Db	800	Gln	Asn	Gln	Ile	Gln	Gln	Trp	Trp	Thr	Asp	Glu	Gly	Thr	Pro	Ser	Met	Arg	Glu	Leu	819				
Qy	2251	CG	T	CG	G	CT	CT	T	T	G	A	G													

Qy	2551	AAGACACAGAACTTGGCAGCTCTCTTCATGCGAATTGCCAGACTCAAAAGGGGGCAGCAA	2618
Dd	:	:	:::::
Dd	920	ThrGlnLysLeuSerLeuIleAlaArgThrValGlyArgHisPheProGlyHisLeu	939
Qy	2611	CTAGCATGGGATTTTGTAAGAGAAAAATTGCACCATCTCTCTGAAAAAATTTGACTTGGGC	2670
Dd	:	:	:::::
Dd	940	LeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeuGly	959
Qy	2671	TCATATGACATAAGGATGATCATCTCTCGGCACAACAGCTCACCTTTCTTCCAAAGGATAAG	2730
Dd	:	:	:::::
Dd	960	SerTyrrThrileGlnSerIleValAlaGlySerThrHisLeuPheSerThrLysThrHis	979
Qy	2731	TTCGAAGAGGTGAACATAATTTTTTGAATCTCTCTGAGGCTCAAGGATCACATCTGGATATT	2790
Dd	:	:	:::::
Dd	980	LeuSerGluValGlnAlaPhePheGluAsnGlnSerGluAlaThrLeuLysLeuArgCys	999
Qy	2791	TTTCAAACTGTTCTGGAAAGGATAACCAAAAATATAAAATGGCTGGAGAGAATCTTCG	2850
Dd	:	:	:::::
Dd	1000	ValGlnGluAlaLeuGluValIleGlnLeuAsnIleGlnTrpMetValArgAsnLeuLys	1019
Qy	2851	ACTCTGAGGACTTGGCTA	2868
Dd	:	:	:::::
Dd	1020	ThrLeuSerGlnTrpLeu	1025
 RESULT 12 LCAP_HUMAN STANDARD; PRT; 1025 AA.			
AC	QUOI6;	Q05145; Q9UIQ7;	
DT	28-FEB-2003	(Rel. 41, Created)	
DE	25-OCT-2004	(Rel. 41, Last sequence update)	
DE	Leucyl-cystinyl aminopeptidase (EC 3.4.11.3) (Cystinyl aminopeptidase)		
DE	(Oxytocinase) (OTase) (Insulin-regulated membrane aminopeptidase)		
DE	(Insulin-responsive aminopeptidase) (IRAP) (Placental leucine		
DE	aminopeptidase) (P-LAP).		
GN	Name=LNPER; Synonyms=OTASE;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 160-168; 319-332; 615-624;		
RP	635-647; 798-814 AND 870-880.		
RC	TISSUE=Placenta;		
RC	MDLINE=S6132882; PubMed=8550619; DOI=10.1074/jbc.271.1.56;		
RX	Rogi T., Tsujimoto M., Nakazato H., Mizutani S., Tomoda Y.;		
PA	"Human placental leucine aminopeptidase/oxytocinase. A new member of		
RT	type II membrane-spanning zinc metalloproteinase family.";		
RL	J. Biol. Chem. 271:56-61(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RC	TISSUE=Placenta;		
RX	MDLINE=P320624; PubMed=9177475; DOI=10.1016/S0167-4781(97)00036-5;		
RA	Lauersen P.G., Rasmussen T.E., Petersen K., Pedraza-Diaz S.,		
RA	Moestrup S.K., Glemann J., Sottrup-Jensen L., Kristensen T.;		
RA	"The complete amino acid sequence of human placental oxytocinase.";		
RL	Biochim. Biophys. Acta 1352:1-7(1997).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).		
RX	MDLINE=20223264; PubMed=10759854;		
RA	Rasmussen T.E., Pedraza-Diaz S., Hardre R., Lauersen P.G.,		
RA	Carroll A.G., Kristensen T.;		
RT	"Structure of the human oxytocinase/insulin-regulated aminopeptidase		
RT	gene and localization to chromosome 5q21.";		
RL	Eur. J. Biochem. 267:2297-2306(2000).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).		
RX	MDLINE=21286092; PubMed=11389728;		
RA	Matsumoto H., Nagasaka T., Hattori A., Rogi T., Tsuruoka N.,		
RA	Mizutani S., Tsujimoto M.;		
RT	"Expression of placental leucine aminopeptidase/oxytocinase in		
RT	neuronal cells and its action on neuronal peptides.";		
RL	Eur. J. Biochem. 268:3259-3266(2001).		

[5]  
CHARACTERIZATION.  
MEDLINE=92117646; PubMed=1731608;  
Tsujiimoto M., Mizutani S., Adachi H., Kimura M., Nakazato H.,  
Tomoda Y.,  
"Identification of human placental leucine aminopeptidase as  
oxytocinase";  
Arch. Biochem. Biophys. 292:388-392 (1992).  
[6]  
FUNCTION.  
MEDLINE=21623680; PubMed=11707427; DOI=10.1074/jbc.C100512200;  
Abistcon A.L., McDowell S.G., Matsacos D., Sim P., Clune E.,  
Mustafa T., Lee J., Mendelsohn F.A., Simpson R.J., Connolly L.M.,  
Chai S.Y.;  
"Evidence that the angiotensin IV (AT(4)) receptor is the enzyme  
insulin-regulated aminopeptidase";  
J. Biol. Chem. 276:48623-48626 (2001).  
-!- FUNCTION: Release of an N-terminal amino acid, cleave before  
cysteine, leucine as well as other amino acids. Degrades peptide  
hormones such as oxytocin, vasopressin and angiotensin III, and  
plays a role in maintaining homeostasis during pregnancy. May be  
involved in the inactivation of neuronal peptides in the brain.  
Cleaves Met-enkephalin and dynorphin. Binds angiotensin IV and may  
be the angiotensin IV receptor in the brain.  
-!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Cys-|-  
xaa, in which the half-cystine residue is involved in a disulfide  
loop, notably in oxytocin and vasopressin.  
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
-!- SUBUNIT: Homodimer. Binds tankyrase 1 and 2.  
-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted.  
During pregnancy serum levels are low in the first trimester, rise  
progressively during the second and third trimester and decrease  
rapidly after parturition. In brain only the membrane-bound form  
is found. The protein resides in intracellular vesicles together  
with GLUT4 and can then translocate to the cell surface in  
response to insulin and/or oxytocin. Localization may be  
determined by dileucine internalization motifs, and/or by  
interaction with tankyrases.  
-!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=3;  
Comment=Experimental confirmation may be lacking for some  
isoforms;  
Name=1;  
IsoId=Q9UIQ6-1; Sequence=VSP\_005448;  
Name=2;  
IsoId=Q9UIQ6-2; Sequence=VSP\_005448;  
Name=3;  
IsoId=Q9UIQ6-3; Sequence=VSP\_005449;  
-!- TISSUE SPECIFICITY: Highly expressed in placenta, heart, kidney  
and small intestine. Detected at lower levels in neuronal cells in  
the brain, in skeletal muscle, spleen, liver, testes and colon.  
-!- PTM: The pregnancy serum form is derived from the membrane-bound  
form by proteolytic processing.  
-!- PTM: N-glycosylated.  
-!- SIMILARITY: Belongs to the peptidase M1 family.  
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or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
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Db 800 GlnAsnGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGluLeu 819
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Qy 2851 ACTCTGAGGACTTCGCTA 2868
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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:R43008E13 product: type 1 tumor necrosis factor
DE receptor, shedding aminopeptidase regulator, full insert sequence.
DE (Fragment).
GN Name=Arts1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK040350; BAC30569.1; -.
DR MGD; MGI:1933403; Arts1.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005615; Extracellular space; TAS.
DR GO; GO:0004178; Fibrinogen aminopeptidase activity; IDA.
DR GO; GO:0004239; Fibrinogen aminopeptidase activity; IDA.
DR GO; GO:0045766; P-positive regulation of angiogenesis; IMP.
DR InterPro; IPR001930; Peptidase_M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
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RP SEQUENCE 694 AA; 80186 MW; B1EA3680BBC60BCB CRC64;
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DB	81	ArgGluSerSerLeuLeuTyraIaAspLysGlyLysSerSerAlaSerSerLysLeuGlyIle	100						
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QY	1570	ATGCTCGCTTCTGGGGGAAATTCAGAGGTCAAGAGATGATGACTACATGACTCTC	1629						
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QY	1630	CAGAAAGGAATCCCTCGTGGTGTAAACAAGACGGGTGTTCACCTCCGACTCCAACAG	1689						
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DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	03-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	MGC69084	protein.	
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OC	Eukaryota;	Metazoa;	Chordata;
OC	Amphibia;	Batrachia;	Anura;
OC	Xenopodinae;	Xenopus.	
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RP	TISSUE=Spleen;		
RC	MEDLINE=22398257;	PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
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RA	Rana S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
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RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
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RC	TISSUE=Spleen;		
RX	MEDLINE=22341132;	PubMed=12454917; DOI=10.1002/dvdy.10174;	
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,		
RA	Richardson P.;		
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus		
RT	initiative."		
RL	Dev. Dyn. 225:384-391(2002).		
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RA	Klein S., Strausberg R.;		
RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.		
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DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
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DR	Pfam; PF01433; Peptidase_M1; 1.		
DR	PRINTS; PR00756; ALADIPTASE.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.		
SQ	SEQUENCE 997 AA; 113619 MW; 46050EC895D2A14 CRC64;		
Alignment Scores:			
Pred. No.:	4e-116	Length:	997
Score:	1847.00	Matches:	383
Percent Similarity:	59.19%	Conservative:	161
Best Local Similarity:	41.68%	Mismatches:	287
Query Match:	36.49%	Indels:	88
DB:	2	Gaps:	16

US-10-039-073-3 (1-2883) x Q6PCGS (1-997)			
QY	157	TTCCAGTAGCCACTAATCGGGAACGATTTCTTGTGCAGGAGCTAAGGCTCCCGAGTGTG	216
Db	150	TyrProIleAlaArgAsnGlyLysValPheProTrpPalaIleSerArgLeuProAsnSer	169
QY	217	GTCAATTCCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTTGTT	276
Db	170	IleLysProIleHisTyrIleLeuThrLeuHisProAsnMetThrThrMetSerPheThr	189
QY	277	GCATCTGAGAAGATCGAAGCTCTTGTGCAGCAATGCTACCCAGTTTATCATCTTGCACAGC	336
Db	190	GlyThrValGlnIleAsnLeuAsnIleThrAlaArgSerLysAsnIleValLeuHisSer	209
QY	337	AAAGATCTTGAATCAGCAATGCCACCTTCAGTCAGAGGAGAGATCAAGATACATGAAA	396
Db	210	SerAspLeuArgIleThrLysAlaAsnVal-----LeuVal	221
QY	397	CCAGGA-----AAAGAACTGAAAGTTTGGATTACCTGCTCATGAACAAATTGCA	447
Db	222	ProGlyGlyThrThrMetAspAlaGluValLeuGluTyrProArgPheGluGluIleAla	241
QY	448	CTGCTGGTTCAGAGAACTTAGCCTCACCTGGAATACTATCTGCTGCTATGACTTCCAA	507
Db	242	IleIleSerProGluSerLeu---ProLysGlyAsnCysLeuLeuThrIleGluTyrThr	260
QY	508	GCCAACTTAGGTGATGGCTTTGAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGT	567
Db	261	SerAsnPheSerSerSeryTyrGlyPheTyrLysIleAspTyrMetAspLysGlySer	280
QY	568	GAACAAGAAATTTCTTCAGTAAACAGATTTTGAGCCAAACCCAGCAGCATGGCTTCCCT	637
Db	281	Lys---ArgSerLeuAlaIaThrGlnPheGluProThrAlaAlaArgLysAlaPhePro	299
QY	628	TGCTTTGATGAACCGTTGTTTCAAAGCCAACTTTTCAATCAAG---ATACGAAGAGAGAC	684
Db	300	CysPheAspGluProAlaPheLysSerThrPheGlnIleAsnIleArgLysAspGlu	319
QY	685	AGGCATATTGCACTATCCAACTGCCCCAAGGTTTAAGACAAATTGAACCTTGAAGGAGGTCTT	744
Db	320	SerMetIleSerLeuSerAsnMetProLysAlaLysThrSerThrThrAsnAspGlyLeu	339
QY	745	TTGGAAGATCACATTTTGAATACTACTGTAAATAAGTAGTACATACCTGTAGCCTACATAGTT	804
Db	340	LeuLeuAspGluPheSerThrSerValLysMetSerThrTyrLeuValAlaPheIleVal	359
QY	805	TGTGATTTCCACTCTCTGAGTGGCTTCATTCATCAGGGGTCAAGGTGCTCATATGCA	864
Db	360	GlyAspIleLysAsnThrThrArgGluThrAsnAspThrLeu---ValSerValTyrThr	378
QY	865	TCCCCAGACAAACGGGAATCAACACATTTATGCTTTTCAGGCATCATCAAGCTTACTTGAT	924
Db	379	ValProGluLysThrAspGlnValLysTyrAlaLeuAspSerAlaValLysLeuLeuAsp	398
QY	925	TTTTATGAAAAGTACTTTTGATATCTACTATCCACTCTCCAAACTGGATTAATTGCTATT	984
Db	399	PheTyrSerAsnTyrTyrGlyIleLysTyrProLeuGluLysLeuAspLeuValAlaIle	418
QY	985	CTGACTTTGACCTGGAGCCATCGGAAATTTGGGGCTCATTCATATAGGGAGAGCTCA	1044
Db	419	ProAspPheGlnAlaAlaMetGluAsnTrpGlyLeuIleThrPheArgGluThrSer	438
QY	1045	CTGCTTTTGGACCCCAAGACCTCTTCTGCTTCGATAAACTGGGGTCCACAGAGTCATA	1104
Db	439	LeuLeuTyrAsnGluAspSerSerIleLysAspLysGlnThrIleThrIleAlaIle	458
QY	1105	GCCCATGAATCGCGCACCAAGTGGTTTGGCAACCTCGTCAATGAATGGTGAATGAT	1164
Db	459	AlaHisGluLeuThrHisGlnTrpPheGlyAsnLeuValThrMetGluTrpTrpAsnAsp	478
QY	1165	ATTGGCTTAAGGAGGGTTTGCAAAATACATGGAACCTTATCGCTGTTAATGCTACATAT	1224
Db		-----	----

Db 479 LeuTrpLeuAsnGluGlyPheAlaThrTyrMetGluTyrPheSerValSerSerLeuPhe 498  
Qy 1225 CCAGAGTCGCAATTTGATGACTATTTTTTGAATGTGTTTTGAAGTAATTTACAAAGAT 1284  
Db 499 ProGluLeuAsnSerGluAsnSerPheLeuLysMetArgPheMetAlaLeuLysLysAsp 518  
Qy 1285 TCATTGAATTCATCCCGCCCTATCTCCAAACAGCGGAAACCCGACCTCAATACAGAA 1344  
Db 519 SerLeuAsnAlaSerHisProIleSerThrAspIleArgSerProGluGlnIleGlu 538  
Qy 1345 ATGTTTGAATGAGTTTCTTATAACAGGGAGCTGTTATTTTGAATATCTCAAGGATTTT 1404  
Db 539 MetPheAsnAspLeuSerTyrIleLysGlyAlaSerIleLeuLeuMetLeuLysThrPhe 558  
Qy 1405 CTGGGTGAGGAAATTCAGAAAGGAATAATTCAGTACTTAAGAAAGTTCAGCTATAGA 1464  
Db 559 LeuSerGluAspMetPheHisLeuSerIleArgSerTyrLeuGlnSerHisGlnTyrGly 578  
Qy 1465 AATGCTAAGATGACTCTGGAGCAGTCTGTCAATAGTGTGTTTGAAGTGTATTT 1524  
Db 579 SerThrThrSerAspSerLeuTrpAspSerLeuAsn----- 590  
Qy 1525 ACATCTGGTGGAGTTGTTCATTCGGATCCCAAGATGACAAGTAAACATGCTCGCCTTTCTG 1584  
Db 591 -----ValValThr 593  
Qy 1585 GGGGAAATGCAGAGGTCAAGAGATGATGACTACATGACTCTCCAGAAAGGAATCCCC 1644  
Db 594 LysGluAsnProAsnValLysAsnMetMetLysThrTrpGlnLysAlaGlyTyrPro 613  
Qy 1645 CTGCTGGTGGTTAAACAGACGGGTTCATCTCCGACTGCAACAGGAGCGTCTCTCCAG 1704  
Db 614 LeuValThrAlaLeuArgLysGlyGluIleThrValArgGlnGluArgPheLeuArg 633  
Qy 1705 GGGGTTTCCAGGAAGACCTGAATGGAGGCGCTCGCAGGAGAGTACTCTGGCATATC 1764  
Db 634 SerThr-----LysProAsp---HisAlaThrAsnAlaSerThrValTrpHisIle 649  
Qy 1765 CCATGACCTACTCCACGAGTTCTTCTAATGTGATCCACAGA-----CAC 1809  
Db 650 ProLeuThrTrpValThrLysLysCysAsnGlyValAspProAspCysAspLysValTyr 669  
Qy 1810 ATTTAAATCAACAGACAGTACTCTGATCTACTGAAAGACAGCTTGGTGAATTT 1869  
Db 670 LeuLeuLysAlaProThrGlyThrIleAsnValSerSerGluPheProTrpValLysPhe 689  
Qy 1870 AATGTGACTCAAATGGTTTACTACATCTCTACATGAGGTCTAGTGGTGGCAACATC 1929  
Db 690 AsnValAsnMetThrGlyTyrTyrIleValAspTyrGlyAlaAspGlyTyrPaspAlaLeu 709  
Qy 1930 ATTACACAGCTGAATCAGAACCCACACTTCTCAGACCTTAAGGACAGAGTAGGTCTGATT 1989  
Db 710 IleGluGlnLeuHisArgAspHisThrValLeuHisSerSerAspArgAlaAsnLeuIle 729  
Qy 1990 CATGATGTGTTTACAGTAGTTGGTCAGGAGACTGACCTAGAACAGCTCTTGACATG 2049  
Db 730 HisAspIlePheMetLeuAlaGlyValGlyLysValProLeuAlaLysAlaPheLysLeu 749  
Qy 2050 ACTTACTACTCCCAATCAACAGACCGCCCGACCTCTCTCGAAGGTCTGAGTTACTTG 2109  
Db 750 LeuGlyTyrLeuValAsnGluThrAspSerAlaProIleIleGlnAla-----Leu 766  
Qy 2110 GAATCGTTTATCCAC-----ATGATGACAGAGGAATATTTACAGATATCTCGAA 2160  
Db 767 HisGlnPheTyrHisIleArgGlyIleLeuLeuLysArgGlyLeuAspAspLeuSerAsp 786  
Qy 2161 AACCTCAAGCGTTACTCTTCCAGTATTTTAAAGCAGTGTATGACCAAGCAAGCTGGAGT 2220  
Db 787 LysLeuMetGluArgGlyLeuAspLeuLeuAsnAsnThrLeuIleLysGlnThrTrpLys 806  
Qy 2221 GACAGGGCTCAGTCTGGACAGGATGCTCGCTCGGCTCTCTTCAAGCTGGCCTGTGAC 2280  
Db 807 AspGluGlyThrLeuAlaGluArgGluLeuArgThrSerLeuLeuAspPheAlaCysSer 826

Qy 2281 CTGAACCATGCTCTTCCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGAATCC 2340  
Db 827 AsnGlyValLeuAsnCysLeuAspArgAlaThrGluLeuPheAsnSerTrp-----Arg 844  
Qy 2341 AGTGGAAATTTAAATATACCAACACAGATGTTTAAAGATTTGTGATTCTTGTGGGTGCAC 2400  
Db 845 PheAsnGluThrArgIleProSerAspValIleAsnIleValPheLysValGlyThrLys 864  
Qy 2401 ACAACACAGCATGGAATACCTTTTAGACAATATCAATCAATGTCAAGTGTGCTGAA 2460  
Db 865 ThrThrGluGlyTyrThrPheLeuArgArgTyrAspSerSerIleTyrGluSerGlu 884  
Qy 2461 CAAAACAAAATTCGTATGCTTTTCTCAACGACGACATCAGGAAAGTACTGACGTTA 2520  
Db 885 LysSerLysIleLeuGluAlaLeuAlaSerThrAspAsnAlaLysAspLeuGlnGlyLeu 904  
Qy 2521 ATTGAACCTAGCAATGGAAGGAAGGTTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580  
Db 905 MetGlnGluSerLeuAlaGlyGlySerIleArgSerGlnGluLeuProAsnValIleSer 924  
Qy 2581 GCGATTCACAGACGTCCTCAAGGGGACAGCAACTAGCATGGGATTTTGAAGAGAAATGG 2640  
Db 925 PheIleCysArgArgSerProGlyTyrLeuLeuAlaTrpAsnPheValLysGlnAsnTrp 944  
Qy 2641 ACCATCTTCTGAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGGC 2700  
Db 945 AsnLeuIleThrGlnLysLeu----- 951  
Qy 2701 ACAACAGCTCACTTT-----TCTTCAAGGATAAGTTGCAAGAGGTGAAACTATTTT 2754  
Db 952 -----LeuHisPhePheAsnSerThrLysGluLysSerArgGluValTyrTyrValLys 969  
Qy 2755 GAATCTCTTGGAGGCTCAAGGATCATCTCGATATTTTCAAACTGTTCTGGAAACGATA 2814  
Db 970 GluAla-----LeuGluThrIle 975  
Qy 2815 ACCAAAATATATAATGCTGGAGAGAACTTCCGACTCTGAGGACTTGGCTAATG 2871  
Db 976 LysLeuAsnIleLysTrpMetLysAsnAsnLeuAspSerLeuLysThrTrpLeuLeu 994

RESULT 15  
Q8WVJ4  
ID Q8WVJ4 PRELIMINARY; PRT; 350 AA.  
AC Q8WVJ4; 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE LRAP protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences."; [2]  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017927; AH17927.1; -.  
DR MEROPS; M01.024; -.  
DR GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR PRINTS; PR00756; ALADIP7ASE.  
SQ SEQUENCE 350 AA; 40060 MW; 5234F40276A81253 CRC64;

Alignment Scores:  
Pred. No.: 1.29e-105 Length: 350  
Score: 1690.00 Matches: 322  
Percent Similarity: 99.69% Conservative: 2  
Best Local Similarity: 99.08% Mismatches: 1  
Query Match: 33.39% Indels: 0  
DB: 2 Gaps: 0

US-10-039-073-3 (1-2883) x Q8WVJ4 (1-350)

QY	1	ATGTTCCATCTCTGCAATGGTTAATTACACAGAAAACCAATGTTTAAACATTCACAGA	60
DB	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
QY	61	GGATTTTACTGCTTAAACAGCCATCTGCCCCAAATATGCATTTGTTCTCAGTTCTCAGTG	120
DB	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnileCysileCysSerGlnPheSerVal	40
QY	121	CCATCTAGTTATCACTTCACTAGGATCTCGGGGCTTCCAGTAGCCACTAATGGGAA	180
DB	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	181	CGATTTCTGGCAGGAGCTAAGGCTCCCGAGTGGTCTATCTCTCCATTATGACCTC	240
DB	61	ArgPheProIrpGlnGluLeuArgLeuProSerValVallleProLeuHisTyrAspLeu	80
QY	241	TTGTGTCACCCCAATCTCACTCTCTGGACTTTGTTGSCATCTGAGAGATCGAAGTCTTG	300
DB	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	301	GTGAGCAATGCTACCCAGTTTATCATCTTCACAGCAAAAGATCTTGAATCAGCAATGCC	360
DB	101	ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
QY	361	ACCTTCAGTCAGAGGAAGATTCAAGATACATGAAACACGAGAAAGAACTGAAAGTTTG	420
DB	121	ThrLeuGlnSerGluGluAspSerLysTyrMetLysProGlyLysGluLeuLysValLeu	140
QY	421	AGTTACCCCTGCTCATGAACAAATTCACACTGCTGTTCCAGAGAACTTAGCCCTCACCTG	480
DB	141	SerTyrProAlaHisGluGlnIleAlaLeuValProGluLysLeuThrProHisLeu	160
QY	481	AAATACATATGGCTATGACTTCCAAAGCCAAAGTTAGGTGATGGCTTTGAAGGTTTTAT	540
DB	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	541	AAAGCACATACAGAACTCTGGTGGTGAACAGATTCCTGCAGTAAACAGATTTTGAG	600
DB	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	601	CCAAACCCAGCAGCATGGCTTTCCCTTGCTTGTGATGAACCGTTGTTCAAAGCCAACTTT	660
DB	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220
QY	661	TCAATCAAGATACGAGAGAGAGCAGGCATATTGCATATCCAAACATGCCAAAGGTTAAG	720
DB	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240

QY	721	ACAATTGAACCTTGAGGAGGTCTTTTGGAGATCACTTTGAAACTACTGTAAAAATGAGT	780
DB	241	ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer	260
QY	781	ACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACATCA	840
DB	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	841	GGGTCGAAGGTGTCCATCTATGCATCCCGACACAAACGGAATCAACACACATATGCTTG	900
DB	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	901	CAGGCATCACTGAAGCTACTTGTATTTTATGAAAAGTACTTTTGATATCTACTATCCACTC	960
DB	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu	320
QY	961	TCCAAACTGGATTTA	975
DB	321	SerLysLeuGlyMet	325

Search completed: September 26, 2005, 07:44:30  
Job time : 537.896 secs

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 26, 2005, 06:04:35 ; Search time 354.781 Seconds  
(without alignments)  
6285.736 Million cell updates/sec

Title: US-10-039-073-3  
Perfect score: 5062  
Sequence: 1 atgttcattcttctgcaat.....ggctaagtgttaactactaa 2883

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO spool\_p/US10039073/runat\_26092005\_070409\_21298/app\_query.fasta\_1.6606  
-DB=A\_Geneseq -QFMT=fatcat -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10039073 @CNC 1 1 933 @runat 26092005\_070409\_21298 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUEY -NEG-SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5052	99.8	960	AAB60299	Human ami
2	5052	99.8	960	AAB60299	Human pro
3	5048	99.7	960	ABP69122	Human pol
4	4141	81.8	785	ABP63022	Human pol
5	3799	75.0	728	ABP63022	Human pol
6	3799	75.0	728	ABP66925	Human pol
7	3770	74.5	722	AAU22999	Novel hum
8	3770	74.5	722	ABP67098	Human pol
9	3770	74.5	722	ABP67098	Human pol
10	3763	74.3	722	ADR41453	Human CD-

11	2515.5	49.7	941	4	AAU07829	Human ART
12	2515.5	49.7	941	5	ABP90347	Human pol
13	2515.5	49.7	941	6	ADA56820	Human sec
14	2515.5	49.7	941	6	ABR47686	Human sec
15	2515.5	49.7	941	6	ABR00040	Human gen
16	2515.5	49.7	941	7	ADB91494	Human sec
17	2515.5	49.7	941	7	ADC74064	Human sec
18	2515.5	49.7	941	7	ADD37852	Human sec
19	2515.5	49.7	944	4	AAAG75607	Human col
20	2512.5	49.6	941	3	AAAY66736	Membrane-
21	2512.5	49.6	941	3	AAAB24422	Human PRO
22	2512.5	49.6	941	4	AAU12403	Human PRO
23	2512.5	49.6	941	4	AAAB65259	Human PRO
24	2512.5	49.6	941	6	ABU58074	Human PRO
25	2512.5	49.6	941	6	ABU59152	Novel hum
26	2512.5	49.6	941	6	ABU82664	Human sec
27	2512.5	49.6	941	6	ABO17847	Novel hum
28	2512.5	49.6	941	6	ABU60583	Human sec
29	2512.5	49.6	941	6	ABU13965	Human PRO
30	2512.5	49.6	941	6	ABU81101	Human PRO
31	2512.5	49.6	941	6	ABU72550	Novel hum
32	2512.5	49.6	941	6	ABU66801	Human PRO
33	2512.5	49.6	941	6	ABU59882	Novel sec
34	2512.5	49.6	941	6	ABU59299	Human sec
35	2512.5	49.6	941	6	ABO25996	Human PRO
36	2512.5	49.6	941	6	ABO25072	Human sec
37	2512.5	49.6	941	6	ABU59005	Human sec
38	2512.5	49.6	941	6	ABU92383	Novel hum
39	2512.5	49.6	941	6	ABU59448	Novel hum
40	2512.5	49.6	941	6	ABU67077	Human sec
41	2512.5	49.6	941	6	ABU92214	Novel hum
42	2512.5	49.6	941	6	ABU10920	Human PRO
43	2512.5	49.6	941	6	ABU81672	Novel hum
44	2512.5	49.6	941	6	ABU88611	Human sec
45	2512.5	49.6	941	6	ABO34125	Human PRO

ALIGNMENTS

RESULT 1  
AAB60299  
ID AAB60299 standard; protein; 960 AA.  
XX

AC AAB60299;

DT 06-APR-2001 (first entry)

XX Human aminopeptidase 17867.

DE Human aminopeptidase 17867.

XX Human aminopeptidase 17867; neutral zinc metalloproteinase;

KW zinc-binding region; M1 aminopeptidase family; lung disorder;

KW colon disorder; lung cancer; colon cancer; breast cancer; tumour;

KW squamous cell carcinoma; insulin-related disorder; diabetes;

KW drug screening.

OS Homo sapiens.

XX WO200100811-A2.

PN 04-JAN-2001.

XX 30-JUN-2000; 2000WO-US018250.

XX 30-JUN-1999; 99US-00345650.

XX (MILL-) MTLENNIUM PHARM INC.

XX PI Kapeller-Libermann R, Williamson M;

XX WPI; 2001-137953/14.

DR N-FSDB; AAF27148.

PT Novel human aminopeptidase polypeptide and polynucleotide useful as

PT target for diagnosis and treatment in aminopeptidase-related disorders  
XX and for identifying modulators of therapeutic use.  
PS Claim 9; Fig 1; 92pp; English.

XX The invention relates to a novel human aminopeptidase, designated  
CC aminopeptidase 17867 (AAB60299) and to cDNA encoding aminopeptidase 17867  
CC (AA227148). Human aminopeptidase 17867 contains a neutral zinc  
CC metalloproteinase zinc-binding region signature motif at residues 367-376,  
CC and an M1 aminopeptidase signature motif at residues 334-338. The  
CC invention also relates to host cells comprising human aminopeptidase  
CC 17867 DNA, the preparation of the protein, an antibody which binds to the  
CC protein, methods of detection of the protein, methods of modulating  
CC activity of the protein, and methods of identifying modulators of protein  
CC activity. Aminopeptidase 17867 proteins and nucleic acids are useful as  
CC targets for diagnosis and treatment in aminopeptidase-related diseases.  
CC Such diseases include a wide variety of lung disorders (e.g., pulmonary  
CC embolism, pulmonary hypertension, emphysema, bronchial asthma) and colon  
CC disorders (e.g., diarrhoea, dysentery, Crohn's disease, ulcerative  
CC colitis). In particular, they may be used in the diagnosis and treatment  
CC of breast and colon carcinoma, lung carcinoma (especially squamous cell  
CC carcinoma), and insulin-related disorders such as diabetes. The  
CC aminopeptidase 17867 proteins are also useful in drug screening methods  
CC to identify modulators of activity, and for raising antibodies for use in  
CC diagnosis and treatment. The present sequence represents human  
CC aminopeptidase 17867

XX SQ Sequence 960 AA;

#### Alignment Scores:

Pred. No.: 0 Length: 960  
Score: 5052.00 Matches: 960  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.80% Indels: 0  
DB: 4 Gaps: 0

US-10-039-073-3 (1-2883) x AAB60299 (1-960)

Qy	1	ATGTTCCATCTTCTGCAATGGTTAAATTCACAGAAACCAACGTTTAACTTCACAGA	60
Db	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
Qy	61	GGATTTTACTCTTAAACAGCCATCTGCCCAATATGCAATTCCTCTCAGTCTCAGTG	120
Db	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
Qy	121	CCATCTAGTTATCACTTCACTGAGGATCTCGGGCTTCCAGTAGCCACTAATGGGAA	180
Db	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
Qy	181	CGATTTCTTGGCAGGAGTAAGCTCCCACTGTGTCTCTCTCCATTATGACCTC	240
Db	61	ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu	80
Qy	241	TTTGTCCACCCCAATCTCACCTCTCTGGACTTGTGTGTCATCTGAGAAGATCGAAGTCTG	300
Db	81	PheValHisProAsnLeuThrSerLeuAspPheValIleSerGluLysIleGluValLeu	100
Qy	301	GTCAGCAATGTCACCAAGTTTATCATCTTGACAGCAAAAGATCTTGAATCACGAATGCC	360
Db	101	ValSerAsnAlaThrGlnPheIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
Qy	361	ACCTTCAGTCAGAGGAAGATTCAGATACATGAAACCCAGAAAGAACTGAAGTTTGTG	420
Db	121	ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140
Qy	421	AGTTACCTGCTCATGAACAATGCACTGCTGTTCCAGAGAACTTACCCCTCACCTG	480
Db	141	SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160
Qy	481	AAATACTATGTGGCTATGCACTTCCAAGCCCAAGTTAGTGTGCTTGAAGGTTTAT	540

Db	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
Qy	541	AAAAGCACATACAGAACTCTTGCTGTGAAACAGAAATCTTCAGTAAACAGATTTTGAG	600
Db	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
Qy	601	CCAACCCAGCAGCATGGCTTCCCTTGTGTTGATGAACCGTTGTTCAAAGCCAACTTT	660
Db	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220
Qy	661	TCAATCAAGATACGAAGAGAGCAGGCATATTGCATATCCAAATGCCAAAGGTTAAG	720
Db	221	SerIleLysIleArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
Qy	721	ACAATTTGAATTCGAAGAGTCTTTTGGAGATCACTTTGAAACTACTGTAAAAATGAGT	780
Db	241	ThrIleGluLeuGlyGlyLeuGluAspHisPheGluThrThrValLysMetSer	260
Qy	781	ACATACCTTGTAGCCTACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCACTTCA	840
Db	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
Qy	841	GGGGTCAAGGTGTCCATCTATGATCCCCAGACAAACGGAATCAACACATTTATGCTTG	900
Db	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
Qy	901	CAGGCATCACTGAAGCTACTTGTATTTTATGAAAGTACTTTTCATATCTACTATCCACTC	960
Db	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrProLeu	320
Qy	961	TCCAAACTGGATTTAAATTTGCTATTCCTGACTTTTGCACCTGGAGCCATGGAAAAATGGGC	1020
Db	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
Qy	1021	CTCATTTACATATAGGAGAGCTGCTCTTTTGGACCCCAAGACCTCTTCTGCTCCGAT	1080
Db	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
Qy	1081	AAACTGTGGTCAACAGAGTCATAGCCCATGAACTGGCGCACCACTGGTTTGGCAACTG	1140
Db	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
Qy	1141	GTCACAATGGAATGGTGAATGATTTTGGCTTAAAGAGGGTTTGCAAAATACATGGAA	1200
Db	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
Qy	1201	CTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTTGATCACTATTTTGAATGTG	1260
Db	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
Qy	1261	TGTTTTGAAAGTAAATTAACAAAGATTCATTAATTCATCCCGCCTATCTCCAAACACAGCG	1320
Db	421	CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla	440
Qy	1321	GAAACCCCGACTCAATACAGGAAATGTTTGTGATGAAGTTTCCATTAAACAGGAGCTTGT	1380
Db	441	GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
Qy	1381	ATTTTGATATGCTCAAGGATTTTTCGGGTGAGAGAAATTCAGAGAGGAATTAATTCAG	1440
Db	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleIleGln	480
Qy	1441	TACTTAAAGAAAGTTTCAAGTATAGAAATGCTAAGAATGATCACTTGTGGAGCAGTCTCTCA	1500
Db	481	TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer	500
Qy	1501	AATAGTTGTTTAAAGAGTGAATTTTACATCTGGTGGAGTTTGTTCATTTCGGATCCCAAGATG	1560
Db	501	AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet	520
Qy	1561	ACAAGTAACTGCTCGCTTCTGGGGGAAATTCAGAGGCTCAAGAGATGATGACTACA	1620
Db	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	540

QY 1621 TGGACTCTCCAGAAAGGAATCCCTCGTGTGGTTAAACAAGACGGGTGTTCACTCCGA 1680  
DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560  
QY 1681 CTGCAACAGGAGCGCTTCTCCAGAGGGGTTTTCCAGGAAGACCCCTGAATGGAGGCGCCCTG 1740  
DB 561 LeuGlnGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 580  
QY 1741 CAGGAGAGGTACTCTGTGGCATATCCCATTTAGCTACTCCACAGATTTCTTAATGTGATC 1800  
DB 581 GlnGluArgTyrLeuTrpHisIleProLeuThrThrSerThrSerSerAsnValIle 600  
QY 1801 CACAGACATTTCTAAATCAAGACAGATCTCTGGATCTACCTGAAAGACCAAGTGG 1860  
DB 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
QY 1861 GTGAATTAATGTCGACTCAATCGTTACTACATCGTTTCACTATGAGGTCATGATGG 1920  
DB 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
QY 1921 GACCAACTCATTACACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAGGACAGATA 1980  
DB 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
QY 1981 GGTCTGATTCATGATGTGTTTTCAGCTAGTGTGTGAGGAGACTGACCTAGACAAAGCT 2040  
DB 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
QY 2041 CTTGACATGACTTACTCTCAACATGAACAGACAGCCCGCACTTCTCGAAGCTGTG 2100  
DB 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700  
QY 2101 AGTTACTTGGAAATCGTTTACCATGATGACAGAGAATATTTACAGATATCTCTGAA 2160  
DB 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720  
QY 2161 AACCTCAAGCGTTACTCTTTCAGTATTTTAAAGCAGTGTATGACAGCAAGCTGGAGT 2220  
DB 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
QY 2221 GACAGGCTCAGTCTGGACAGGATGCTCCGCTGGCTCTTTCAGCTGCGCTGCAC 2280  
DB 741 AspyLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
QY 2281 CTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGGAATCC 2340  
DB 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
QY 2341 AGTGAATAATTAATATACCAACAGATGTTTAAAGATGTGTATTTCTGTGGTCTCAG 2400  
DB 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800  
QY 2401 ACAACAGCAGGATGGAATACCTTTTAGGCAATATGAATGCTCAATGCTCAAGTCTGAA 2460  
DB 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820  
QY 2461 CAAACAAATTTCTGTATCTTGTTCACAGCAAGCATCAGAAAAGTTACTGAAGTTA 2520  
DB 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840  
QY 2521 ATTGAACATAGGAATGGAAGGAAGTTATCAAGACACAGAACTTCGCGAGCTCTCTTCAT 2580  
DB 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeuLeuHis 860  
QY 2581 GCGATTGCCAGAGTCCAAAGGGGAGCAACTAGCATGGATTTTGAAGAGAAATGG 2640  
DB 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
QY 2641 ACCCATCTTCTGAAAAATTTCTGACCTTGGGCTCATATGACATAGATGATATCTCTGGC 2700  
DB 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900

QY 2701 ACACAGCTCACTTTTCTTCCAGGATAAGTTGCAAGAGGTGAACATATTTTGAATCT 2760  
DB 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920  
QY 2761 CTTGAGGCTCAAGGATCACATCTCGATATTTTCAAACTGTTCTCGAAACGATAACCAA 2820  
DB 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940  
QY 2821 AATATAAATGGCTGGAGAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAATACT 2880  
DB 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960  
RESULT 2  
ID AAE04879 standard; protein; 960 AA.  
XX AAE04879;  
XX 10-SEP-2001 (first entry)  
XX Human protease protein-6 (PRTS-6).  
XX Human; protease protein-6; PRTS-6; cytostatic; hypotensive; gene therapy;  
KW gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;  
KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;  
KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;  
KW acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;  
KW developmental disorder; epithelial disorder; eczema; dementia; neuropathic;  
KW neurological disorder; reproductive disorder; infertility; teratogenesis;  
KW immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;  
KW anaemia; antitumour; antiviral; antibacterial.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT Peptide 1..35  
FT Protein /label= Signal\_peptide  
FT Binding-site 36..960 /note= "Mature human PRTS-6"  
FT Binding-site 367..377 /label= Zinc\_binding\_region  
FT Binding-site 367..376 /label= Zinc\_binding\_region  
XX WO200146443-A2.  
XX 28-JUN-2001.  
XX 19-DEC-2000; 2000WO-US034811.  
XX 23-DEC-1999; 99US-0172055P.  
XX 21-JAN-2000; 2000US-0177334P.  
XX 28-JAN-2000; 2000US-0178884P.  
XX 02-FEB-2000; 2000US-0179903P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;  
PI Yue H, Nguyen DB, Tang VT, Yao MG, Lal P;  
XX WPI; 2001-418080/44.  
DR N-PSDB; AAD09543.  
XX Novel human protease proteins (PRTS) useful for diagnosing, treating,  
PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,  
PT cell proliferative disorders associated with abnormal expression of PRTS.  
XX Claim 1; Page 110-112; 129pp; English.  
XX The present sequence is human protease protein (PRTS-6). Human PRTS and  
CC its nucleic acid molecule are useful for the diagnosis, treatment and  
CC prevention of disorders associated with increased or decreased expression  
CC of PRTS. Examples of such disorders include, gastrointestinal disorder

CC such as anorexia, dysphagia; cardiovascular disorder such as  
 CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as  
 CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative  
 CC disorder such as actinic keratosis, cirrhosis; developmental disorder  
 CC such as epilepsy, anaemia; epithelial disorder such as allergic contact  
 CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,  
 CC dementia and reproductive disorder such as infertility and teratogenesis.  
 CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or  
 CC transgenic animals (mice or rats) to model human disease. PRTS DNA is  
 CC also in use for therapy. PRTS and its immunogenic fragments are  
 CC useful for screening libraries of compounds in several drug screening  
 CC assays. PRTS is useful for analysing the proteome of a tissue or cell  
 CC type

xx SQ Sequence 960 AA;

Alignment Scores:

Pred. No.: 0 Length: 960  
 Score: 5052.00 Matches: 960  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.80% Indels: 0  
 DB: 4 Gaps: 0

US-10-039-073-3 (1-2883) x AAE04879 (1-960)

Qy 1 ATGTTCCATTCTCTGCAATGGTTAAATTCACACAGAAAACCAATGTTTAACTTCACAGA 60  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20  
 Qy 61 GGATTTTACTGCTTAACAGCCATCTTGCCCCAANAATATGCAATTTGTTCTCAGTCTCAGTG 120  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
 Qy 121 CCATCTAGTTATCACTCACTGAGATCCTGGGCTTCCAGTAGGACCTAATGGGAA 180  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
 Qy 181 CGATTTCTTGGCAGGAGTAAGGCTCCCAAGTGTGGTCAATCTCTCCATTAATGACCTC 240  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
 Qy 241 TTTGTCCACCCCAATCTCCTCTGAGCTTTGTCATCTTGAGATCTGAGAGATCGAAGTCTTG 300  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
 Qy 301 GTCAGCATGCTACCCAGTTATCATCTTCACAGCAAGATCTTGAATCAGCAATGCC 360  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
 Qy 361 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAACACGAGMAAAGAACTGAAAGTTTG 420  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
 Qy 421 AGTTACCTGCTCATGAACAAATTCGACTGCTGGTCCAGAGAACTTACCCCTCACCTG 480  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
 Qy 481 AAATACTATGTGGCTATGGACTTCCAGCCAGTAGTAGTGTGCTTTGAGGGTTTAT 540  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
 Qy 541 AAAAGACATACAGAACTCTTGGTGGTGAACAAGAAATCTTTCAGTAACAGATTTTGAG 600  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200  
 Qy 601 CCAACCCAGGCAACCATGGCTTCCCTTGTGTTGATGAACCGTTGTTTCAAAGCCAACTTT 660  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
 Qy 661 TCATCAAGATACCAAGAGAGAGAGCATATTCACATNTCCACATGTCACCAAGGTTAAG 720  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240

Qy 721 ACAATTGAACCTGAAGAGAGTCTTTTGGAGATCACCTTTGAAACTACTGTAAAAATGAGT 780  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 241 ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260  
 Qy 781 ACATACCTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA 840  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 261 ThrTyrLeuValAlaTyrIleValCysAppPheHisSerLeuSerGlyPheThrSerSer 280  
 Qy 841 GGGGTCAAGGTGTCCATCTATGATCATCCACAGACAAACGGAATCAAAACACATATGCTTTG 900  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
 Qy 901 CAGGCATCACTGAAGCTACTTGAATTTTATGAAAGTACTTTTCATCTACTATCCACTC 960  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
 Qy 961 TCCAAACTGGATTAATTTGCTATTCCTGACTTTTGACCTGGAGCCATGGAAAATTTGGGGC 1020  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTyrGly 340  
 Qy 1021 CTCATTTACATATAGGAGAGCTCACCTGCTTTTGGACCCCAAGACCTCTTCTGCTCCGAT 1080  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
 Qy 1081 AAACCTGGGTCAACAGAGCTATAGCCCATGAATCGCGCACCGAGTGGTTTGGCAACCTG 1140  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 361 LysLeuTyrValThrArgValIleAlaHisGluLeuAlaHisGlnTyrPheGlyAsnLeu 380  
 Qy 1141 GTCACAAATGGAATGGTGGAAATGATATTTGGCTTAAGAGGGTTTTCGAAAATCATGGAA 1200  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 381 ValThrMetGluTyrTrpAsnAspIleTyrLeuLysGluGlyPheAlaLysTyrMetGlu 400  
 Qy 1201 CTTATCGCTGTTAATCTCATATCCAGAGCTGCAATTTGAGACTATTTTGGATGTG 1260  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420  
 Qy 1261 TGTTTTGAAGTAAATTAACAAAGATTCATTTGAATTCATCCCGCCCTATCTCCAAACACAGCG 1320  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
 Qy 1321 GAAACCCCGACTCAAAATACAGGAATGTTTGTATGAAGTTTCTTATAACAGGGAGCTTGT 1380  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 441 GluThrProThrGlnIleGlnMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
 Qy 1381 ATTTTCAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGATAAATTCAG 1440  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480  
 Qy 1441 TACTTAAAGAAAGTTCAGCTATAGAAATGCTAGAATGATGACTTGTGGAGCAGTCTGTCA 1500  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTyrPheSerLeuSer 500  
 Qy 1501 AATAGTTGTTTGAAGAGTGAATTTATCTGGTGGAGTTTGTTCATTTCCGATCCCAAGATG 1560  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 501 AsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520  
 Qy 1561 ACAAGTAAACATGCTCCCTTCTGGGGGAAATTCAGAGGTCAAGAGATGATGACTACA 1620  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540  
 Qy 1621 TGGACTCTCCAGAAAGAAATCCCTCTGCTGGTGGTTTAAACAAGACGGGTGTTTCACTCCGA 1680  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 541 TrpThrLeuGlnLysGlyIleProLeuLeuValValLysGlnAspGlyCysSerLeuArg 560  
 Qy 1681 CTGCAACAGAGAGGCTTCTCCAGGGGGTTTTCAGGAAGAAGCCCTGAATGGAGGGCCCTG 1740  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTyrArgAlaLeu 580  
 Qy 1741 CAGGAGAGTACTGTGGCATATCCCATTCAGCTACTCCACGAGTCTTCTTAATGTGATC 1800  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsnValIle 600

```
QY 1801 CACAGACATTTCTAAATCAAGACAGACATCTCTGGATCTTACCTGAAAAGACAGTTGG 1860
Db |||||||
QY 601 HIsArGHIsIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
Db |||||||
QY 1861 GTGAATTTAATGTGCGATCAATGTTACTACATCGTTTCACTATGAGGTCATGATGG 1920
Db |||||||
QY 621 VAlLySPHeAsnValAspSerAsnGlyTrpYrIleValHisTrpGluGlyHisGlyTrp 640
Db |||||||
QY 1921 GACCAACTCATTTACAGCTGAATCAGAACCAACACACTTCTCAGACCTTAAGGACAGAGTA 1980
Db |||||||
QY 641 AspGlnLeuLeuThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
Db |||||||
QY 1981 GGTCTGATTCATGATGTTTTCAGCTAGTGTGTGAGGAGACTGACCTCAGACAAAGCT 2040
Db |||||||
QY 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
Db |||||||
QY 2041 CTTGACATGCTACTTACCTCAACATGAACAACAGCAGCCCGCACTTCTCGAAGTCTG 2100
Db |||||||
QY 681 LeuAspMetThrTrpYrTrpLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
Db |||||||
QY 2101 AGTTACTTGGAAATCGTTTACCACATGATGAGCAGAAGGAATATTTTCAGATATCTCTGAA 2160
Db |||||||
QY 701 SerTyLeuGluSerPheTrpHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720
Db |||||||
QY 2161 AACCTCAGCGTTACTCTTTCAGTATTTTAAAGCCAGTATGACAGGAAAGCTGGAGT 2220
Db |||||||
QY 721 AsnLeuLysArgTyLeuLeuGlnTrpPheLysProValIleAspArgGlnSerTrpSer 740
Db |||||||
QY 2221 GACAGGGCTCAGTCTGGACAGGATGCTCCGCTGGCTCTCTGAACTGGCTGGCTGAC 2280
Db |||||||
QY 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
Db |||||||
QY 2281 CTGAACCATGCTCTTGTGATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATGAATCC 2340
Db |||||||
QY 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780
Db |||||||
QY 2341 AGTGAAAATTAATATATACCAACAGATGTTTTAAAGATGTGTATTTCTGTGGTGCTCAG 2400
Db |||||||
QY 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTrpSerValGlyAlaGln 800
Db |||||||
QY 2401 ACACAGCAGGATGAATTACTCTTTAGGCAATATGAACTGTCAATCTCAAGTCTGAA 2460
Db |||||||
QY 801 ThrThrAlaGlyTrpAsnTrpLeuLeuGluGlnTrpGluLeuSerMetSerSerAlaGlu 820
Db |||||||
QY 2461 CAAAAAATAATCTGTATGCTTGTCAACAGCAGCATCTCAGAAAGTACTGAAGTTA 2520
Db |||||||
QY 821 GlnAsnLysIleLeuTyAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840
Db |||||||
QY 2521 ATTGAACCTAGGAATCGAAGGATTTATCAAGACACAGAACTTGGCAGCTCTCTTCTCAT 2580
Db |||||||
QY 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860
Db |||||||
QY 2581 GCGATTGCCAGCTCCAAAGGGGAGCACTAGCATGGATTTTGTAAAGAAAATTTGG 2640
Db |||||||
QY 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880
Db |||||||
QY 2641 ACCCATCTTCTGAAAAATTTGACTTGGCTCATATGACATGAAGATGATCATCTCTGGC 2700
Db |||||||
QY 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyAspIleArgMetIleIleSerGly 900
Db |||||||
QY 2701 ACAACAGCTCACTTTTCTTCCAGGATTAAGTTGCAAGGTTGAATACTATTTTGAATCT 2760
Db |||||||
QY 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920
Db |||||||
QY 2761 CTTGAGGCTCAGGATTCATCTGATATTTTCAACTGTCTCGAACCATACCAAA 2820
Db |||||||
QY 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940
Db |||||||
QY 2821 AATATAAATGCTCGAGAGAAATCTTCCGACTCTGAGGACTTGGCTTAATGGTTAATACT 2880
Db |||||||
QY 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960
Db |||||||
```

RESULT 3

```
ABP69122
ID ABP69122 standard; protein; 960 AA.
XX
AC ABP69122;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1169.
XX
Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
antiarthritic.
XX
Homo sapiens.
XX
WO200270539-A2.
XX
12-SEP-2002.
XX
05-MAR-2002; 2002WO-US005095.
XX
05-MAR-2001; 2001US-00799451.
XX
(HYSE-) HYSEQ INC.
XX
Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
Wehrman T, Wang J, Wang D, Drmanac RT;
XX
WPI; 2002-759812/82.
DR
N-PSDB; ABZ11339.
XX
New polynucleotides comprising sequences assembled from expressed
sequence tags (ESTs), useful for treating cell-proliferative,
neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
or coagulation disorders.
XX
Claim 9; SEQ ID NO 1169; 1012pp + Sequence Listing; English.
XX
The invention relates to an isolated polynucleotide (I) comprising a
nucleotide sequence selected from any of 948 sequences (ABZ11119-
ABZ12066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for
identifying expressed genes or for physical mapping of human genome. The
encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
markers, as a food supplement, for generating antibodies, in medical
imaging, screening and diagnostic assays and for treating cell-
proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
platelet or coagulation disorders, wound, burns, incision, ulcers, liver
or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
arthritis, etc. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 960 AA;
SQ
Alignment Scores:
Pred. No.: 0 Length: 960
Score: 5048.00 Matches: 959
Percent Similarity: 100.00% Conservativeness: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 5 Gaps: 0
US-10-039-073-3 (1-2883) x ABP69122 (1-960)
```

QY 1 ATGTTCCATTCTTCTGCAATGGTTAAATTTCACACAGAAAAACCAATGTTTAAACATTTCACAGA 60  
Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20  
QY 61 GGATTTTACTCTCTAAACAGCCATCTTGCCCAAAATATGCAATTCTTCAGTTCTCAGTG 120  
Db 21 GlyPheTyrCysLeuThrAlaIleuProGlnIleCysIleCysSerGlnPheSerVal 40  
QY 121 CCATCTAGTTATCACTTCACCTGAGGATCCTCGGGCTTTCCAGTAGCACCTAAATGGGGAA 180  
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
QY 181 CGATTTCTTGGCAGGAGCTAAGGCTCCCAAGTGTGTCATCTCTCCATTATGACCTC 240  
Db 61 ArgPheProTyrGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
QY 241 TTTGTCCACCCCAATCTCACCTCTCTGACCTTCTGCATCTGAGAGATCGAAGTCTTG 300  
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluIlyIleGluValLeu 100  
QY 301 GTCAGCAATGTCACCCAGTTTATCATCTTGCA CAGCAAAAGATCTTGAATCACCAGATGCC 360  
Db 101 ValSerAsnAlaThrGlnPheIleIleuHisSerLysAspLeuGluIleThrAsnAla 120  
QY 361 ACCCTTCAGTCAGAGGAAGATCAAGATACATGATAACACAGGAAAAGAACTGAAAGTTTG 420  
Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
QY 421 AGTTACCCCTGCTATGAACAATTCGACTGCTGCTCCAGAGAACTTACGCCTCACCTG 480  
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
QY 481 AAATACTATGTGGCTATGGACTTCCAAAGCCCAAGTTAGTGATGGCTTTGAAGGGTTTAT 540  
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
QY 541 AAAAGCATACAGAACTCTTGGTGGTGAACAAGAAATCTTGCAGTAACAGATTTTGAG 600  
Db 181 LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200  
QY 601 CCACCCAGGCACCATGGCTTCCCTTGTCTTTCATGAACCGTGTTCAAAGCCCACTTT 660  
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
QY 661 TCAATCAAGATACGAAGAGAGCAGGCATATTCACCTATCCAAATGCCCCAAAGGTTAAG 720  
Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
QY 721 ACAATTGAACCTTGAAGGAGGTCTTTTGAAGATCACCTTTGAAATCACTGTAAATAAGT 780  
Db 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260  
QY 781 ACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTTCATCA 840  
Db 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
QY 841 GGGGTCAAGGTGTCATCTATGCATCCCGACACAAACGGAATCAACACATATTATGCTTTG 900  
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
QY 901 CAGGCATCACTGAAGCTACTTGATTTTTATGAAAAGTACTTTTGATATCTACTATCCACTC 960  
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
QY 961 TCCAAACTGGAATTAATGCTATTCTGACTTTCGACTTTCGACTGGAGCCATGGAAATGGGGC 1020  
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
QY 1021 CTCATTACATATAGGAGAGCTGCTACTGCTTTTTCACCCCAAGACCTCTCTGCTTCOGAT 1080  
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
QY 1081 AAACGTGGGTCAACAGAGTCATACCCCATGAACCTGGCGCACAGTGGTTTGGCAACCTG 1140

Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
QY 1141 GTCACAATGAATGGTGGAAATGATATTGGCTTAAGAGAGGTTTTCGAAATAACATCGAA 1200  
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400  
QY 1201 CTTTATCGCTGTTAATGCTCATATCCAGAGCTGCAATTTTGAATGACTATTTTGAATGTG 1260  
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspPhePheLeuAsnVal 420  
QY 1261 TGTTTTGAAGTAATTAACAAAGATTTCATTGAATTATCCCGCCCTATCTCCAAACACAGCG 1320  
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
QY 1321 GAAACCCCGACTCAAATACAGGAAATGTTTGTGTAAGATTTCCTATACAAAGGAGCTTGT 1380  
Db 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
QY 1381 ATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAAGGAATAATTTCAG 1440  
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleIleGln 480  
QY 1441 TACTTAAAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTGTGGAGCAGTCTGTCA 1500  
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500  
QY 1501 AATAGTTGTTTACAAAGATGATTTTATCATCTGGTGGAGTTTGTTCATTCGGATCCCAAGATG 1560  
Db 501 AsnSerCysLeuGlnSerAspPheThrSerGlyGlyValCysHisSerAspProLysMet 520  
QY 1561 ACAAGTAACATGCTCGCCCTTCTGGGGGAAAAATGCAGAGGTCAAAGAGATGATGACTACA 1620  
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540  
QY 1621 TGACCTCTCCAGAAAGAAATCCCTCTGCTGGTGGTTAAACAAGACCGGTGTTCACTCCGA 1680  
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560  
QY 1681 CTGCAACAGGAGCGCTCTCCAGGGGTTTCCAGGAAAGACCCTCAATGGAGGGCCCTG 1740  
Db 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580  
QY 1741 CAGGAGAGGTACCTGTGGCATATCCCATTTGACCTACTCCACGAGTTCTTCTAATGTATC 1800  
Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600  
QY 1801 CACAGACACATTTCTAAATCAAAGACAGATACCTCGATCTACCTGAAAGACAGTTGG 1860  
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
QY 1861 GTGAAATTTAATGTGACTCAAATGGTTACTCATCTGTTCACTATCAGGTGCATGATGG 1920  
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
QY 1921 GACCAACTCATTACACAGCTGAATCAGAACCCACACACTTCTCAGACCTTAAGGACAGAGTA 1980  
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
QY 1981 GGTCTGATTCATGATGTGTTTACGTAGTTGGTGCAGGAGAGCTGACCTTAGACAAAGCT 2040  
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
QY 2041 CTTGACATCACTTACTACTCCAAATGAAACAAGCAGCCCGCACTCTCCGAAAGTCTG 2100  
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700  
QY 2101 AGTTACTTGGAAATCGTTTTACCACATGATGAGCAGAGGAATAATTTTCAGATATCTCGAA 2160  
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIleSerGlu 720  
QY 2161 AACCTCAAGCGTTACCTTCTTCAGTATTTTAAAGCCAGTGATTCACAGGCAAGCTGGAGT 2220

Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
QY 2221 GACAAAGGCTCAGTCGGACAGGATGCTCCGCTCGGTCTCTTGAAGCTGCGCTGTGAC 2280  
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
QY 2281 CTGAACCATGCTCCTTGGATCCAGAAAGCTGCTGAACCTCTTCCAGTGGATGAATCC 2340  
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
QY 2341 AGTGGAAAATTAATATACCAACAGATGTTTTAAAGATTGTATTCTGTGGTGTCTCAG 2400  
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800  
QY 2401 ACAACAGCAGGATGGAATTTACCTTTTAGACCAATATGAACCTGTCAATGTCAAGTCTGAA 2460  
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820  
QY 2461 CAAAACAAAATTTCTGTATGCTTTGTCAAGCAGCAAGCATCAGGAAAAGTTACTGAAGTTA 2520  
Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLysLeu 840  
QY 2521 ATTGAACCTAGGAATCGAAGGAAGTATTCAAGACACAGAACTTGCAGCTCTCTTCAT 2580  
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860  
QY 2581 GCGATTGCCAGCGTCCAAAGGGCAGCAACTAGCATGGATTTTGTGAAGAGAAAATTGG 2640  
Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
QY 2641 ACCCATCTTCTGAAAAATTTGACTTGGCTCATATGACATATGACATAGCATCATCTCTGGC 2700  
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900  
QY 2701 ACAACAGCTCACTTTCTTCCAGGATGAAGTTCAGAGGTGAAGTAACTATTTTGAATCT 2760  
Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920  
QY 2761 CTTGAGGCTCAAGGATCACTGATATTTTCAAACTGTTCTGAAACGATACCAAA 2820  
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940  
QY 2821 AATATAAATGGCTGGAGAGAAATCTTCGACTCTGAGACTTGCTGCTTAATGTTAATCT 2880  
Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960

RESULT 4  
ABP63022  
ID ABP63022 standard; protein; 785 AA.  
XX AC ABP63022;  
XX DT 14-OCT-2002 (first entry)  
XX DE Human polypeptide SEQ ID NO 459.  
XX KW Human; vulnery; dermatological; neuroprotective; nootropic; cancer;  
KW antiParkinsonian; immunostimulant; cytostatic; immunosuppressive;  
KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;  
KW burn; central nervous system disorder; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; immune disorder;  
KW autoimmune disorder; multiple sclerosis; diabetes; allergy.  
XX OS Homo sapiens.  
XX PN WO200218424-A2.  
XX PD 07-MAR-2002.  
XX PF 31-AUG-2001; 2001WO-US027093.  
XX PR 01-SEP-2000; 2000US-00654935.

(HYSE-) HYSEQ INC.  
Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;  
WPI: 2002-583321/62.  
N-PSDB; ABQ93501.  
New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.  
Claim 20; SEQ ID NO 459; 284pp + Sequence Listing; English.  
The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (I), (II) and (III) are useful for diagnostic evaluation of disorders. (I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 785 AA;  
SQ  
Alignment Scores:  
Pred. No.: 0 Length: 785  
Score: 4141.00 Matches: 782  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 2  
Query Match: 81.81% Indels: 0  
DB: 5 Gaps: 0  
US-10-039-073-3 (1-2883) x ABP63022 (1-785)  
QY 1 ATGTTCCATTCTTCTGCAATGGTTAATTCACACAGAAAACCAATGTTTAACTTCACAGA 60  
Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20  
QY 61 GGATTTTACTGCTTAAACAGCCATCTTCCCCCAATATGATCTTCTCTCAGTCTTCAGTG 120  
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
QY 121 CCATCTAGTTATCACTTCACTGAGGATCCTGGGGCTTTCCAGTAGCCACTAATGGGAA 180  
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
QY 181 CGATTTCTTGGCAGGAGCTTAAGGCTCCCAGTGTGTCATCTCTCCATATGACCTC 240  
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
QY 241 TTTGTCACCCCAATCTCACTCTCTGACCTTTTGTGATCTGAGAGATCGAAGTCTTG 300  
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
QY 301 GTCAGCAATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACAATGCC 360  
Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
QY 361 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAACACAGAGAAAGAACTGAAAGTTTG 420  
Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
QY 421 AGTTACCTGCTCATGAACAAAATTCAGCTGCTGGTCTCCAGAGAACTTACGCTCACCTG 480  
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160

QY 481 AAATACATATGGCTATGGACTTCCAAAGCCCAAGTTAGGTGATGGCTTTGAAGGTTTAT 540  
Db LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
QY 541 AAAAGCACATACAGAACTCTGGTGGTGGACAGAAATCTTCAGATAACAGATTTTGAG 600  
Db LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu 200  
QY 601 CCAACCCAGGCACCATCGGCTTCCCTTGGCTTTTCATGAACCGTGTTCAAAGCCCAACTTT 660  
Db ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
QY 661 TCAATCAAGATACGAAGAGAGAGCAGCATATTCACATATCCAAACATGCCAAAGGTTAAG 720  
Db SerIleLysIleArgAspGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
QY 721 ACAATTGAACCTTGAAGAGGTCTTTTGGAGATCACCTTTGAAACTACTGTAAAAATCAGT 780  
Db ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrValLysMetSer 260  
QY 781 ACATACCTTGTAGCTACATAGTTTGTGATTCCACTCTCTGAGTGGCTTCACATTCATCA 840  
Db ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
QY 841 GGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACGGAATCAAAACACATTTATGCTTTG 900  
Db GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
QY 901 CAGGCATCACTGAGCTACTGATTTTATGAAAGTACTTTGATATCTACTATCCATC 960  
Db GlnAlaSerLeuLysLeuLeuAspPheTyrGlnLysTyrPheAspIleTyrTyrProLeu 320  
QY 961 TCCAACTGGATTAAATGGCTATTCTCCTGACTTTGCACCTGGAGCATCGAAATTTGGGGC 1020  
Db SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
QY 1021 CTCAATACATATAGGAGAGCTACTGCTTTTTCACCCCAAGACCTCTTCGCTCCGAT 1080  
Db LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
QY 1081 AAATGTGGTCCACAGAGTCATAGCCCATGCACTGGCCAGCCAGTGGTTGGCAACTG 1140  
Db LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
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Db ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400  
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QY 1381 ATTTTGAATATGCTCAAGGATTTTCTCGGTGAGAGAAATTCAGAAAGGAATTAATTCAG 1440  
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QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGAAAGACCTCAATGGAGGGCCCTG 1740  
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QY 1801 CACAGACATCTTAAATCAAAAGACAGATACCTCTGATCTACTCTGAAAGACAGTTGG 1860  
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Db AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
QY 2221 GACAAGGCTCAGTCTGGACAGGATGCTCCGCTCCGCTCTCTTGAAGCTGGCTGTGAC 2280  
Db AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLysLeuAlaCysAsp 760  
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Db LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheGlnTrpMetGluSer 780  
QY 2341 AGTGGAAATTA 2352  
Db SerGlyLysLeu 784  
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ID ABB10338 standard; protein; 728 AA.  
XX ABB10338;  
AC ABB10338;  
XX  
DT 10-JAN-2002 (first entry)  
XX  
DE Human cDNA SEQ ID NO: 646.  
XX  
KW Human; gene therapy; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW proliferative disorder; inflammation.  
XX  
OS Homo sapiens.

PN	WO200154474-A2.	PR	29-SEP-2000; 2000US-0236327P.
XX		PR	29-SEP-2000; 2000US-0236367P.
PD	02-AUG-2001.	PR	29-SEP-2000; 2000US-0236368P.
XX		PR	29-SEP-2000; 2000US-0236369P.
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PR	25-SEP-2000; 2000US-0234997P.	XX	
PR	25-SEP-2000; 2000US-0234998P.	XX	(HUMA-) HUMAN GENOME SCI INC.
PR	26-SEP-2000; 2000US-0235484P.	XX	Rosen CA, Barash SC, Ruben SM;
PR	27-SEP-2000; 2000US-0235834P.	PI	
PR	27-SEP-2000; 2000US-0235836P.		

XX WPI; 2001-476161/51.  
DR N-PSDB; ABA06560.  
XX  
PT Isolated nucleic acid molecule encoding an inflammation-associated  
FT polypeptide is used in preventing, treating or ameliorating a medical  
XX condition.  
PS  
XX Claim 11; SEQ ID NO 646; 859pp + Sequence Listing; English.  
PS  
XX The present invention provides human cDNAs, proteins and related genomic  
CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence  
CC is a protein of the invention  
XX  
SQ Sequence 728 AA;  
Alignment Scores:  
Pred. No.: 0 Length: 728  
Score: 3799.00 Matches: 722  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 75.05% Indels: 0  
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Db 7 ValysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLys 26  
QY 775 ATGAGTACATACCTTGTAGCCTACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCAC 834  
Db 27 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 46  
QY 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACCGAATCAAAACACATTAT 894  
Db 47 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 66  
QY 895 GCTTTGAGGATCAGTGAAGTACTTGTATTTTATGAAAGTACTTTGTATCTACTAT 954  
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QY 955 CCACCTCTCCAACTGGGATTTAATTGCTATTCTGCTTTTGCACCTGGAGCCATGGAAAAAT 1014  
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QY 1495 CTGTCAAAATAGTTGTTTAAAGAGTGAATTTTACATCTGTGGAGCTTGTGTCTTCGATCC 1554  
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QY 2095 GGTCTGAGTTACTTGAATCGTTTTCACCATGATGGACAGAAAGGAATATTTTCAGATATC 2154  
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QY 2275 TGTGACCTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACCTCTTCTCCAGTGGATG 2334  
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ABP66925

ID ABP66925 standard; protein; 728 AA.

XX AC ABP66925;

XX DT 09-DEC-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 646.

XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

XX KW antiparkinsonian; antiscickling; antianaemic; antiarthritic; cancer;

XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;

XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;

XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;

XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

XX US2002090672-A1.

XX PN 11-JUL-2002.

XX PD 17-JAN-2001; 2001US-00764853.

XX PF 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180629P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 07-JUL-2000; 2000US-0216647P.

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XX PR 11-JUL-2000; 2000US-0217487P.

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XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

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PR 21-SEP-2000; 2000US-0234223P.

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PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

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PR 13-OCT-2000; 2000US-0239935P.

PR 20-OCT-2000; 2000US-0240960P.

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PR 01-NOV-2000; 2000US-0244617P.

PR 17-NOV-2000; 2000US-0249299P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX PI Rosen CA, Ruben SM, Barash SC;

XX WPI: 2002-681727/73.

XX N-PSDB, ABV83897.

DR Novel polypeptide useful for diagnosis, prognosis, prevention, and

XX treatment of immune, hyperproliferative, renal, respiratory,

PT cardiovascular, reproductive, endocrine, gastrointestinal and

PT neurological disorders.

XX Claim 11; SEQ ID NO 646; 369pp + Sequence Listing; English.

PS The invention relates to novel genes (ABV83682-ABV84101) and proteins

XX (ABP66710-ABP67129) useful for preventing, treating or ameliorating

CC medical conditions e.g. by protein or gene therapy. The genes are

CC isolated from a range of human tissues disclosed in the specification.

CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic

CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing

CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)

CC infectious diseases such as viral, bacterial, fungal and parasitic

CC infections. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 728 AA;

Alignment Scores:

Pred. No.: 0 Length: 728

Score: 3799.00 Matches: 722

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Query Match:	75.05%	Indels:	0
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Qy	775	ATGAGTACATACCTTTGAGCCTACATAGTTTGTGATTTCACCTCTCTGAGTGGCTTCAC	834
Db	27	MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr	46
Qy	835	TCATCAGGGGTCAAGGTGCTCATCTATGCATCCCCAGACAAACCGAATCAACACATTAT	894
Db	47	SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr	66
Qy	895	GCTTTGCAGGCATCACTGAAGCTACTTGATTTTATGAAAAGTACTTTTGATATCTACTAT	954
Db	67	AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr	86
Qy	955	CCACTCTCCAACTGGATTAAATTGCTATTCTCTGACTTTTGCCACCTGGAGCCATGGAAAAAT	1014
Db	87	ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn	106
Qy	1015	TGGGGCTCATATCATATAGGAGACGTCACTGCTTTTGGACCCCAAGACTCTCTCTGCT	1074
Db	107	TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla	126
Qy	1075	TCCGATAAACTGTGGGTCAACAGAGTCATAGCCCATGAACCTGGCGCACCACTGTTTGGC	1134
Db	127	SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly	146
Qy	1135	AACCTGTGTCAAATGGTGAATGCATATTTGGCTTAAAGGAGGTTTTGCAAAATAC	1194
Db	147	AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr	166
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Qy	1375	GCTTGATTTTGAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGNATA	1434
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Qy	1435	ATTCACTACTTAAAGAGTTTCAGCTATAGAAATGCTAAGAAATGATGACTTTGTGAGCAGT	1494
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Qy	1615	ACTACATGGACTCTCCAGAAAGGAATCCCTCGCTGGTGGTTAAACAAGACGGGTGTCA	1674
Db	307	ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer	326
Qy	1675	CTCCGACTGCAACAGGAGCGCTTCCTCCAGGGGTTTTCCAGGAAGACCTCGAATGAGG	1734

Db	327	LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg	346
Qy	1735	GCCTCCAGGAGAGGTACCTGTGGCATATCCCATTTGACCTTACCCTGAGGTTCTTCTAAT	1794
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Qy	1795	GTGATCCACAGACACATTTCTAAATCAAAGACAGATACTCTGGATCTCTACCTGAAAAGACC	1854
Db	367	VallIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr	386
Qy	1855	AGTTGGGTGAAATTTAATGTGGACTCAAATGGTTACTACATCTTCACTATGAGGTCAT	1914
Db	387	SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis	406
Qy	1915	GGATGGGACCACTCATTAACAGCTGAATCAGAACACACACTTCTCAGACCTAAGGAC	1974
Db	407	GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp	426
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Db	427	ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp	446
Qy	2035	AAAGCTCTTGACATGACTTACTACCTCCCAACATGAAACAAGACGCCCGCACTTCTCGAA	2094
Db	447	LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu	466
Qy	2095	GGTCTCAGTTACTTGAATCGTTTACCACATGATGACAGAGGAAATTTTCAGATATC	2154
Db	467	GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle	486
Qy	2155	TCTGAAAACTCAAGCGTTACCTTCTTCAGTATTTTAAAGCCAGTGTGACAGGCCAAAGC	2214
Db	487	SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer	506
Qy	2215	TGAGGTGACAAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGGCC	2274
Db	507	TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla	526
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Db	527	CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet	546
Qy	2335	GAATCAGTGGAAAAATAAATATACCAACAGATGTTTTAAAGATTCTGTATCTGTGGGT	2394
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Qy	2395	GCTCAGACAAACAGCAGGATGGAATTAACCTTTTAGACCAATATGAACCTGCTCAAGT	2454
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Qy	2455	GCTGAACAAAACAAAATTCGTATGCTTTGTCAACGACGACATCAGGAAAAGTTACTG	2514
Db	587	AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu	606
Qy	2515	AAGTTAATTGAACCTAGGAAATGGAAGGAAAGTTTATCAAGACACAGAACTTGGCAGCTCTC	2574
Db	607	LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu	626
Qy	2575	CTTCATGCGATTGCCAGAGCTCCAAAGGGCGAGCAACTAGCATGGATTTTGTAAAGAA	2634
Db	627	LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu	646
Qy	2635	AATTGGACCCATCTCTGAAAAAATTTGACTTGGGCTCATATGACATATAGGATGATCATC	2694
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DT 18-DEC-2001 (first entry)  
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DE Novel human enzyme polypeptide #85.  
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KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
KW autoimmune disorder; neurological disorder; metabolic disorder;  
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;  
KW nephrotropic; anticoagulant.  
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OS Homo sapiens.  
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 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Baraesh SC, Ruben SM;  
 XX  
 XX WPI; 2001-465566/50.  
 DR N-PSDB; AAS40869.  
 XX

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Claim 11; SEQ ID NO 995; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 722 AA;

Alignment Scores:  
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 Score: 3770.00 Matches: 717  
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 Best Local Similarity: 99.31% Mismatches: 5  
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US-10-039-073-3 (1-2883) x AAU22999 (1-722)

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XX Human cDNA SEQ ID NO: 819.  
DE XX Human; gene therapy; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW proliferative disorder; inflammation.  
XX Homo sapiens.  
XX WO200154474-A2.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US001349.  
PF 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
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XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM,  
XX WPI; 2001-476161/51.  
DR N-PSDB; ABA06733.  
XX  
XX Isolated nucleic acid molecule encoding an inflammation-associated  
PT polypeptide is used in preventing, treating or ameliorating a medical  
PT condition.  
XX  
XX Claim 11; SEQ ID NO 819; 859pp + Sequence Listing; English.  
XX  
XX The present invention provides human cDNAs, proteins and related genomic  
CC DNAs. These can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence  
CC is a protein of the invention  
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SQ Sequence 722 AA;  
  
Alignment Scores:  
Pred. No.: 0 Length: 722  
Score: 3770.00 Matches: 717  
Percent Similarity: 99.31% Conservative: 0  
Best Local Similarity: 99.31% Mismatches: 5  
Query Match: 74.48% Indels: 0  
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AC ABP67098;  
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XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
XX antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;  
XX antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
XX antiallergic; antidiabetic; antidiulcer; anticonvulsant; antifungal;  
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
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11-JUL-2002.  
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 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 XX  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 FI Rosen CA, Ruben SM, Barash SC;  
 XX  
 DR WPI; 2002-681727/73.  
 DR N-PSDB; ABV84070.  
 XX  
 PT Novel polypeptide useful for diagnosis, prognosis, prevention, and  
 PT treatment of immune, hyperproliferative, renal, respiratory,  
 PT cardiovascular, reproductive, endocrine, gastrointestinal and  
 PT neurological disorders.  
 XX  
 PS Claim 11; SEQ ID NO 819; 369pp + Sequence Listing; English.  
 PS  
 XX  
 CC The invention relates to novel genes (ABV83682-ABV84101) and proteins  
 CC (ABP6710-ABP67129) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune

CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsies; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pt\_sequences  
 XX  
 SQ Sequence 722 AA;

## Alignment Scores:

Pred. No.: 0 Length: 722  
 Score: 3770.00 Matches: 717  
 Percent Similarity: 99.31% Conservative: 0  
 Best Local Similarity: 99.31% Mismatches: 5  
 Query Match: 74.48% Indels: 0  
 DB: 5 Gaps: 0

US-10-039-073-3 (1-2883) x ABP67098 (1-722)

QY 715 GTTAAGACAAATTGAAGAGAGGTCTTTGGGAAGATCACCTTGAAGAACTACTGTAAAA 774  
 Db 1 ValLysThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrThrValLys 20  
 QY 775 ATGAGTACATACCTCTGTAGCCTACATAGTTTGATTTCCACTCTCTGAGTGGCTTCACT 834  
 Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40  
 QY 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACGGAATCAAAACACATTAT 894  
 Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60  
 QY 895 GCTTTCAGGCATCACTGAAGCTACTTGATTTTATGAAAAGTACTTTGATATCTACTAT 954  
 Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80  
 QY 955 CCACTCTCCAAAGCTGGATTATTTGCTATTCTGACTTTTGACCTCGAGCCATGGAAT 1014  
 Db 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100  
 QY 1015 TGGGGCTCATATACATATAGGAGAGCTCACTGCTTTTGGACCCCAAGACCTCTTCTGCT 1074  
 Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120  
 QY 1075 TCCGATAAACTGTGGGTCAACAGATCATAGCCCATGAAGTGGCGCACACAGTGGTTGGC 1134  
 Db 121 SerAspLysLeuTyrValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140  
 QY 1135 AACCTGGTCACAATGGAATGGTGAATGATATTTGGCTTAAGGAGGTTTTCGAAAATAC 1194  
 Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160  
 QY 1195 ATGGAACTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTTGATGACTATTTTTTG 1254  
 Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspTyrPheLeu 180  
 QY 1255 AATGCTGTTTGAAGTAATTACAAAGATTTCATTCGAATTCATCCCGCCCTATCTCAA 1314  
 Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200  
 QY 1315 CCAGCGGAAACCCCGACTCAAAATACAGGAAATGTTTGTAGTGAAGTTCCTTATACCAAGGGA 1374  
 Db 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220  
 QY 1375 GCTTGTTATTTGAATATGCTCAAGGATTTCCTGGGTGAGAGAAAATTCAGAGAAGAATA 1434  
 Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPhe\*\*\*LysGlyIle 240  
 QY 1435 ATTCACTACTTAAAGAGTTTCAGCTATAGAAATGCTAAGATGATGACTGTGGAGCAGT 1494  
 Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer 260

QY 1495 CTGTCAGATAGTTGTTTAAAGTGAATTTTACATCTGGTGGAGTTTGTCTATTCGATCCC 1554  
Db 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 280  
QY 1555 AAGATGACAAAGTAAACATGCTCGCCCTTCTGGGGGAAATGACAGAGTCAAGAGAGATG 1614  
Db 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGlu\*\*\*LysGluMetMet 300  
QY 1615 ACTACATGGACTCTCCAGAAAGAAATCCCTGCTGGTGGTAAACAAGACGGGTTC 1674  
Db 301 ThrThrTrpThrLeuGlnLysGlyLeuProLeuLeuValValLysGlnAspGlyCysSer 320  
QY 1675 CTCCGACTGCAACAGAGCGCTTCTCCAGGGGGTTTCCAGGAAGACCCGTAATGGAGG 1734  
Db 321 LeuArgLeuGlnGlnArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340  
QY 1735 GCCTGTCAGGAGAGTACTCTGGGCATATCCATTGACCTACTCCACGAGTTCTCTAAT 1794  
Db 341 AlaLeuGlnGluArgGlyLeuTrpHisLeuProLeuThrThrSerSerSerAsn 360  
QY 1795 GTGATCCACAGACACATTTAAATCAAGACAGATCTCTGGATCTACCTGAAAGACC 1854  
Db 361 ValIleHisArgHisLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380  
QY 1855 AGTGGGTGAATTTAATGTGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAT 1914  
Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrtyrIleValIleHisGlyHis 400  
QY 1915 GGATGGGACCACTCATACAGCTGAATCAGACACACACTCTCAGACCTTAAGGAC 1974  
Db 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420  
QY 1975 AGAGTAGTGTGATTCATGATGTTTTCAGCTAGTTGGTGCAGGAGACTGACCCCTAGAC 2034  
Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440  
QY 2035 AAAGCTCTTGACATGACTTACTCTCAACATGAAACAAGCAGCCCCGCTCTCTCGAA 2094  
Db 441 LysAlaLeuAspMetThrTyrtyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 460  
QY 2095 GGTCTGAGTACTTGGAAATCGTTTACCACATGATGGACAGAGAAATTTTCAGATATC 2154  
Db 461 GlyLeuSerTyrrLeuGluSerPheTyrrHisMetMetAspArgAsnIleSerAspIle 480  
QY 2155 TCTGAAAAACCTCAAGCGTTACCTCTTCAGTATTTTAAAGCCAGTGATTCAGAGCAAGC 2214  
Db 481 SerGluAsnLeuLysArgTyrrLeuLeuGlnTyrrPheLysProValIleAspArgGlnSer 500  
QY 2215 TGGAGTGACAGGGCTCAGTCTGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGGCC 2274  
Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520  
QY 2275 TGTGACCTGAACCACTGCTTGCATCCAGAAAGCTGCTGAACCTTCTCCAGTGGATG 2334  
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540  
QY 2335 GAATCCAGTGGAAAAATTAATATACCAACAGATGTTTAAAGATTGTATTCTGTGGGT 2394  
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrrSerValGly 560  
QY 2395 GCTCAGACAAACAGCAGGATGGAATTAATCTTTTAGAGCAATATGAATCTCAATGTCAAGT 2454  
Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrrLeuLeuGluGlnTyrrGluLeuSerMetSerSer 580  
QY 2455 GCTGAACAAACAAATTTCTGTATGCTTGTTCACAGCAGCAAGCATTCAGAAAGTACTG 2514  
Db 581 AlaGluGlnAsnLysIleLeuTyrrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu 600  
QY 2515 AAGTTAAATTGACTAGGAATGGAAGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTC 2574  
Db 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeu 620

QY 2575 CTTTCATGGATTGCCAGACGCTCCAAAGGGGCGAGCAACTAGCATGGGATTTTGTAGAGAA 2634  
Db 621 LeuHisAlaIleAlaAaArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640  
QY 2635 AATTGGACCCCATCTTCTGMAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATC 2694  
Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrrAspIleArgMetIleIle 660  
QY 2695 TCTGGCCAAACAGCTCACTTTTCTTCCAAAGATTAAGTTGCAAGGTTGAAACTATTTTTT 2754  
Db 661 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePhe 680  
QY 2755 GAATCTCTTGGGCGCTCAAGGATCATCTCGATATTTTCAAACTGTTCTCGAACCGATA 2814  
Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700  
QY 2815 ACCAAAAATATAAATGGCTGGAGAAGAACTCTCCGACTCTGAGGACTTGGCTAATGTT 2874  
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu\*\*\*\*\* 720  
QY 2875 AATACT 2880  
Db 721 \*\*\*Thr 722  
RESULT 10  
ID ADR41453 standard; protein; 722 AA.  
XX ADR41453;  
XX AC ADR41453;  
XX DT 07-OCT-2004 (first entry)  
XX DE Human CD-like molecule HAIDK30, SEQ ID NO:252.  
XX KW Human; CD-like molecule; cluster of differentiation; diagnosis;  
KW prevention; immune disorder; immunodeficiency; autoimmune disorder;  
KW blood-related disorder; haematological disorder; haemostatic disorder;  
KW thrombolytic disorder; hyperproliferative disorder; cancer; tumour;  
KW apoptotic disorder; cardiovascular disorder; respiratory disorder;  
KW angiogenic disorder; neovascularisation; neurological disorder;  
KW endocrine disorder; reproductive system disorder; infectious disease;  
KW gastrointestinal disorder; drug screening; tissue regeneration;  
KW chemotaxis; gene therapy; antibody therapy; drug targeting;  
KW chromosome mapping; forensic analysis; immunophenotyping; cytostatic;  
KW haemostatic; tranquiliser; vulnery; anti-inflamatory; nephrotropic;  
KW cardiant; antiallergic; anti-HIV; antirheumatic; antiarthritic;  
KW antipsoiatric; immunosuppressive; vasotropic; nootropic; neuroprotective;  
KW antithyroid; thyromimetic; gynaecological; virucide; hepatotropic;  
KW antibacterial; dermatological; chromosome 16.  
XX OS Homo sapiens.  
XX OS WO200226930-A2.  
XX PN 04-APR-2002.  
XX FD 25-SEP-2001; 2001WO-US029838.  
XX PF 26-SEP-2000; 2000US-0235484P.  
XX XX (HUMA-) HUMAN GENOME SCI INC.  
XX XX Rosen CA, Birse CE;  
XX XX WPI; 2002-405050/43.  
XX XX N-PSDB; ADR41277.  
XX DR Novel polynucleotides and polypeptides useful for treating, preventing or  
XX ameliorating cardiovascular, renal, neurovascular, and autoimmune  
XX disorders.  
XX PS Claim 11; SEQ ID NO 252; 1243pp; English.

CC The invention relates to 167 novel human CD (cluster of differentiation)-  
 CC like molecules (ADR41388-ADR41563) and to cDNAs encoding them (seqid:11)-  
 XX  
 SQ Sequence 722 AA;

Alignment Scores:  
 Pred. No.: 0 Length: 722  
 Score: 3763.00 Matches: 717  
 Percent Similarity: 99.31% Conservative: 5  
 Best Local Similarity: 99.31% Mismatches: 0  
 Query Match: 74.34% Indels: 0  
 DB: 5 Gaps: 0

US-10-039-073-3 (1-2883) x ADR41453 (1-722)

QY 715 GTTAAGCAATGAACCTTGAGGAGCTCTTTGGAGATCACCTTTGAACTACTGTAAA 774  
 Db 1 VallysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrVallys 20  
 QY 775 ATGAGTACATACCTTGAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 834  
 Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40  
 QY 835 TCATCAGGGTCAAGGTGTCATCTATGCATCCCGACAGCAAAACGGAATCAAAACATATAT 894  
 Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60  
 QY 895 GCTTTGAGGAGCATCACAGACTCTGATTTTATGAAAGTACTTTGATATCTACTAT 954  
 Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80  
 QY 955 CCATCTCCAAACTGGATTTAAATTGCTATTCTGACTTTGCACCTGGAGGCATGGAAAAT 1014  
 Db 81 ProluSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100  
 QY 1015 TGGGGCTCATTAATATAGGAGACGTCACTGCTGTTTTGACCCCAAGACTCTCTCGCT 1074  
 Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 120  
 QY 1075 TCCGATAAAGCTGGGTCCAGAGTCATAGCCCATCAACTGGCGCACCAAGTGGTGGC 1134  
 Db 121 SerAspLysLeuThrValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140  
 QY 1135 AACCTGCTCAAAATGGTGAATGATAATTTGGCTTAAGGAGGGTTTTGCAAAATAC 1194  
 Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160  
 QY 1195 ATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGTATGATCTATTTTGG 1254  
 Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180  
 QY 1255 AATGTGTGTTTGAAGTAATTACAAAAGATTCTATTGAATTCATCCCGCCCTATCTCCAA 1314  
 Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200  
 QY 1315 CCAGCGAAACCCGACTCAAAATACAGAAATGTTTGTATGAAGTTTCTTATAACAAGGGA 1374  
 Db 201 ProAlaGluThrProThrGlnIleGlnGluMet\*\*\*AspGluValSerTyrAsnLysGly 220  
 QY 1375 GCTTGTATTTGAATATGCTCAAGGATTTCTGGGTGAGGAGAAATTCAGAAAGGAATA 1434  
 Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIle 240  
 QY 1435 ATTCAAGTACTTAAGAGAGTTCAGCTATAGAAATGCTAAGATGATGACTTGTGGCGAGT 1494  
 Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSer 260  
 QY 1495 CTGTCAAAATAGTCTTTAGAAAAGTGAATTTACATCTGGTGGAGTTTGTCAATCGGATCCC 1554  
 Db 261 LeuSerAsnSer\*\*\*LeuGluSerAspPheThrSerGlyValCysHisSerAspPro 280  
 QY 1555 AAGATGACAGATTAACGTCTGCTCTTCTGGGGGAAAATGCAGAGGTCAAAAGATGATG 1614  
 |||||

Db 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMet 300  
 QY 1615 ACTACATGAGCTCTCCAGAAAGGAATCCCCCTGCTGTTGTTAAACAAGACGGGTGTCA 1674  
 Db 301 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 320  
 QY 1675 CTCGACTGCACAGGAGCGCTTCTCCAGGGGGTTTCCAGGAAGACCCCTGAAATGAGG 1734  
 Db 321 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340  
 QY 1735 GCCCTGCAGAGAGGTACTCTGGGCATATCCCATTCACCTACTCCACGAGTCTTCTTAAT 1794  
 Db 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 360  
 QY 1795 GTGATCCACAGACACATCTAAATCAAAAGACAGATACTCTGCATCTACTCTGAAAAGACC 1854  
 Db 361 ValIleHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380  
 QY 1855 AGTTGGGTGAAATTTAATGTGGACTCAAAATGGTTACTACATCGTTCACATATGAGGGTCAT 1914  
 Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 400  
 QY 1915 GATGGGACCAACTCATACAGCTGAATCAGAACACACACATCTCTCAGACCTAAGGAC 1974  
 Db 401 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 420  
 QY 1975 AGAGTAGGTCTGATTCATGATGTTTTCAGCTAGTTGGTGAGGGAGACTGACCTAGAC 2034  
 Db 421 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 440  
 QY 2035 AAAGCTCTTTGACATGACTTACTACCTCCAAACATGAAACAAGCAGCCCCGACTTCTCGAA 2094  
 Db 441 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 460  
 QY 2095 GGTCTGAGTTACTTGAATCGTTTACACATGATCGACAGAAAGGAATATTTCAGATATC 2154  
 Db 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle 480  
 QY 2155 TCTGAAAACTCAAGGTTTACCTTCTTCAGTATTTTAAAGCCAGTGTATGACAGGCAAGC 2214  
 Db 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500  
 QY 2215 TGGAGTGACAAGGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCC 2274  
 Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520  
 QY 2275 TGTGACTGAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCCCGAGTGGATG 2334  
 Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540  
 QY 2335 GAATCCAGTGGAAAATTAATAATATACCAACAGATGTTTAAAGATTCTGTATTCTGTGGGT 2394  
 Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560  
 QY 2395 GCTCAGACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAACGTGTCATGTCAAGT 2454  
 Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580  
 QY 2455 GCTGAACAAAAACAAATCTCTGTATGTTGTCACGAGCAAGCATCAGGAAAGTTACTG 2514  
 Db 581 AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeu 600  
 QY 2515 AAGTTAATTTGAACCTAGGAATGGAAGGAAAGTTTATCAAGACACAGAACTTGGCAGCTCTC 2574  
 Db 601 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeu 620  
 QY 2575 CTTTCATGCGATGCCAGACGTCAAAAGGGCGACCAACTAGCATGGGATTTTGTAAAGAA 2634  
 Db 621 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 640  
 QY 2635 AATTGACCCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATC 2694  
 |||||  
 Db 641 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 660

QY 2695 TCTGCAACAGCTCATTCTTCCAAAGATAGTTGCAAGAGTGAACTATTTTT 2754  
 Db 661 SerGlyThrAlaHisPheSerLysAspLysLeuGlnGluValLysLeuPhePhe 680  
 QY 2755 GAATCTCTTGAGGCTCAAGGATCACATCTGGATATTTTCAAACCTGTTCTCGAAACGATA 2814  
 Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700  
 QY 2815 ACCAAAAATATAAATGGCTGAGAGAAATCTTCCGACTCTGAGACTGGCTAATGGTT 2874  
 Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu\*\*\*\*\* 720  
 QY 2875 AATACT 2880  
 Db 721 \*\*\*Thr 722  
 RESULT 11  
 AAU07829  
 ID AAU07829 standard; protein; 941 AA.  
 AC AAU07829;  
 DT 04-DEC-2001 (first entry)  
 XX Human ARTS-1 polypeptide.  
 DE Human; aminopeptidase regulator of type I; cytokine signalling; ARTS-1;  
 KW tumour necrosis factor receptor ectodomain shedding; interleukin-1;  
 KW interleukin-6; immune disorder; TNF-mediated immune disease;  
 KW inflammatory disorder; anti arthritic; vasotropic; immunomodulator;  
 KW immunosuppressive; antibacterial; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 350..361  
 FT /label= Zinc\_binding domain  
 FT Domain 353..376  
 FT /label= Zinc\_metalloproteinase\_catalytic\_motif  
 FT Domain 372..379  
 FT /label= Zinc\_binding\_catalytic\_site  
 XX  
 PN WO200164856-A2.  
 XX  
 XX 07-SEP-2001.  
 XX  
 XX 28-FEB-2001; 2001WO-US006464.  
 XX  
 XX 28-FEB-2000; 2000US-0185586P.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Levine S;  
 XX  
 DR WPI; 2001-550175/61.  
 DR N-PSDB; AAS09227.  
 XX  
 XX Novel polypeptide useful for the regulation of ectodomain shedding of  
 PT type I, tumor necrosis factor receptor and other cytokine receptors and  
 PT for treating disorders and diseases of the immune system.  
 XX  
 XX Claim 2; Fig 1; 139pp; English.  
 XX  
 XX The present invention relates to the isolation of a novel human  
 CC polypeptide, defined as aminopeptidase regulator of type I, 55 kDa tumour  
 CC necrosis factor (TNF) receptor ectodomain shedding (ARTS-1), and the  
 CC polynucleotide sequence encoding for ARTS-1. The invention describes  
 CC compositions and methods for the regulation of cytokine signalling  
 CC through the TNF pathway. The ARTS-1 polypeptide and antibodies that bind  
 CC ARTS-1 are useful for regulating the shedding of the extracellular domain  
 CC of a cytokine receptor such as type-1 tumour necrosis factor receptor,  
 CC type I or II interleukin-1 cytokine receptor and interleukin-6 cytokine

CC receptor alpha-chain gp80, by delivering the molecules to a tissue  
 CC comprising one or more cells expressing the cytokine receptor or their  
 CC plasma membrane extracellular surface. The ARTS-1 sequences are  
 CC useful for treating a subject, preferably human, displaying, suspected  
 CC of, or at risk of displaying a pathology resulting from abnormal cytokine  
 CC activity, such as tumour necrosis factor alpha, interleukin-lalpha, lbeta  
 CC or interleukin-6. A vector comprising the polynucleotide encoding ARTS-1  
 CC is useful in gene therapy. The ARTS-1 sequences are useful in diagnostic  
 CC and therapeutic regimens in treating immune disorders (e.g. TNF-mediated  
 CC immune diseases) and inflammatory disorders (e.g. rheumatoid arthritis).  
 CC The present sequence represents human ARTS-1 polypeptide  
 XX  
 SQ Sequence 941 AA;

Alignment Scores:  
 Pred. No.: 2e-246 Length: 941  
 Score: 2516.50 Matches: 478  
 Percent Similarity: 69.34% Conservative: 171  
 Best Local Similarity: 51.07% Mismatches: 268  
 Query Match: 49.71% Indels: 19  
 DB: 4 Gaps: 7

US-10-039-073-3 (1-2883) x AAU07829 (1-941)

QY 67 TACTGCTTAACAGCCATCTTGGCCCAATATGCATTGTTCTCAGTTCAGTGCCATCT 126  
 Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30  
 QY 127 AGTTATCACTCACTGAGGATCCTGGGGCTTCCAGTAGCCACTAATGGGAACGATT 186  
 Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47  
 QY 187 CTTGGCAGGAGCTAAGGCTCCCGAGTGTGCTTCTCTCCATTATGACCTCTTTGTC 246  
 Db 48 ProTrpAsnLysIleArgLeuProGluTy-ValIleProValHisTyAspLeuLeu 67  
 QY 247 CACCCCAATCTCACTCTCGGACTTTGTCATCTCAGAGATCGAGTCTTGTCAGC 306  
 Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87  
 QY 307 AATGCTACCCAGTTTATCATCTTGACAGCAAGAGATCTGAAATCAGCAATGCCACCTT 366  
 Db 88 GlnProThrSerThrIleIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 107  
 QY 367 CAGTCAGAGGAAGATTCAAGATACATGAAACCAAGAAAGAACTGAAGTTTTCAGTTAC 426  
 Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125  
 QY 427 CTTGCTCATGAACAAATTGCACCTGCTGTTCCAGAGAAACTTACGCTCAGCTGAAATAC 486  
 Db 126 ProArgGlnGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145  
 QY 487 TATGTGCTATGGACTTCCAAAGCCAAAGTTAGGTAGTGGCTTTGAAGGGTTTATAAAGC 546  
 Db 146 ThrValValIleHisTyAlaGlyAsnLeuSerGluThrPheHisGlyPheTyLysSer 165  
 QY 547 ACATACAGAACTCTTGTGCTGGAACAAAGAAATTTCTCCAGTAACAGATTTTGAGCCAAAC 606  
 Db 166 ThrTyArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 185  
 QY 607 CAGCAGCATGGCTTTCCCTTGTGTTGATGAACCGTTGTTCAAGGCAACTTTTCAATC 666  
 Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205  
 QY 667 AAGATACGAAGAGAGACGAGCATATTGCACTATCCAAACATGCCAAAGGTTAAGACAATT 726  
 Db 206 LysIleArgGlnProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal 225  
 QY 727 GAATCTGAAGAGAGGCTCTTTGGAGAGATCACTTTGAAACTACTGTAAATAATGAGTACATAC 786  
 Db 226 ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr 245  
 QY 787 CTTGTAGCCTACATAGTTTGTGATTCCACTCTCTGAGTGGCTTCACTTCAATCAGGGGTC 846

Db 246 LeuValAlaPheIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 265  
Qy 847 AAGGTGCCATCATATCCAGACAAACGGNATCAACACATATATGCTTTGCAGGCA 906  
Db 266 LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla 285  
Qy 907 TCAGTGAAGTACTGTATTTTATGAAAGTACTTTTGATATCTACTATCCACTCTCCAAA 966  
Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305  
Qy 967 CTGGATTAAATGCTATTCTGACTTTGCACCTGGAGCCATGGAAAAATGGGGCTCAT 1026  
Db 306 GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr 325  
Qy 1027 ACATATAGGAGAGCTCAGTCTTTTGGACCCCAAGACCTCTCTGCTTCGGATAACTG 1086  
Db 326 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerLysLeu 345  
Qy 1087 TGGGTCAACAGAGTCATAGCCCAAGTGGCGCACAGTGGTTTGGCAACCTGGTCACA 1146  
Db 346 GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 365  
Qy 1147 ATGGAATGGTGAATGATATTTGGCTTAAGAGGGTTTTCGAAAAATACATGGAACTTATC 1206  
Db 366 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 385  
Qy 1207 GCTGTTAATGCTACATATCCAGAGCTCAATTTGATGACTATTTTGAATGTGTGTTT 1266  
Db 386 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 405  
Qy 1267 GAAGTAATTACAAAGATTCATTGAATTCATCCCGCTATCTCCAAACCCAGCGAAACC 1326  
Db 406 AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn 425  
Qy 1327 CCGACTCAATACAGGAAATGTTTGATGAAATTCCTATACAAAGGGAGCTGTGATTTTG 1386  
Db 426 ProAlaGlnIleArgGluMetPheAspValSerTyrAspLysGlyAlaCysIleLeu 445  
Qy 1387 AATATGCTCAAGGATTTCTGGGTGAGGAGAAATCCAGAAAGGAATAATTCAGTACTTA 1446  
Db 446 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 465  
Qy 1447 AAGAAGTTCAGCTATAGAAATGCTAAGAATGATGACTGTGGAGCAGTCTGTCAAATAGT 1506  
Db 466 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 485  
Qy 1507 TGTTTAGAAGTGAATTTACATCTGGT-----GGAGTTTGTCTCATTCGGATCCCAAGATG 1560  
Db 486 Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis 503  
Qy 1561 ACAAGTAACATGCTCGCTTCTGGGGGAAATGCAGAGTCAAGAGATGATGACTACA 1620  
Db 504 SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr 523  
Qy 1621 TGGACTCTCAGAAAGAAATCCCTCTGCTGGTGTAAACAAGACGGGTGTCTACTCCGA 1680  
Db 524 TrpThrLeuGlnLysGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 543  
Qy 1681 CTGCAACAGGAGCGCTTCTCCAGGGGTTTCCAGGAAGACCCCTGAATGGAGGGCCCTG 1740  
Db 544 MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro 557  
Qy 1741 CAGGAGAGTACCTGTGGCATATCCCATTCACCTACTCCAGAGTCTTCTAATGTGATC 1800  
Db 558 AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAspMetVal 577  
Qy 1801 CACAGACACATTCATAAATCAAGACAGATACTCTGGATCTACCTGAAAAGACAGCTGG 1860  
Db 578 HisArgPheLeuLeuLysThrLysThrAspValLeuLeuLeuProGluGluValGluTrp 597  
Qy 1861 GTGAAATTTAATGGGACTCAAATGGTTTACTACATCGTTTCACTATGAGGTCATGGATGG 1920  
:::|||||

Db 598 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617  
Qy 1921 GACCAACTCATTTACACAGCTGAATCAGAACACACACTTCTCAGACTTAAGGACAGTA 1980  
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637  
Qy 1981 GGTCTCATTCATGATGTGTTTTCAGCTAGTTGGTGCAGGAGAGCTGACCCCTAGACAAAGCT 2040  
Db 638 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla 657  
Qy 2041 CTTGACATGACTTACCTACCTCCAAATGAAACAGCAGCCCGCAGCTTCTCGAAGTCTG 2100  
Db 658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677  
Qy 2101 AGTTACTTCGGAATCGTTTACCACATGATGGACAGAGGAATATTTTCAGATATCTCTGAA 2160  
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697  
Qy 2161 AACCTCAAGCGTTTACCTTCTTTCAGTATTTTAAACCCAGTGAATTCACAGGCAAGCTCGAGT 2220  
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuAspLeuLeuAspLysGlnThrTrpThr 717  
Qy 2221 GACAGGGCTCAGTCTGGGACAGGATGCTCCGCTCCGCTCTCTTGAAGCTGGCTGTGAC 2280  
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuAlaCysVal 737  
Qy 2281 CTGAACATGCTCCTTGGCATCCAGAAAGCTGTGAATCTTCTCCAGTGGATGGAATCC 2340  
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757  
Qy 2341 AGTGGAAAAATTAATATACCAACAGATGTTTAAAGATTGTGTATTCTGTGGTGTCTCAG 2400  
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777  
Qy 2401 ACACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAATGCTCAATGTCAAGTCTGAA 2460  
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797  
Qy 2461 CAAAACAAATCTGTATCTTGTCAACGAGCAAGCATCAGAAAGTTACTGAAGTTA 2520  
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817  
Qy 2521 ATTGAATAGGAATGGAAGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580  
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837  
Qy 2581 GCGATTGCCAGCTCCAAAGGGCGAGCAACTAGCATGGGATTTGTAGAGAAATGGS 2640  
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857  
Qy 2641 ACCCATCTTCTGAAAAATTTGACTTTGGCTCATATGACATAGGATGATCATCTCTGGC 2700  
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerIleAlaHisMetValMetGly 877  
Qy 2701 ACAACAGCTCACCTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2760  
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluValLysGlyPhePheSerSer 897  
Qy 2761 CTTGAGGCTCAAGGATCAGATCTGGATATTTTCAAACTGTTCTGGAACAGATAACAA 2820  
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917  
Qy 2821 AATATAAATGCTGGAGAGAAATCTTCGACTCTCGACTCTCGAGGACTTGGCTA 2868  
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933  
RESULT 12  
ABB90347  
ID ABB90347 standard; protein; 941 AA.  
XX ABB90347;  
AC ABB90347;  
DT 24-MAY-2002 (first entry)



Qy	1327	CCGACTCAAAATACACAGAAATGTTTGATGAAGATTTCTTATAACACAGGAGCTTGATTTTG	1386
Db	426	ProAlaGlnIleAArgGluMetPheAspAspValSerTyrAspIysGlyAlaCysIleLeu	445
Qy	1387	AATATGCTCAAGGATTTTCTGGGTGAGGAGNAATCCAGAAAGGAATAATTCAGTACTTA	1446
Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheIysSerGlyIleValGlnTyrLeu	465
Qy	1447	AAGAAGTTTCAGCTATAGAAATGCTAAAGATCATGACTTGTGGAGCAGCTCTGTCAAATAGT	1506
Db	466	GlnIysHisSerTyrIysAsnThrLysAsnGluAspLeuTyrAspSerMetAlaSerIle	485
Qy	1507	TGTTTGAAGATGATTTTACATCTGGT-----GGAGTTTGTTCATTCCGGATCCCAAGATG	1560
Db	486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerAArgSerGlnHis	503
Qy	1561	ACAAGTAACATGCTCGCTTCTGGGGGAAATGCACAGAGTCAAAGAGATGATGACTACATA	1620
Db	504	SerSerSerSerHisIstPheHisGlnGluGlyValAspValLysThrMetAsnThr	523
Qy	1621	TGGACTCTCCAGAAAGGAATCCCCCTGCTGGTGTTAAACAAGACGGGTGTTCACTCCGA	1680
Db	524	TrpThrLeuGlnAArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
Qy	1681	CTGCAACAGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGAATGGAGGGCGCTG	1740
Db	544	MetLysGlnGluHisTyrMetLysGly-----SerAspGlyAlaPro	557
Qy	1741	CAGGAGAGGTACCTGTGGCATATCCCATCTGACCTTCTCCAGAGTTCCTTAATGTGATC	1800
Db	558	AspThrGlyTyrLeuTyrPheHisValProLeuThrPheIleThrSerIysSerAspMetVal	577
Qy	1801	CACAGACACATTTCAAATCAAGACAGATACTCTGGATCTACCTGAAAAAGACCATGTGG	1860
Db	578	HisArgPheLeuLeuLysThrLysThrAspValLeuIleLeuProGluValGluTyr	597
Qy	1861	GTGAAATTTAATGTGGACTCAATGGTTACTACATCGTTCACTATGAGGCTCATGATGG	1920
Db	598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTyr	617
Qy	1921	GACCAACTCATATACACAGCTGAATCAACAACACACACTCTCTCAGACCTAAGGACAGATA	1980
Db	618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
Qy	1981	GGTCTGATTCATGATGTGTTTTCAGTCTAGTTGGTGACGGAGACTGACCCCTAGACAAAGCT	2040
Db	638	SerLeuIleAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGluLysAla	657
Qy	2041	CTTGACATGACTTACTACTCTCAACATGAACAACAGACGCCCGCAGCTTCTCGAAGGCTCTG	2100
Db	658	LeuAspLeuSerLeuTyrLeuLysHisIsgluThrGluIleMetProValPheGlnGlyLeu	677
Qy	2101	AGTTACTTGAATCGTTTATACCACATCATGACAGAGGAATATTTCCAGATATCTCTGAA	2160
Db	678	AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr	697
Qy	2161	AACCTCAAGCGTTACTCTTCTCAGTATTTTAAGCCAGTATTCAGACGGCAAGCTGGAGT	2220
Db	698	GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrIstPThr	717
Qy	2221	GACAAGGGCTCAGTCTGGGACAGATGCTCGCTCGCTCTCTTGAAGCTGSCCTGTGAC	2280
Db	718	AspGluGlySerValSerGluAArgMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal	737
Qy	2281	CTGAACCATGCTCTTCATCCCAAGAGCTGCTGAACCTTCTTCCCACTGGATGGAAATCC	2340
Db	738	HisAsnTyrGlnProCysValGlnAArgAlaGluGlyTyrPheArgLysTyrLysGluSer	757
Qy	2341	AGTGGAAAAATTAATATACCAACAGATGTTTTAAAGATTGTGTATTTCTGGGTGCTCAG	2400
Db	758	AsnGlnAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln	777

Qy	2401	ACAACACGACGATGAAGATTACCTTTTAGACGATATATGAACATGTCAATGTCAAGTGCTGAA	2460
Db	778	SerThrGluGlyTrpAspPheLeuTySerLysTyfGlnPheSerLeuSerSerThrGlu	797
Qy	2461	CAAAACAAAATCTGTATGCTTTGTCAACGACGACGATCAGAGAAAAGTTACTGAAGTTA	2520
Db	798	LysSerGlnIleGluPheAlaLeuCyArgThrGlnAsnLysGluLysLeuGlnTrpLeu	817
Qy	2521	ATTGAACCTAGGAATGGAAGAAAAGTTATCAAGACACACAGAACTTGGCAGCTCTCCTTCAT	2580
Db	818	LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr	837
Qy	2581	GGGATTCACGACGTCCTCAAGGGGCGACAACTAGCATGGGATTTGTGAAGAGAAAATTGG	2640
Db	838	LeuIleGlyArgAsnProValGlyTyProLeuAlaTrpGlnPheLeuAlaGlyAsnTrp	857
Qy	2641	ACCATCTTCTGAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCTGGC	2700
Db	858	AsnLysLeuValGlnLysPheGluLeuGlySerSerIleAlaHisMetValMetGly	877
Qy	2701	ACAACAGCTCACCTTTCTTCCAAGGATAAGTCTCAAGAGGTGAAACTATTTTTTGAATCT	2760
Db	878	ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer	897
Qy	2761	CTTGAGGCTCAAGGATCACATCTGGATATTTTTTCAACATGTTCTCGAAACGATAACAA	2820
Db	898	LeuLysGluAsnGlySerGlnLeuArgCyValGlnGlnThrIleGluThrIleGluGlu	917
Qy	2821	AATATAAATGGCTGGAGAGATCTCCGACTCTGAGGACTTGGCTA	2868
Db	918	AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu	933
RESULT	13		
AD	AD56820		
ID	AD56820 standard; protein; 941 AA.		
XX	ADA56820;		
XX	20-NOV-2003 (first entry)		
DT	Human secreted protein #103.		
DE	immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;		
KW	cytostatic; cerebroprotective; neuroprotective; nootropic;		
KW	cardiovascular; antiarteriosclerotic; gene therapy;		
KW	human secreted protein; immune disorder; inflammation;		
KW	respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;		
KW	inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;		
KW	multiple sclerosis; ischemic brain injury; Parkinson's disease;		
KW	Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;		
XX	triple helix formation; antisense gene therapy; forensic biology.		
OS	Homo sapiens.		
XX	WO2002102994-A2.		
XX	27-DEC-2002.		
XX	19-MAR-2002; 2002WO-US008278.		
XX	21-MAR-2001; 2001US-0277340P.		
PR	19-JUL-2001; 2001US-0306171P.		
PR	13-NOV-2001; 2001US-0331287P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
FA	Rosen CA, Ruben SM;		
PI	WPI: 2003-167512/16.		
DR	N-PSDB; ADA55924.		
DR	New human secreted polypeptides and polynucleotides, useful for		
PT	diagnosing, treating or preventing e.g. immune disorders, inflammatory		







```
Db 638 SerLeuIleAsnAenAlaPheGlnLeuValSerIleGlyLysLeuSerIleGlyLysAla 657
Qy 2041 CTTGACATGACTTACTACCTCCACATGAAACAGCAGCCCGCAGCTTCTCGAAGGTCTG 2100
Db 658 LeuAspLeuSerLeuTyLysLeuValSerIleGlyLysLeuValSerIleGlyLysAla 677
Qy 2101 AGTTACTTGAATCGTTTACCACATGATGACAGAGGAATATTTTCAGATATCTCTGAA 2160
Db 678 AsnGluLeuIleProMetTyLysLeuMetGluLysArgAspMetAsnGluValGluThr 697
Qy 2161 AACCTCAAGCGTTACCTTCTCAGTATTTTAAGCCAGTATTCACAGGGAAGCTGAGT 2220
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuAspLeuIleAspLysGlnThrTrpThr 717
Qy 2221 GACAGGCGTCACTGGACAGGATGCTCGCTCGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGluLeuLeuLeuAlaCysVal 737
Qy 2281 CTGAACCATGCTCTCCATCCAGAAAGCTGCTGAACCTCTTCCAGTGGATGGAATCC 2340
Db 738 HisAsnTyrglnProCysValGlnArgAlaGluGlyTyrglnPheArgLysTrpLysGluSer 757
Qy 2341 AGTGGAAATTAATATACCAACAGATGTTTAAAGATTGTGTATCTGTGGGTGCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777
Qy 2401 ACAACAGCAGATGGAATACCTTTTAGACACATATGAATCAAGTCAAGTCTGAA 2460
Db 778 SerThrGluGlyTrpAspPheLeuTyrglnPheSerLeuSerLeuThrGlu 797
Qy 2461 CAAACAAAATTCGTATGCTTTTCAACGAGCAGATCAGGAAAGATTTACTGAAGTTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
Qy 2521 ATTGAATAGGAATGGAAGAAAGTTATCAGACAGACAGATTTGGCAGCTCTCTTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnPheProGlnIleLeuThr 837
Qy 2581 GCGATTCGCCAGCTCCAAAGGGCCAGCACTAGCATGGGATTTTGTAAAGAAATTTGG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyrglnPheLeuAlaTrpGlnPheLeuLysAsnTrp 857
Qy 2641 ACCCATCTCTGAAAAATTTGACTGGGTTCATATGACATAGGATGATCATCTCTGGC 2700
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
Qy 2701 ACAACAGCTCACTTTCTTCCAGGATAAGTTGCAAGAGTGGAACATAATTTTGAATCT 2760
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897
Qy 2761 CTTGAGGCTCAAGCATCACATCTGGATATTTTCAAACTGTTCTGGAACAGTAAACCAA 2820
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917
Qy 2821 AATATAAAATGGCTGGAGAAAGATCTTCCGACTCTGAGGAACTTGGCTA 2868
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933
```

## RESULT 15

ABR00040

ID ABR00040 standard; protein; 941 AA.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunosuppressive; vulnery; chromosome 5q14.3.

Homo sapiens.

WO200276488-A1.

03-OCT-2002.

19-MAR-2002; 2002WO-US008276.

21-MAR-2001; 2001US-0277340P.

19-JUL-2001; 2001US-0306171P.

13-NOV-2001; 2001US-0331287P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2003-029900/02.

N-PSDB; AB271219.

New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.

Claim 13; Page 953-955; 1216pp; English.

AB271190-AB271478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. AB271479-AB271540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, oesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the treatment of immune disorders, inflammation, infection, hyperproliferative disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein of the invention

Sequence 941 AA;

Alignment Scores:  
Pred. No.: 2,53e-246 Length: 941  
Score: 2515.50 Matches: 477  
Percent Similarity: 69.34% Conservative: 172  
Best Local Similarity: 50.96% Mismatches: 268  
Query Match: 49.69% Indels: 19  
DB: 6 Gaps: 7

US-10-039-073-3 (1-2883) x ABR00040 (1-941)

Qy 67 TACTGCTTAACAGCCATCTTGTCCCAAAATATGCAATTTGTTCTCAGTTCAGTGCCATCT 126

15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30

Qy 127 AGTTATCATCTTCACTGAGGATCCCTGGGCTTCCAGTACCCACTAATGGGACGATTT 186

31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47

Qy 187 CCTTGCAGGAGCTAAAGCTCCCGAGTGTGTCATTCCTCCATATGACCTTTTGTC 246

48 ProTrpAsnLysIleArgLeuProGluTyrrValIleProValHisTyrrAspLeuLeu 67





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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: September 26, 2005, 06:43:03 ; Search time 369.314 Seconds  
(without alignments)  
6354.782 Million cell updates/sec

Title: US-10-039-073-3  
Perfect score: 5052  
Sequence: 1 atgttcattcttctgcaat.....ggctaatgggttaactactaa 2883

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 3653108

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=PublishedApplications\_AA -QMTS=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcr -THR MAX=100  
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-MAXLEN=200000000 -USER=US10039073@cgn 1 1 921 @runat\_26092005\_070411\_21348  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5052	99.8	960	13	US-10-039-073-1 Sequence 1, Appli
2	5052	99.8	960	14	US-10-168-425-6 Sequence 6, Appli
3	4141	81.8	785	15	US-10-363-616-459 Sequence 646, App
4	3799	75.0	728	9	US-09-764-853-646 Sequence 819, App
5	3770	74.5	722	9	US-09-764-853-819 Sequence 2, Appli
6	2516.5	49.7	941	15	US-10-220-443-2 Sequence 2723, App
7	2515.5	49.7	941	18	US-10-472-533-329 Sequence 329, App
8	2515.5	49.7	941	18	US-10-472-533-329 Sequence 329, App
9	2515.5	49.7	941	14	US-10-106-698-6381 Sequence 6381, Ap
10	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
11	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
12	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
13	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
14	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
15	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
16	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
17	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
18	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
19	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
20	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
21	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
22	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
23	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
24	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
25	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
26	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
27	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
28	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
29	2512.5	49.6	941	9	US-09-989-722-353 Sequence 353, App
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31	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
32	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
33	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
34	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
35	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
36	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
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38	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
39	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
40	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
41	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
42	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
43	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
44	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App
45	2512.5	49.6	941	10	US-09-989-722-353 Sequence 353, App

ALIGNMENTS

RESULT 1  
US-10-039-073-1  
; Sequence 1, Application US/10039073  
; Publication No. US20020098177A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: 17867, A No. US20020098177A1 Human Amino-peptidase  
; FILE REFERENCE: 35800/240749(5800-36  
; CURRENT APPLICATION NUMBER: US/10/039,073  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 09/345,650  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-039-073-1

## Alignment Scores:

Pred. No.: 0 Length: 960  
Score: 5052.00 Matches: 960  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.80% Indels: 0  
DB: 13 Gaps: 0

US-10-039-073-3 (1-2883) x US-10-039-073-1 (1-960)

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DB 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
QY 121 CCATCTAGTTATCACTTCACAGGATCCCTGGGGCTTTCCAGTAGCCACTTAATGGGGAA 180  
DB 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
QY 181 CGATTTCTTGGCAGGAGCTTAAGGCTCCCGAGTGTGCTCATTTCTCTCCATTATGACCTC 240  
DB 61 ArgPheProTTPGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
QY 241 TTTGTCACCCCAATCTCACTCTCTGACCTTGTGCACTCTGAGAGATCGAAGTCTTG 300  
DB 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
QY 301 GTACAGCAATGCTACCCAGTATTATCATCTTGACAGCAAGATCTTGAAATCACGAATGCC 360  
DB 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
QY 361 ACCCTTCAGTCAGAGGAGATTCAAGATACATGAATCAACAGCAAGAACTGAAAGTTTGT 420  
DB 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
QY 421 AGTTACCTGCTCATGAACAAATTCGACTGCTGTTCCAGAGAACTTAGCCCTCACCTG 480  
DB 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
QY 481 AAATACTATGTGGCTATGGACTTCCAAAGCCAAAGTTAGTGTGCTTGAAGGTTTAT 540  
DB 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
QY 541 AAAAGCACATACAGAACTCTTGGTGGTGAACAGAAATTTCTGCAGTAAACAGATTTTGAG 600  
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QY 601 CCAACCCAGGACGCATGGCTTTCCCTTGTGATGAACGGTTGTTCAAGCCAACTTT 660  
DB 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
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DB 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
QY 721 ACAATTGAATCTGAAGGAGTCTTTTGGAGATCACTTTTGAAACTACTGTAAAAATGAGT 780  
DB 241 ThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLysMetSer 260  
QY 781 ACATACCTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCA 840  
DB 261 ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer 280  
QY 841 GGGGTCAAGGTGTCATCTATGATCCCGACAGAAACGGAAATCAACACATTAATGCTTTG 900  
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DB 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
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DB 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
QY 1021 CTCATTACATATAGGAGAGCTCACCTGCTTTTTCAGCCCAAGACCTCTCTGCTTCGCAT 1080  
DB 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
QY 1081 AAATCTGGGTGTCACAGAGTCATAGCCCATGAATCTGGCGCACAGTGTGTTGGCAACTG 1140  
DB 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
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QY 1201 CTTATCGCTGTTAATGCTACATATCCAGAGCTCAATTTTGATGACTATTTTGAATGTG 1260  
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QY 1261 TGTGTTGAAAGTAATTAACAAAGATTCATTGAATTCATCCCGCCTATCTCCAAACACAGCG 1320  
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DB 441 GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
QY 1381 ATTTTCAATATGCTCAAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATAAATTCAG 1440  
DB 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPheGlnLysGlyIleGln 480  
QY 1441 TACTTAAAGAGTTCAGCTATAGAAATGCTAAGAAATGCTAAGATGATGACTGTGGACAGTCTGCTCA 1500  
DB 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500  
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QY 1621 TGGACTCTCCAGAAAGAAATCCCCCTGCTGCTGTTGTTAAACAGACGGGTGTTCACTCCGA 1680  
DB 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg 560  
QY 1681 CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCAGGAGACCCCTGAATGAGGGCCCTG 1740  
DB 561 LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580  
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DB 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
QY 1921 GACCAACTCATTAACAGCTGAAATCAGAACCAACACACTTCTCAGACTTAAGGACAGAGTA 1980  
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QY 1981 GGTCTGATTCATGATGTTTTCAGCTAGTGTGGTGCAGGGAGACTGACCTTAGACAAAGCT 2040  
DB 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680

QY 2041 CTTGACATGACTTACTACTCTCAACATGAACAACAGCAGCCCGCACTTCTCGAAGTCTG 2100  
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QY 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700  
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QY 2101 AGTTACTTGGAACTCGTTTACCACATGATGGACAGAAGAAATATTTTCAGATATCTCTGAA 2160  
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QY 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnHisSerAspHisSerGlu 720  
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QY 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValHisAspArgGlnSerTrpSer 740  
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QY 2221 GACAAAGGCTCAGTCTGGACAGGATGCTCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280  
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QY 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760  
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QY 2281 CTGAACCATGCTCCTTGGATCCAGAAAGCTGCTGAACCTCTTCCAGTGGATGAATCC 2340  
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QY 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
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QY 2401 ACAACAGCAGGATGAATTTACTCTTTAGCAATATGAACCTGCTCAATGCTCAAGTCTGAA 2460  
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QY 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820  
Db |||||||  
QY 2461 CAACAACAAATTCGTATGCTTGTGTCACGAGCAGCATCGAAGAACTTACTGAAGTTA 2520  
Db |||||||  
QY 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGluLysLeuLeuLysLeu 840  
Db |||||||  
QY 2521 ATTGAACTAGGAATCGAAGAAAGTATTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580  
Db |||||||  
QY 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860  
Db |||||||  
QY 2581 GCGATTGCCAGCTGCCAAAGGGCAGCAACTAGCATGGATTTTGTGAAGAGAAATGG 2640  
Db |||||||  
QY 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
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QY 2641 ACCCATCTCTGAAAAATTTGACTTGGCTGCATATGACATGAAGGATCATCTCTGGC 2700  
Db |||||||  
QY 881 ThrHisLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900  
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Db |||||||  
QY 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920  
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QY 2761 CTTGAGGCTCAAGGATCACTCTGGATATTTTCAAACTGTTCTGGAAACGATTAACCAA 2820  
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QY 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940  
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RESULT 2

US-10-168-425-6  
; Sequence 6, Application US/10168425  
; Publication No. US20030124706A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YANG, Junming  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: BURFORD, Neil  
; APPLICANT: LU, DYOUNG, Janice  
; APPLICANT: LU, DYOUNG, Aina M.  
; APPLICANT: REDDY, Roopa  
; APPLICANT: YUE, Henry  
; APPLICANT: NGUYEN, DANNIEL B.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YAO, Monique G.

; APPLICANT: LAL, Preeti  
; TITLE OF INVENTION: PROTEASES  
; FILE REFERENCE: PI-0003 PCT  
; CURRENT APPLICATION NUMBER: US/10/168,425  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903  
; PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PERL Program  
; SEQ ID NO 6  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030124706A1 60116897CD1  
US-10-168-425-6  
Alignment Scores:  
Pred. No.: 0 Length: 960  
Score: 5052.00 Matches: 960  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.80% Indels: 0  
DB: 14 Gaps: 0  
US-10-039-073-3 (1-2883) x US-10-168-425-6 (1-960)  
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Db 1 MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg 20  
QY 61 GGATTTTACTGCTTAAACAGCCATCTTGCCTCAATATGCAATTTGTTCTCAGTTCTCAGTG 120  
Db 21 GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal 40  
QY 121 CCATCTAGTTATCATCTTCACTGAGATCCTGGGCTTCCAGTAGCCACTAAATGGGAA 180  
Db 41 ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu 60  
QY 181 CGATTTCTTGGCAGGAGCTAAGGCTCCCACTGGTGGTTCATCTCTCCATTATGACCTC 240  
Db 61 ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu 80  
QY 241 TTTGTCACCCCAATCTCACCTCTCTGACTTTGTTGTCATCTGAGAAAGATCGAAGTCTTG 300  
Db 81 PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu 100  
QY 301 GTACGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAATCAGCAATGCC 360  
Db 101 ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla 120  
QY 361 ACCCTTCAGTCAGAGGAAGATTCAAGATACATGAAACCAGGAAAGAACTGAAAGTTTG 420  
Db 121 ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu 140  
QY 421 AGTTACCTGCTCATGAACAAATTTGCACTGCTGTTCCAGAGAACTTTACGCTCACCTG 480  
Db 141 SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu 160  
QY 481 AATATCTATGTGGCTATGGACTTCCAGCCCAAGTTAGTGTAGTGGCTTTGAAGGTTTAT 540  
Db 161 LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr 180  
QY 541 AAAAGCACATACAGAACTCTTGGTGGTGAACAAGAAATCTTTCAGTAACAGATTTTCAG 600  
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QY 601 CCAACCCAGGCACGATGGCTTTCCCTTGTGTTGATGAACCGTGTGTTCAAGCCAACTTT 660  
Db 201 ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe 220  
QY 661 TCAATCAAGATACGAAGAGAGAGCAGGCATATTGCATATTCCACATGCCAAAGGTTAAG 720

Db 221 SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys 240  
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Db 241 ThrIleGluLeuGluGlyLeuLeuGluAspHisPheGluThrValLysMetSer 260  
Qy 781 ACATACCTTGAGGCTACATAGTTGTGATTCTCCACTCTCTGAGTGGCTTCACTTCATCA 840  
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Qy 841 GGGGTCAAGGTGTCATCTATGATCCCGACACAAACGGAATCAAACACATATTGCTTTG 900  
Db 281 GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu 300  
Qy 901 CAGGCATCACTGAAGCTACTTGATTTTATGAAAGTACTTTGATATCTACTATCCACTC 960  
Db 301 GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyrProLeu 320  
Qy 961 TCCAAACTGGATTAAATTGCTATTCTGACTTTGCACTCGAGCCATGGAAAATTGGGGC 1020  
Db 321 SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly 340  
Qy 1021 CTCAATTACATATAGGAGAGCTCACTGCTTTTGGACCCCAAGACCTTTCTGCTTCGAT 1080  
Db 341 LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp 360  
Qy 1081 AACTGTGGGTCAACGAGTCATAGCCCATGAACTGGCGCCACCGATGGTTTGGCAACTG 1140  
Db 361 LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu 380  
Qy 1141 GTCAAACTGGAATGCTGGATGATTTTGGCTTAAGGAGGTTTGGCAAAATACATGGAA 1200  
Db 381 ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu 400  
Qy 1201 CTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTAATTTTGAATGTG 1260  
Db 401 LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal 420  
Qy 1261 TGTTTTCAAGTAAATACAAAGATTCATTAAGTTCATCCCGCCCTACTCCAAACCCAGCG 1320  
Db 421 CysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLysProAla 440  
Qy 1321 GAAACCCCGACTCAAAATACAGGAAATGTTGATGAAGTTTCCCTATAACAAGGAGCTTGT 1380  
Db 441 GluThrProThrGlnIleGlnMetPheAspGluValSerTyrAsnLysGlyAlaCys 460  
Qy 1381 ATTTTGAATATGCTCAAGGATTTTCTCGGTGAGGAGAAATCCAGAAAGGAATAATTCAG 1440  
Db 461 IleLeuAsnMetLeuLysAspPheLeuGlyGluLysPheGlnLysGlyIleIleGln 480  
Qy 1441 TACTTAAGAGATTCAAGTATAGAAATGCTAAGATGATGACTGTGTGGACAGTCTGTCA 1500  
Db 481 TyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspAspLeuTrpSerSerLeuSer 500  
Qy 1501 AATAGTTGTTTAGAAAGTGAATTTTACATCTGGTGGAGTTTGTCAATCCGATCCCAAGATG 1560  
Db 501 AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet 520  
Qy 1561 ACAAGTAACTGCTCGCTTTCTGGGGGAAATGACAGAGTCAAAGAGATGATGATCA 1620  
Db 521 ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr 540  
Qy 1621 TGGACTCTCCAGAAAGAAATCCCTGCTGGTGTAAACAGACGGGTCTTCACTCCGA 1680  
Db 541 TrpThrLeuGlnLysGlyIleProLeuLeuValLysLysGlnAspGlyCysSerLeuArg 560  
Qy 1681 CTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAGACCTCGAATGGAGGGCCCTG 1740  
Db 561 LeuGlnGlnLysArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu 580  
Qy 1741 CAGGAGAGTACCTGTGGCATATCCCATTTGACCTTACCTCCACGAGTTCTTCAATGTGATC 1800

Db 581 GlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerSerAsnValIle 600  
Qy 1801 CACAGACACATTTCTAAATCAAAGACAGATACTCTGATCTACTCTGAAAGACAGTTGG 1860  
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620  
Qy 1861 GTCAAAATTTAATGTGACTCAAAATGCTTACTACATCGTTTCACTATGAGGCTCATGGATGG 1920  
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640  
Qy 1921 GACCAACTCATTTACACAGCTGAATCAGAACCAACACACTTCTCAGACTTAAGACAGAGTA 1980  
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660  
Qy 1981 GGTCTCATTCATGATCTGTTTCACTAGTTGGTCAGGAGACTGACCTTAGACAAAGCT 2040  
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680  
Qy 2041 CTTGACATGACTTACTACCTCCAACATGAAACAAGCGCCCGCACCTTCTCGAAGGTCTG 2100  
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700  
Qy 2101 AGTTACTTGGATCGTTTACACATGATGGACAGAGGAATATTTCCAGATATCTCGAA 2160  
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720  
Qy 2161 AACCTCAAGCTTACCTTCTTCAAGTATTTAAGCCAGTATTGACAGGCAAGCTGGAGT 2220  
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740  
Qy 2221 GACAAGGCTCAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280  
Db 741 AspLysGlySerValTrpAspArgMetLeuAspSerAlaLeuLeuLysLeuAlaCysAsp 760  
Qy 2281 CTGAACCATGCTCTTGGCATCCAGAAAGCTGCTGAACTCTTCCACAGTGGATGGAATCC 2340  
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMetGluSer 780  
Qy 2341 AGTGGAAATTAATATACCAAGATGTTTAAAGATTGTGTATTCTGTGGGTGCTCAG 2400  
Db 781 SerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGlyAlaGln 800  
Qy 2401 ACAACAGCAGGATGGAATTAACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTCTGAA 2460  
Db 801 ThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSerAlaGlu 820  
Qy 2461 CAAAACAAAATCTGTATGCTTTGTCAACGACGACATCAGGAAAGATTACTGAAGTTA 2520  
Db 821 GlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGlnLysLeuLeuLysLeu 840  
Qy 2521 ATTGAACCTAGGAATGGAAGGAAAGTTATCAACACACAGAACTTGGCAGCTCTCCTTCAT 2580  
Db 841 IleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaLeuLeuHis 860  
Qy 2581 GCGATTGCCAGACGCTCCAAAGGGGACGAACTAGCATGGGATTTTGTAAAGAAAAATTGG 2640  
Db 861 AlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGluAsnTrp 880  
Qy 2641 ACCCATCTTCTGAAAAAATTTGACTTGGGCTCATATGACATAGGATGATCATCTCGGC 2700  
Db 881 ThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIleSerGly 900  
Qy 2701 ACAACAGCTCACATTTTCTTCCAAAGGATAAGTTTCAAGAGGTGAAACTATTTTGTGAATCT 2760  
Db 901 ThrThrAlaHisPheSerSerLysAspLysLeuGlnGluValLysLeuPhePheGluSer 920  
Qy 2761 CTTGAGGCTCAAGGATCACATCTGGGATAATTTTCAAACTGTTCTGAAACGATGAACAAA 2820  
Db 921 LeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIleThrLys 940  
Qy 2821 AATATAAATGGCTGAGAGAAATCTCCGACTCTGAGGACTTGGCTTAATGTTAATCT 2880  
Db 941 AsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetValAsnThr 960

## RESULT 3

US-10-363-616-459  
; Sequence 459, Application US/10363616  
; Publication No. US20040044181A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-113 (793)  
; CURRENT APPLICATION NUMBER: US/10/363,616  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 09/654,935  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 490  
; SEQ ID NO 459  
; LENGTH: 785  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-363-616-459

## Alignment Scores:

Pred. No.:	0	Length:	785
Score:	4141.00	Matches:	782
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	2
Query Match:	81.81%	Indels:	0
DB:	15	Gaps:	0

US-10-039-073-3 (1-2883) x US-10-363-616-459 (1-785)

QY	1	ATGTTCCATTCTTCGCAATGTTTAATTCACACAGAAACCAATGTTTAACATTCACAGA	60
DB	1	MetPheHisSerSerAlaMetValAsnSerHisArgLysProMetPheAsnIleHisArg	20
QY	61	GGATTTTACTGCTTAACGCCATCTGCCCAAAATGATGTTTCTCAGTTCCTCAGTG	120
DB	21	GlyPheTyrCysLeuThrAlaIleLeuProGlnIleCysIleCysSerGlnPheSerVal	40
QY	121	CCATCTAGTTATCACTTCACTCAGGATCCTGGGGCTTTCCAGTAGCCCAATAGGGGAA	180
DB	41	ProSerSerTyrHisPheThrGluAspProGlyAlaPheProValAlaThrAsnGlyGlu	60
QY	181	CGATTTCTTGGCAGAGCTAAGGCTCCCGAGTGGTCATTCCTCTCCATTAACCTC	240
DB	61	ArgPheProTrpGlnGluLeuArgLeuProSerValValIleProLeuHisTyrAspLeu	80
QY	241	TTTGTCCACCCCAATCTCACCCTCTGGACTTTGTCATCTGAGAGATCGAAGCTCTTG	300
DB	81	PheValHisProAsnLeuThrSerLeuAspPheValAlaSerGluLysIleGluValLeu	100
QY	301	GTCAGCAATGTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAATCACGAATGCC	360
DB	101	ValSerAsnAlaThrGlnPheIleIleLeuHisSerLysAspLeuGluIleThrAsnAla	120
QY	361	ACCCTTCAGTCAGAGAAAGATCAAGATACATGAAACCCAGGAAAGAACTGAAAGTTTG	420
DB	121	ThrLeuGlnSerGluGluAspSerArgTyrMetLysProGlyLysGluLeuLysValLeu	140
QY	421	AGTTACCTGCTCATGACAAATTCGCTGCTGGTTCAGAGAACTTACGGCTCACCTG	480
DB	141	SerTyrProAlaHisGluGlnIleAlaLeuLeuValProGluLysLeuThrProHisLeu	160
QY	481	AAATACTATGTGGCTATGACTTCCAAGCCAAGTAGTTAGGTGATGGCTTTGAAGGGTTTAT	540
DB	161	LysTyrTyrValAlaMetAspPheGlnAlaLysLeuGlyAspGlyPheGluGlyPheTyr	180
QY	541	AAAGCACATACAGAACTCTTGGTGGTGAAACAAGAAATCTTGCAGTAACAGATTTGAG	600
DB	181	LysSerThrTyrArgThrLeuGlyGlyGluThrArgIleLeuAlaValThrAspPheGlu	200
QY	601	CCAAACCCAGGACGATGCTTCCCTTGTGATGACCCCTGTTTCAAGGCCAATCTT	660
DB	201	ProThrGlnAlaArgMetAlaPheProCysPheAspGluProLeuPheLysAlaAsnPhe	220

QY	661	TCAATCAAGATACGAAGAGAGAGAGGAGATATTCACATATCCAAACATGCCAAAGGTTAAG	720
DB	221	SerIleLysIleArgArgGluSerArgHisIleAlaLeuSerAsnMetProLysValLys	240
QY	721	ACAATTGAACCTTGAGGAGGCTTTTGGACAGTCACTTTGAAACTTACTGTAAAAATGAGT	780
DB	241	ThrIleGluLeuGluGlyGlyLeuGluAspHisPheGluThrValLysMetSer	260
QY	781	ACATACCTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACCTCATCA	840
DB	261	ThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThrSerSer	280
QY	841	GGGTCAAGGTGCTCATCTATGCAATCCCGACAGAAAACGGAATCAACACATATGCTTGTG	900
DB	281	GlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyrAlaLeu	300
QY	901	CAGGCATCACTGAAGCTACTGTTTATGAAAGTACTTTGATATCTACTATCTACCTC	960
DB	301	GlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTrpProLeu	320
QY	961	TCCAAACTGGAATTTAATTTGCTTATTCCTGACTTTTGACCTGGAGCCATCGAAAATGGGCG	1020
DB	321	SerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsnTrpGly	340
QY	1021	CTCATTTACATATAGGAGACGTCACGCTGTTTGTGACCCCAAGACCTCTTCTGCTTCCGAT	1080
DB	341	LeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAlaSerAsp	360
QY	1081	AACTGTGGTCCACAGAGTCATAGCCCATGAACTGGCGCACCCAGTGCTTTGGCAACCTG	1140
DB	361	LysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeu	380
QY	1141	GTCAAAATGGAATCGTGAATGATATTGGCTTAAGGAGGCTTTGCAAAATACATGAA	1200
DB	381	ValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyrMetGlu	400
QY	1201	CTTATCGCTGTTAATGTACATATCCAGAGCTGCAATTTGATGACTATTTTGAATGTG	1260
DB	401	LeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeuAsnVal	420
QY	1261	TGTTTTCGAATTAATACAAAGATTCATTTGAATTCATCCCGCCCTATCTCCAAACCCACG	1320
DB	421	CysPheGluValIleThrLysAspSerLeuAsnSerArgProIleSerLysProAla	440
QY	1321	GAACCCCGACTCAAAATACAGAAATGTTTCATCAAGTTTCCCTATAACAAGGAGCTTGT	1380
DB	441	GluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGlyAlaCys	460
QY	1381	ATTTTGAATATGCTCAAGGATTTTCTGGTGAGAGAAATTCAGAAAGGAATTAATTCAG	1440
DB	461	IleLeuAsnMetLeuLysAspPheLeuGlyGluGlyLysPheGlnLysGlyIleIleGln	480
QY	1441	TACTTAAGAGATTCAGCTATAGAAATCTAAGATGATGATCTGTGGAGCAGTCTGTCA	1500
DB	481	TyrLeuLysLysPheSerTyrArgAsnAlaAsnAsnAspAspLeuTrpSerSerLeuSer	500
QY	1501	AATAGTTTGTAGAAAGTATTTACATCTCGTGGAGTTTCTCATTCGGATCCCAAGATG	1560
DB	501	AsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspProLysMet	520
QY	1561	ACAAAGTAACATGCTCGCTTTCTGGGGGAAATTCAGAGGTCAAAGAGATGATGACTACA	1620
DB	521	ThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGluValLysGluMetMetThrThr	540
QY	1621	TGGACTCTCCAGAAAGGAATCCCTCTGCTGGTGTAAACAAGCGGTGTTCTACTCGA	1680
DB	541	TrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSerLeuArg	560
QY	1681	CTGCAACAGGAGCGCTCTCCTCCAGGGGTTTTCAGGAAGACCCCTGAATGAGGGGCCCTG	1740
DB	561	LeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArgAlaLeu	580

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Qy 1741 CAGGAGAGGTACCTGTGGCATATCCCATTTGACCTACTCCAGAGTCTTCTTAATGTGATC 1800
Db 581 GlnGluArgTyrLeuThrPheHisLeuProLeuThrTyrSerThrSerSerAsnValIle 600
Qy 1801 CACAGACACATTCATAAATCAAGACAGATACCTCTGGATCTACCTGAAAGACCAAGTTGG 1860
Db 601 HisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThrSerTrp 620
Qy 1861 GTGAAATTTAATGTGGACTCAAATGGTTACTACATCGTTCACTATGAGGGTCTAGGATGG 1920
Db 621 ValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHisGlyTrp 640
Qy 1921 GACCAATCATTAACAGCTGAATCAGAACACACACTTCTCAGACCTAAGACAGAGTA 1980
Db 641 AspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAspArgVal 660
Qy 1981 GGTCTGATTCATGATGTGTTTCAGCTAGTTGGTCCAGGGAGACTGACCTAGACAAAGCT 2040
Db 661 GlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAspLysAla 680
Qy 2041 CTTGACATGACTTACTACTCCAACTCAAACATGAACAAGCAGCCCCGCACTTCTCGAAGGTCTG 2100
Db 681 LeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGluGlyLeu 700
Qy 2101 AGTTACTTGGAAATCGTTTACCACATGATGACAGAAAGGAATATTTTCAGATATCTCTGAA 2160
Db 701 SerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIleSerGlu 720
Qy 2161 AACCTCAAGCGTTACCTTCTCAGTATTTAAGCCAGTGTGACAGGCAAGCTGGAGT 2220
Db 721 AsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSerTrpSer 740
Qy 2221 GACAAGGCTCAGTCTGGGACAGGATGCTCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 741 AspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAlaCysAsp 760
Qy 2281 CTGAACCATGCTCTTCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATCC 2340
Db 761 LeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPhePheGlnTrpMetGluSer 780
Qy 2341 AGTGGAAATTA 2352
Db 781 SerGlyLysLeu 784
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RESULT 4
US-09-764-853-646
; Sequence 646: Application US/09764853
; Patent No. US2002090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 646
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-646
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Alignment Scores:
Pred. No.: 0 Length: 728
Score: 3799.00 Matches: 722
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 75.05% Indels: 0
DB: 9 Gaps: 0
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US-10-039-073-3 (1-2883) x US-09-764-853-646 (1-728)

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Db 7 ValLysThrIleGluLeuGluGlyGlyLeuLeuGluAspHisPheGluThrThrValLys 26
Qy 775 ATGAGTACATACCTTGTAGCTACATAGTTTGTGATTTCACACTCTCTGAGTGGCTTCACT 834
Db 27 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 46
Qy 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCCAGACAAACCGGAATCAAAACACATTAT 894
Db 47 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 66
Qy 895 GCTTTCGAGGCATCCTGAAAGCTACTTGAATTTTATGAAAAGTACTTTGATATCTACTAT 954
Db 67 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 86
Qy 955 CCNACTCTCCAAATCGATTTAATTTGCTATTTCTGACTTTTCACCTCGAGCCATGGAAAT 1014
Db 87 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 106
Qy 1015 TGGGGCTCATTTACATATAGGGAGAGCTCACTGCTTTTGTGACCCCAAGACCTCTTCTGCT 1074
Db 107 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerSerAla 126
Qy 1075 TCCGATAAACTGTGGTCCACAGAGTCATAGCCCATGAACTGGCGCACCAAGTGGTTGGC 1134
Db 127 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 146
Qy 1135 AACCTGGTCACATGAAGTGTGGAATGATATTTGGCTTAAGGAGGTTTTCGAAATAC 1194
Db 147 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 166
Qy 1195 ATGGAATCTTATCGCTGTAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGTG 1254
Db 167 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspLysTyrPheLeu 186
Qy 1255 AATGTGTGTTTGAAGTAATTCAAAAAGATTCATTTGAATTCATCCCGCCCTATCTCCAAA 1314
Db 187 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 206
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Db 207 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 226
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Db 247 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 266
Qy 1495 CTGTCAAATAGTTGTTAGAAAGTGAATTTTACATCTGTGGAGTTTGTTCATTCGGATCCC 1554
Db 267 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyGlyValCysHisSerAspPro 286
Qy 1555 AAGATCACAAAGTAAACATGCTCGCTTTCGGGGGAAAAATTCAGAGCTCAAAAGAGATGATG 1614
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Qy 1615 ACTACATGACTCTCCAGAAAGGAATCCCCCTGCTGGTGGTTAAACAAGACGGGTGTTC 1674
Db 307 ThrThrTrpThrLeuGlnLysGlyIleProLeuLeuValLysGlnAspGlyCysSer 326
Qy 1675 CTCGAGTCCAAACAGGAGGCTTCTCCAGGGGTTTTCAGGAAGACCTGATGAGG 1734
Db 327 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 346
Qy 1735 GCCCTCAGGAGAGGTACCTGTGGCATATCCCATTCACCTACTCCACGAGTCTTCTTAAT 1794
Db 347 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 366
Qy 1795 GTGATCCACAGACACATTCATAAATCAAAAGACAGATACCTCTGGATCTTCTGAAAAGACC 1854
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Db 367 VALLIEHISARGHISILEULYSERLYSTHRASPThrLeuAspLeuProGluLysThr 386
QY 1855 ACTTGGGTGAATTAATGTGGACTCAAAATGGTTACTACATCGTTCACTATGAGGGTCAT 1914
Db 387 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 406
QY 1915 GGATGGGACCACTCATACAGAGCTGAATCAGAACCCACACACTCTCTCAGACCTAAGAC 1974
Db 407 GlyTrpAspGlnLeuIleThrGlnLeuAsnGlnAsnHisThrLeuLeuArgProLysAsp 426
QY 1975 AGAGTAGGTCGATTCATCATGTGTTTCAGCTAGTTGGTGGCAGGAGACTGACCCCTAGAC 2034
Db 427 ArgValGlyLeuIleHisAspValPheGlnLeuValGlyAlaGlyArgLeuThrLeuAsp 446
QY 2035 AAGAGCTCTTGACATGACTTACTACCTCCAACATGAACACAGCAGCCCGCACTTCTCGAA 2094
Db 447 LysAlaLeuAspMetThrTyrTyrLeuGlnHisGluThrSerSerProAlaLeuLeuGlu 466
QY 2095 GGTCTGAGTTACTTGAATCGTTTACACATGATGGACAGAGAAATATTCAGATATC 2154
Db 467 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgAsnIleSerAspIle 486
QY 2155 TCTGAAACCTCAAGCGTTACCTTCTTCAGTATTTTAAGCCAGTATTCACAGCGCAAGC 2214
Db 487 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 506
QY 2215 TGGAGTCAGCAAGGGTCAGTCTGGGACAGGATGCTCCGCTCGCTCTCTTGAAGCTGGCC 2274
Db 507 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 526
QY 2275 TGTGACCTGAACCATGCTCTTTCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGAG 2334
Db 527 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 546
QY 2335 GAATCCAGTGGAAATTAATATATACCAACAGATGTTTAAAGATTGTGTATCTGTGGGT 2394
Db 547 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 566
QY 2395 GCTCAGACAAACAGCAGGATGGAATTAACCTTTTAGACATATGAACCTGCAATGTCAAGT 2454
Db 567 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 586
QY 2455 GCTGAACAAACAAATTCGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTG 2514
Db 587 AlaGluGlnAsnLysIleLeuTyrAlaLeuSerThrSerLysHisGlnGlnLysLeuLeu 606
QY 2515 AGTTAATTAAGTAACTAGGAATGAAGAAAGTTATCAAGACACAACTTGGCAGCTCTC 2574
Db 607 LysLeuIleGluLeuGlyMetGluGlyLysValIleLysThrGlnAsnLeuAlaAlaLeu 626
QY 2575 CTTTCATGCGATTGCCAGAGCTCCAAAGGGGACCACTAGCATGGGATTTTGTAAAGAA 2634
Db 627 LeuHisAlaIleAlaArgArgProLysGlyGlnGlnLeuAlaTrpAspPheValArgGlu 646
QY 2635 AATTGGACCCATCTTCTGAAAAAATTTGACTTTGGGCTCATATGACATGAAGATGATCATC 2694
Db 647 AsnTrpThrHisLeuLeuLysLysPheAspLeuGlySerTyrAspIleArgMetIleIle 666
QY 2695 TCTGGCACACAGCTCATCTTTCTTCCAGGATAAGTTGCAAGAGGTGAACACTATTTTTT 2754
Db 667 SerGlyThrThrAlaHisPheSerSerLysAspLysLeuGlnGlnValLysLeuPhePhe 686
QY 2755 GAATCTCTTGAGGCTCAAGGATCACATCTGGATATTTTTTCAACCTGTTCTCGAAGCATA 2814
Db 687 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 706
QY 2815 ACCAAAAATATAAATGGCTGGAGAGAAATCTTCCGACTCTCAGGACTTGGCTTAATGGTT 2874
Db 707 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeuMetVal 726
QY 2875 AATACT 2880
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Db 727 AsnThr 728
RESULT 5
US-09-764-853-819
; Sequence 819, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 819
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (237)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (719)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (720)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (721)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-819
Alignment Scores:
Pred. No.: 0 Length: 722
Score: 3770.00 Matches: 717
Percent Similarity: 99.31% Conservative: 0
Best Local Similarity: 99.31% Mismatches: 5
Query Match: 74.48% Indels: 0
DB: 9 Gaps: 0
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QY 775 ATGAGTACATACCTTTGTAGCCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACT 834
Db 21 MetSerThrTyrLeuValAlaTyrIleValCysAspPheHisSerLeuSerGlyPheThr 40
QY 835 TCATCAGGGGTCAAGGTGTCCATCTATGCATCCCGACAAACCGAATCAACACATTAT 894
Db 41 SerSerGlyValLysValSerIleTyrAlaSerProAspLysArgAsnGlnThrHisTyr 60
QY 895 GCTTTGACGGCATCACGAAGCTACTGATTTTATGAAAAGTACTTTGATATCTACTAT 954
Db 61 AlaLeuGlnAlaSerLeuLysLeuLeuAspPheTyrGluLysTyrPheAspIleTyrTyr 80
QY 955 CCATCTCCAAACCTGGATTTAATTGCTATTCTCCTGCTTTTGCACCTTGGAGCCATGGAAAT 1014
Db 81 ProLeuSerLysLeuAspLeuIleAlaIleProAspPheAlaProGlyAlaMetGluAsn 100
QY 1015 TGGGGCTCATATACATAGGGAGACGTCACTGCTTTTTTGACCCCAAGACCTTCTGCT 1074
Db 101 TrpGlyLeuIleThrTyrArgGluThrSerLeuLeuPheAspProLysThrSerAla 120
QY 1075 TCCGATAACTGTGGGTCCACCAGAGTATAGCCCATGAACCTGGCGCACCAGTGGTTGGC 1134
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Db 121 SerAspLysLeuTrpValThrArgValIleAlaHisGluLeuAlaHisGlnTrpPheGly 140  
Qy 1135 AACCTGGTCAAAATGGATGGTGAATGATATTTGGCTTAAGGAGGGTTTTGCAAAATAC 1194  
Db 141 AsnLeuValThrMetGluTrpTrpAsnAspIleTrpLeuLysGluGlyPheAlaLysTyr 160  
Qy 1195 ATGGAACCTTATCGCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGACTATTTTGTG 1254  
Db 161 MetGluLeuIleAlaValAsnAlaThrTyrProGluLeuGlnPheAspAspTyrPheLeu 180  
Qy 1255 AATGTGTTTGTGAAGTAATACAAAAGATTCATTGAATTCATCCCGCCCTATCTCCAAA 1314  
Db 181 AsnValCysPheGluValIleThrLysAspSerLeuAsnSerSerArgProIleSerLys 200  
Qy 1315 CCAGCGAAACCCGACTCAAATACAGAAATGTTTCATGAAGTTTCTCTATAACAAGGGA 1374  
Db 201 ProAlaGluThrProThrGlnIleGlnGluMetPheAspGluValSerTyrAsnLysGly 220  
Qy 1375 GCTTGTATTTTGAATATGCTCAAGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATA 1434  
Db 221 AlaCysIleLeuAsnMetLeuLysAspPheLeuGlyGluGluLysPhe\*\*LysGlyIle 240  
Qy 1435 ATTCACTACTTAAAGAAGTTCAGCTATAGAAATCTAAGATGATGACTTGTGGAGCAGT 1494  
Db 241 IleGlnTyrLeuLysLysPheSerTyrArgAsnAlaLysAsnAspLeuTrpSerSer 260  
Qy 1495 CTGTCAAATAGTCTTTAGAAAGTGAATTTACATCTGTGGAGTTTGTCAATTCGGATCCC 1554  
Db 261 LeuSerAsnSerCysLeuGluSerAspPheThrSerGlyValCysHisSerAspPro 280  
Qy 1555 AAGATGACAAATACATGCTCGCTTCTCGGGGAAATGACAGAGTCAAGAGATGATG 1614  
Db 281 LysMetThrSerAsnMetLeuAlaPheLeuGlyGluAsnAlaGlu\*\*LysGluMetMet 300  
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Qy 1675 CTCCGACTGCAACAGGAGCGCTTCTCGAGGGGTTTTCCAGGAAGACCCCTGAATGGAGG 1734  
Db 321 LeuArgLeuGlnGlnGluArgPheLeuGlnGlyValPheGlnGluAspProGluTrpArg 340  
Qy 1735 GCCTGCGAGGAGGTACTCTGGCATATCCATTGACCTACTCCAGAGTCTTCTTAAT 1794  
Db 341 AlaLeuGlnGluArgTyrLeuTrpHisIleProLeuThrTyrSerThrSerSerAsn 360  
Qy 1795 GTGATCCACAGACACATCTAAATCAAGACATCTCTGGATCTACCTGAAAGACC 1854  
Db 361 ValIleHisArgHisIleLeuLysSerLysThrAspThrLeuAspLeuProGluLysThr 380  
Qy 1855 AGTTGGGTGAAATTTAATGTGCACTCAAATGGTTACTACATCGTTCACTATGAGGGTCAT 1914  
Db 381 SerTrpValLysPheAsnValAspSerAsnGlyTyrTyrIleValHisTyrGluGlyHis 400  
Qy 1915 GGATGGGACCAACTCATTTACACAGCTGAATCAGAACCAACACTTCTCAGACCTTAAGGAC 1974  
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Qy 1975 AGAGTAGGCTGATTCATGATGTTGTTTTCAGTACTTGTGTCAGGAGACTGACCTAGAC 2034  
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Qy 2035 AAAGCTCTTGACATGACTTACTACTCTCAACATGAAACAAGCAGCCCGCAGCTTCTCGAA 2094  
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Qy 2095 GGTCTGATTTACTTGGAAATCGTTTTTACACATGATGACAGAAAGAAATATTTTCAGATATC 2154  
Db 461 GlyLeuSerTyrLeuGluSerPheTyrHisMetMetAspArgArgAsnIleSerAspIle 480  
Qy 2155 TCTGAACACCTCAGCGGTACTCTTTCAGTATTTTAAAGCCAGTGATGACAGCGCAAGC 2214  
Db 481 SerGluAsnLeuLysArgTyrLeuLeuGlnTyrPheLysProValIleAspArgGlnSer 500

Qy 2215 TGGAGTGACAAGGGCTCAGTCTGGGACAGGATGCTCGGCTCGGCTCTCTTTGAAAGCTGGCC 2274  
Db 501 TrpSerAspLysGlySerValTrpAspArgMetLeuArgSerAlaLeuLeuLysLeuAla 520  
Qy 2275 TGTGACTGAAACCATGCTCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCAGTGGATG 2334  
Db 521 CysAspLeuAsnHisAlaProCysIleGlnLysAlaAlaGluLeuPheSerGlnTrpMet 540  
Qy 2335 GAATCAGTGGAAAAATTAATATACCAACAGATGTTTAAAGATTGTGTATTCTGTGGGT 2394  
Db 541 GluSerSerGlyLysLeuAsnIleProThrAspValLeuLysIleValTyrSerValGly 560  
Qy 2395 GCTCAGACAACAGCAGGATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGT 2454  
Db 561 AlaGlnThrThrAlaGlyTrpAsnTyrLeuLeuGluGlnTyrGluLeuSerMetSerSer 580  
Qy 2455 GCTGAACAAAACAAAATCTCTGTATGCTTGTCAACGAGCAGCATCAGGAAAGTACTG 2514  
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Qy 2575 CTTTCATCGCATTCGCCAGAGCTCCAAAAGGGCAGCAACTAGCATGGGATTTTGTAAAGAA 2634  
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Qy 2635 AATTGACCCCATCTCTGAAAAAATTTGACTTGGGCTCATATCACAATAAGGATGATCATC 2694  
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Qy 2695 TCTGGCACAAACAGCTCACTTTTCTTCCAAAGGATAAGTTGCAAGAGGTGAAACTATTTTT 2754  
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Qy 2755 GAATCTCTTGGAGCTCAAGGATCACATCTGGATATTTTCAAACTGTTCGTGAAACGATA 2814  
Db 681 GluSerLeuGluAlaGlnGlySerHisLeuAspIlePheGlnThrValLeuGluThrIle 700  
Qy 2815 ACCAAAAATATAAATGGCTGGAGAGAATCTTCCGACTGAGGACTTGGCTAATGGTT 2874  
Db 701 ThrLysAsnIleLysTrpLeuGluLysAsnLeuProThrLeuArgThrTrpLeu\*\*\*\*\* 720  
Qy 2875 AATACT 2880  
Db 721 \*\*\*Thr 722  
RESULT 6  
US-10-220-443-2  
; Sequence 2, Application US/10220443  
; Publication No. US20030215820A1  
; GENERAL INFORMATION:  
; APPLICANT: Levine, Stewart  
; TITLE OF INVENTION: REGULATORS OF TYPE-1 TUMOR NECROSIS FACTOR RECEPTOR AND OTHER CYT  
; TITLE OF INVENTION: RECEPTOR SHEDDING  
; FILE REFERENCE: 218732  
; CURRENT APPLICATION NUMBER: US/10/220,443  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/06464  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/185,586  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 941  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-220-443-2  
Alignment Scores:

Pred. No.:	5.2e-228	Length:	.941
Score:	2516.50	Matches:	478
Percent Similarity:	69.34%	Conservative:	171
Best Local Similarity:	51.07%	Mismatches:	268
Query Match:	49.71%	Indels:	19
DB:	15	Gaps:	7
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Qy	127	AGTTATCACTTCACGTAGGATCCCTGGGGCTTTCCAGTAGCACCTAATGGGAACGATT	186
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Qy	187	CCTTGGCAGGAGCTAAGGCTCCCGAGTGTGTCTCTCTCCATTATGACCTCTTTGTC	246
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Qy	247	CACCCCAATCTCACCTCTCGACTTTGTCATCTGAGAAGATCGAAGTCTTGTCACG	306
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Qy	307	AATGCTACCCAGTTTATCATCTTGACACGAAGAATCTTGAATCAGCAATGCCACCCCT	366
Db	88	GlnProThrSerThrIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107
Qy	367	CAGTCAGAGGAAGATTCAAGATACATGAACACAGAAAGAATCTGAAGATTTTGAGTTAC	426
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Qy	487	TATGTGCTGTGACTTCCCAAGCCAAGTTAGTGATGGCTTTGAAGGGTTTTATAAAGC	546
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
Qy	547	ACATACAGAACTCTTGGTGTGAACAAAGAAATCTTGCAGTAAACAGATTTGAGCCAAAC	606
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Qy	607	CAGCAGCATGGCTTTCCCTGCTTTTGATCAACCGTGTGTTCAAGCCAACTTTTCAATC	666
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Qy	667	AAGATACGAAGAGAGCAGGCATATTGCACATATCCAACTATCCAAAGTTTAAGACAACT	726
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Qy	787	CTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCATTCATCAGGGGTC	846
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Qy	847	AAGGTGTCCATCTATGATCCCAAGCAAAACGGAAATCAACACATTTATGCTTTCAGCA	906
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Qy	907	TCACTGAAGCTACTTGATTTTATGAAAGTACTTTGATATCTACTACTCCACTCTCCAAA	966
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Qy	967	CTGATTTAATTCCTATTCCTGACTTTGCCACTGGAGCCATGGAAAATTTGGGGCTCAT	1028
Db	306	GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325

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Qy 2221 GACAAGGCGTCAGTCTGGGACAGATGCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280
Db 718 AspGluGlySerValSerGluArgMetLeuArgSerGlnLeuLeuLeuLeuAlaCysVal 737
Qy 2281 CTGAACCATGCTCTTGTGATCCAGAAAGCTGCTGAACTTCTCCCAAGTGATGGAATCC 2340
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
Qy 2341 AGTCGAAATTAATATACCAACAGATGTTTAAAGATTGTGTATCTGTGGGTGCTCAG 2400
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValAlaGln 777
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Qy 2461 CAAACAAATTCGTATGCTTGTCTCAACGAGCAAGCATCAGGAAAGTTACTGAACTTA 2520
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817
Qy 2521 ATTCAACTAGGAATGGAGGAAGGTTATCAAGACACAGAACTTGGCAGCTCTCTTCAT 2580
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837
Qy 2581 GCGATTGCCAGCTCCAAAGGGCGCAGCAACTAGCATGGATTTTGTAAAGAAATTTGG 2640
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857
Qy 2641 ACCCATCTTCAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGC 2700
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877
Qy 2701 ACAACAGCTCACTTTCTTCCAAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2760
Db 878 ThrThrAsnGlnPheSerThrThrArgThrArgLeuGluGluValLysGlyPhePheSer 897
Qy 2761 CTGAGGCTCAAGGATCACATCTGGATATTTTCAAACTGTCTTGGAAACGATAACCAA 2820
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Qy 2821 AATATAAATGGCTGGAGAGAATCTTCCGACTCTGAGGACTGGCTA 2868
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RESULT 7

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US-10-264-237-2723
; Sequence 2723, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P131P1
; CURRENT APPLICATION NUMBER: US/10/264, 237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2723
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2723
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Alignment Scores:
Pred. No.: 6,46e-228 Length: 941
Score: 2515.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 49.69% Indels: 19
DB: 15 Gaps: 7

US-10-039-073-3 (1-2883) x US-10-264-237-2723 (1-941)

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Qy 127 AGTTATCACTTCACTCAGGATCCTGGGGCTTCCAGTAGTCCACTAATGGGGAACGATTT 186
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47
Qy 187 CTTTGGCAGGAGCTAAGGCTCCCGAGTGGTTCATTCCTCTCCATATGACCTTTTGTGTC 246
Db 48 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeu 67
Qy 247 CACCCCAATCTCACTCTCTGGACTTTTGTGATCTGAGAGATCGAAGTCTTGGTCAGC 306
Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrLysValGluIleThrAlaSer 87
Qy 307 AATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTTGAATCAGCAATGCACCTT 366
Db 88 GlnProThrSerThrIleIleLeuHisSerHisIleGlnIleSerArgAlaThrLeu 107
Qy 367 CAGTCAGAGGAAGATTCAAGATACATGAAACCAAGGAAAGAACTGAGAAAGTTTGGATTAC 426
Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125
Qy 427 CTGCTCATGAACAAATTCGACTGCTGCTTCCAGAGAAACTTACGCTCACCTGAAATAC 486
Db 126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145
Qy 487 TATGTGGCTATGGACTTCCAAAGCAAGTAGGTAGGTGGCTTTGAAGGGTTTATAAAGC 546
Db 146 ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165
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Qy 607 CAGGCAGCATGCTTTCCTTCTGATTTTGTATGACCGTCTTCAAGCCAACTTTTCAATC 666
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Qy 727 GAACTTGAAGGAGGTCTTTTGGAAAGATCACTTTGAAACTACTGTAAATAGTGTACATAC 786
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Db 286 AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys 305
Qy 967 CTGGATTTAATGCTATTCTGACTTTTGACCTGGAGCCATGGAATTTGGGGCCCTCATT 1026
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; ORGANISM: Homo sapiens									
US-10-472-533-329									
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Percent Similarity:	69.34%	Conservative:	172						
Best Local Similarity:	50.96%	Mismatches:	268						
Query Match:	49.69%	Indels:	19						
DB:	18	Gaps:	7						
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Db	15	PhelLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer	30	Db	306	GlnAspLeuAlaAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325		
Qy	127	AGTTATCATCTCACTGAGGATCTCGGGCTTCCAGTAGCCACCAATAGGGGAACGATTT	186	Qy	1027	ACATATAGGAGAGCAGTCACCTGCTTTTGAACCCCAAGACCTCTTCTGCTTCCGATAAACTG	1086		
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47	Db	326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345		
Qy	187	CTTTGGCAGGAGCTAAGGCTCCCGAGTGTGGTCAATCTCTCCATTATGACCTCTTTGTC	246	Qy	1087	TGGGTCCACAGAGTCATAGCCCATGAATCGCGCCACAGTGGTTTGGCAACCTGGTCACA	1146		
Db	48	ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle	67	Db	346	GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365		
Qy	247	CACCCCAATCTCACTCTCGGACTTTGTCATCTGAGAGATCGAAGTCTTGGTCAGC	306	Qy	1147	ATGGAATGTGGAATGATATTTGGCTTAAGAGGGTTTTGC AAAATACATGGAACCTTATC	1206		
Db	68	HisAlaasnLeuThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87	Db	366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385		
Qy	307	AATGCTACCCAGTTTATCATCTTCGACAGCAAGATCTTGAATACAGAAATGCGCCCTT	366	Qy	1207	GCTGTTAATGCTACATATCCAGAGCTGCAATTTGATGATCACTATTTTTCGAATGTGTGTTT	1266		
Db	88	GlnProThrSerThrIleIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu	107	Db	386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405		
Qy	367	CAGTCAGGGAAGATTCAAGATACATGAAACCGAGGAAAGAACTCAAAGTTTTCAGTTAC	426	Qy	1267	GAAGTAATTACAAAAGATTCATTGAATTCATCCGCCCTATCTCCAAAACAGCGGAAC	1326		
Db	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125	Db	406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425		
Qy	427	CTGTGCTCATGAACAAATGCACTGCTGGTTCAGAGAAACTTACGCCTCACTGAAATAC	486	Qy	1327	CCGACTCAAAATACAGAAATGTTTGAATGTTTCTATAACAAGGGAGCTTGTATTTTG	1386		
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145	Db	426	ProAlaGlnIleArgGluMetPheAspValSerTyrAspLysGlyAlaCysIleLeu	445		
Qy	487	TATGTGCTATGAGCTTCCAGCCAAAGTATAGTGATGGCTTTGAAGGGTTTATAAAGC	546	Qy	1387	AATATGCTCAAGATTTTCTGGGTGAGGAGAAATTCAGAAAGAAATTAATTCAGTACTTA	1446		
Db	146	ThrValValIleHisTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165	Db	446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465		
Qy	547	ACATACAGAACTCTGGTGGTGAACAGATTTCTGCAGTAACAGATTTTGAGCCCAACC	606	Qy	1447	AGAAGTTCTCAGCTATAGAAATGCTAAGAATGATGACTTGTGGAGCAGTCTGCTCAAAATAGT	1506		
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Qy	667	AAGATACGAAGAGAGCAGGCATATTGCACTATCCACATGCCAAAGTTTGAAGCAATT	726	Db	504	SerSerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523		
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Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245	Qy	1681	CTGCAACAGGAGCGCTTCTCCAGGGGGTTTTCCAGGAAGACCTGAAATGGAGGGCCCTG	1740		
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Db	266	LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla	285	Qy	1801	CACAGACACATCTTAAATCAAAAGACAGATACCTCTGGATCTACTGAAAAACAGCAGTTGG	1860		
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Db	286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305	Qy	1861	GTGAAATTTAATGTGAGCTCAAAATGGTTACTACATCGTTCATGAGGGTCAATGATGG	1920		

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Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757
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RESULT 9
US-10-106-698-6381
; Sequence 6381, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
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; SEQ ID NO 6381
; LENGTH: 944
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6381

Alignment Scores:
Pred. No.: 6,47e-228 Length: 944
Score: 2515.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 49.69% Indels: 19
DB: 14 Gaps: 7

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QY 127 AGTTATCATCTTCACTGAGGATCTCGGGGCTTTCAGTAGCCACTAATGGGAAGATT 186
Db 34 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 50
QY 187 CTTGGCAGGAGCTAAGCTCCCGAGTGTGCTCATTTCTCTCCATTATGACTCTTTGTC 246
Db 51 ProTrpAsnLysIleArgLeuProGluTyrValIleProValHisTyrAspLeuLeuIle 70
QY 247 CACCCCAATCTCACTCTCTGACTTTGTTGCATCTGAGAAGATCGAAGTCTTGGTCAGC 306
Db 71 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 90
QY 307 AATGCTACCCAGTTTATCATCTTCACAGCAAGATCTTGAATCAGCAATGCCACCTT 366
Db 91 GlnProThrSerThrIleIleLeuHisSerHisLeuGlnIleSerArgAlaThrLeu 110
QY 367 CAGTCAGAGGAGGATTCAGATATCATGAAACCAGGAAGAACTGAAAGTCTTGAATAC 426
Db 111 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 128
QY 427 CTTGCTCATGAACAAATTTGCACTGCTGTTCCAGAGAACTTTAGCGCTCAGCTGAAATAC 486
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QY 487 TATGTGCTATGACTTTTCCAAAGCCCAAGTTAGGTAGTGGCTTTGAAGGGTTTATAAAGC 546
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Db 169 ThrTyrArgThrLysGluGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr 188
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QY 787 CTTGTAGCTACATAGTTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCAATCAGGGGTC 846
Db 249 LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal 268
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Db 269 LysValSerValTyrAlaValProAspLysMetAsnGlnAlaAspTyrAlaLeuAspAla 288
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Qy 1027 ACATATAGGAGAGCGTCACTGCTTTTGGACCCCAAGACCTCTCTCGCTCCGATAAACTG 1086  
Db 329 ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu 348  
Qy 1087 TGGGTCAACAGAGCATAGCCCATGAAGTGGCGCACCGAGTGGTTTGGCAACCTGGTCACA 1146  
Db 349 GlyIleThrMetThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr 368  
Qy 1147 ATGGAATGGTGAATGATATTTGGCTTAAGAGAGGTTTGGCAAAATACATGAACCTTATC 1206  
Db 369 MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal 388  
Qy 1207 GCTGTTAATGCTACATATCCAGAGCTGCAATTTTCATGACTATTTTGAATGTGTGTTT 1266  
Db 389 SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe 408  
Qy 1267 GAAGTAATTACAAAGATTTCATTAATTCATCCCGCCCTATCTCCAAACACGCGGAAC 1326  
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Qy 1327 CCGACTCAATACAGGAATGTTTGAATGCAAGTTCCTTAACAGGGAGCTGTGATTTTG 1386  
Db 429 ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu 448  
Qy 1387 AATATGCTCAAGGATTTCTGGTGAGGAGAAATTCAGAAAGGAATAAATTCAGTACTTA 1446  
Db 449 AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu 468  
Qy 1447 AAGAAGTTCAGCTATAGAAATGCTAAGAATGATCACTTGTGGACAGCTGTCTCAAAATG 1506  
Db 469 GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle 488  
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Qy 1621 TGGACTCTCCAGAAGGAATCCCTCTGCTGTGTGTTAAACAAGACGGGTGTCTACCGA 1680  
Db 527 TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis 546  
Qy 1681 CTGCAACAGGAGCGCTCTCCAGGGGTTTCCAGGNAGCCCTGATGGAGGGCCCTG 1740  
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Qy 1741 CAGGAGAGTACCTGTGGCATATCCATCCACTACTCCAGAGTCTCTCTAAATGTGATC 1800  
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Qy 1801 CACGACACATTTCAAAATCAAGACAGATACTCTGGATCTCTACCTGAAAGACAGTTGG 1860  
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Qy 1861 GTGAATTAATGGACTCAATGGTTTACTACATCGTTTCACTATGAGGGTCATGGATGG 1920  
Db 601 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 620  
Qy 1921 GACCAACTCATTACACACTGAATCAGAAACACACACTTCTCAGACCTTAAGACACAGATA 1980  
Db 621 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 640  
Qy 1981 GGTCTGATTCATGATGTTTTCAGCTAGTTGGTGAGGAGACTGACCTTAGACAAAGCT 2040

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## RESULT 10

US-09-989-722-353  
; Sequence 353, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
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PRIOR FILING DATE: 1998-06-03  
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PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
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PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1,24e-227 Length: 941
Score: 2512.50 Matches: 477
Percent Similarity: 69.34% Conservative: 172
Best Local Similarity: 50.96% Mismatches: 268
Query Match: 19 Indels: 19
DB: 7 Gaps: 7

US-10-039-073-3 (1-2883) x US-09-989-722-353 (1-941)

Qy 67 TACTGCTTAACGCCATCTTGCCCAATATGCAATTTGTTCTCAGTTCTCAGTCCCATCT 126
   :: |||:::||||| :: :: |||:::|||||
Db 15 PheLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer 30

Qy 127 AGTTATCACTTCACTCAGGATCCTGGGGCTTCCAGTAGCCACTAATAGGGGACGATTT 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe 47

Qy 187 CTTTGGCAGGAGTAAGGCTCCCCAGTGTGGTCATTCTCTCCATTATGACCTCTTTGTC 246
   ||||| ::|||:::||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 48 ProTrpAsnLysileArgLeuProGluTyrValIleProValHisTyrAspLeuIle 67

Qy 247 CACCCCAATCTCACTCTCTGAGACTTTGTTGTCATCTGAGAGATCGAAGTCTTGGTCAGC 306
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68 HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer 87

Qy 307 AATGCTACCCAGTTTATCATCTTGACAGCAAGATCTTGAATCACCAAGTCCACCCCTT 366
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 88 GlnProThrSerThrIleIleIleHisSerHisLeuGlnIleSerArgAlaThrLeu 107

Qy 367 CAGTTCAGAGGAAGATTCAAGATACATGAACACCGAGGAAGAACTGAAAGTTTTCAGTTAC 426

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**Alignment Scores:**

Pred. No.:	1,248-227	Length:	941
Score:	2512.50	Matches:	477
Percent Similarity:	69.34%	Conservative:	172
Best Local Similarity:	50.96%	Mismatches:	268
Query Match:	49.63%	Indels:	19
DB:	9	Gaps:	7

US-10-039-073-3 (1-2883) x US-09-989-723-353 (1-941)

Qy	67	TACTGCTTAAACAGCCATCTTGCCCCCAANATATGCATTTGTTCTCAGTTCTTCTCAGTGCCCATCT	126
Db	15	PhuLeuLeuSerSerLeuLeuAlaLeuLeuThrVal-----SerThrProSer	30
Qy	127	AGTTATCACTTCACGTAGGATCCTCGGGCTTTCCAGCTAGCCACTAATGGGAACGATTT	186
Db	31	TrpCysGlnSerThrGlu-----AlaSerProLysArgSerAspGlyThrProPhe	47
Qy	187	CTTTGGCAGGAGCTAAGGCTCCCCAGTGTGGTCATTCTCTCCATTATGACCTCTTTGTGTC	246
Db	48	ProTyrAsnLysIleargLeuProGluTyrValIleProValHisIstyrAspLeuLeuIle	67
Qy	247	CACCCCAATCTCACTCTCTGAGCTTTGTTGGCATCTGAGAAGATCGAAGTCTTGGTCAGC	306
Db	68	HisAlaAsnLeuThrThrLeuThrPheTrpGlyThrThrLysValGluIleThrAlaSer	87
Qy	307	AATGCTTACCAGTTTATCATCTTGACAGCAAGATCTTGAATACAGAAATGCCACCCCTT	366
Db	88	GlnProThrSerThrIleIleLeuHisSerHisIleGluGlnIleSerArgAlaThrLeu	107
Qy	367	CAGTCAGAGGAAGATTCAAGATACATGAAACCCAGGAAGAACTGAAAGTTTTCAGTTAC	426
Db	108	ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis	125
Qy	427	CCTGCTCATGAACAAATTGCACTGCTGTTCCAGAGAAACTTAGCCCTCACTGAAATAC	486
Db	126	ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr	145
Qy	487	TATGTGGCTATGCACTTCCAAGCCAAAGTTAGTGTGATGGCTTTGAAGGGTTTATAAAGC	546
Db	146	ThrValValIleHisIstyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer	165
Qy	547	ACATACAGAACTCTTGGTGGTGAACAAAGAATCTTCGCAGTAAACAGATTTTGAGCCAAC	606
Db	166	ThrTyrArgThrLysAsnGlyGluLeuArgIleLeuAlaSerThrGlnPheGluProThr	185
Qy	607	CAGGCAGCATGGCTTTCCTTGCTTTGATGAACGGTTGTTCAAGCCAACTTTTCAATC	666
Db	186	AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle	205
Qy	667	AGATACGAAGAGAGAGCAGGCATATTCATCTCCAACTCCCAAGCTGCAAGGTTTAAACAAT	726
Db	206	LysIleArgArgGluProArgHisLeuAlaIleSerAsnMetProLeuValLysSerVal	225
Qy	727	GAACTTGAAGGAGGTCTTTTGAAGATCACTTTTGAAACTACTGTAAAAATGAGTACATAC	786
Db	226	ThrValAlaGluGlyLeuIleGluAspHisPheAspValThrValLysMetSerThrTyr	245
Qy	787	CTTGAGCCTACATAGTTTGTGATTCTTCACCTCTCTGAGTGGCTTCATCTCATCAGGGTTC	846
Db	246	LeuValAlaPheIleIleSerAspPheGluSerValSerLysIleThrLysSerGlyVal	265
Qy	847	AAGGTCTCCATCTATGTCATCCCCACAAACCGGAATCAAAACATATATGCTTTTGACGCA	906
Db	266	LysValSerValTyrAlaValProAspLysIleAsnGlnAlaAspTyrAlaLeuAspAla	285
Qy	907	TCATCGAAGCTACTTGATTTTTTATGAAAGACTTTTGTATCTACTATTCACCTCTCCAAA	966

286	AlaValThrLeuLeuGluPheTyrGluAspTyrPheSerIleProTyrProLeuProLys	305
967	CTGATTAAATTCGTATTCCTGACTTTGACCTGGAGCCATGAGAAATGGGCGCTCAT	1026
306	GlnAspLeuAlaIleProAspPheGlnSerGlyAlaMetGluAsnTrpGlyLeuThr	325
1027	ACATATAGGAGACGTCACTGCTTTTGTGACCCCAAGACCTCTTCTGCTCCGATAAATCG	1086
326	ThrTyrArgGluSerAlaLeuLeuPheAspAlaGluLysSerSerAlaSerSerLysLeu	345
1087	TGGGTCCACAGAGTCATAGCCCATGAACCTGGCGCACCACTGGTTTGGCAACCTGGTCACA	1146
346	GlyIleThrValThrValAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThr	365
1147	ATGGAATGGTGGAAATGATATTTCGCTTAAGCAGGGTTTGCAGAAATACATGGAACATTATC	1206
366	MetGluTrpTrpAsnAspLeuTrpLeuAsnGluGlyPheAlaLysPheMetGluPheVal	385
1207	GCTGTTAAATGCTACATATCCAGAGCTGCAATTTTGATGACTATTTTGAATGTGCTTTT	1266
386	SerValSerValThrHisProGluLeuLysValGlyAspTyrPhePheGlyLysCysPhe	405
1267	GAAGTAATTACAAAAGATTCATTGAAATTCATCCGCGCTATCTCCAAAACCGCGGAACCC	1326
406	AspAlaMetGluValAspAlaLeuAsnSerSerHisProValSerThrProValGluAsn	425
1327	CCGACTCAAAATACAGAAATGTTTGATGAAGTTTCCTATAACAAGGAGAGCTGTATTTTG	1386
426	ProAlaGlnIleArgGluMetPheAspAspValSerTyrAspLysGlyAlaCysIleLeu	445
1387	AATATGCTCAAGGATTTTCTGGGTGAGAGAAATTCAGAAAAGGAATAATTCAGTACTTA	1446
446	AsnMetLeuArgGluTyrLeuSerAlaAspAlaPheLysSerGlyIleValGlnTyrLeu	465
1447	AAGAAGTTCAGCTATAGAAATGCTAGAAATGATGACTTGTGGAGCAGCTGTGCAATAGT	1506
466	GlnLysHisSerTyrLysAsnThrLysAsnGluAspLeuTrpAspSerMetAlaSerIle	485
1507	TGTTTAGAAGTCATTTTACATCTCGT-----GGAGTTTGTTCATTCGGATCCCAAGATG	1560
486	Cys---ProThrAspGlyValLysGlyMetAspGlyPheCys---SerArgSerGlnHis	503
1561	ACAAGTAACATGCTGCCTTTCTGGGGGAAATGCGAGAGTCAAAGAGATGATGACTACA	1620
504	SerSerSerSerHisTrpHisGlnGluGlyValAspValLysThrMetMetAsnThr	523
1621	TGCACTCTCCAGAAAGAAATCCCTCTGCTGGTGGTTAAACAAGACGGGTGTTCACTCCGA	1680
524	TrpThrLeuGlnArgGlyPheProLeuIleThrIleThrValArgGlyArgAsnValHis	543
1681	CTCAACAGAGCGCTTCTCCAGGGGGTTTCCAGGAAGACCCCTGAATGGAGGGCCCTG	1740
544	MetLysGlnGlnHisTyrMetLysGly-----SerAspGlyAlaPro	557
1741	CAGGAGAGGTACTCTGTGGCATATCCCATCTGACCTACTCCACAGAGTTCTTCTAATGTGATC	1800
558	AspThrGlyTyrLeuTrpHisValProLeuThrPheIleThrSerLysSerAsnMetVal	577
1801	CACAGACACATTTAAATCAAAGACAGATACTCTGGATCTCTACCTGAGAAAGCACGTTGG	1860
578	HisArgPheLeuLysThrLysThrAspValLeuIleLeuProGluGluValGluTrp	597
1861	GTCAAAATTAATGTGACCAATAGTTACTCATCTGTTTCACTATGAGGGTCAATGATCGS	1920
598	IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspGlyTyr	617
1921	GACCAACTATTACACAGCTGAATCAGAACACCACACTTCTCAGACCTTAAGGACAGATGA	1980
618	AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla	637
1981	GGTCTGATTCATGATGTGTTTCAGCTAGTTGTGTGAGGAGACTGACCCCTAGACAAAGCT	2040
638	SerLeuIleAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGlyLysAla	657



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; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1.24e-227	Length:	941
Score:	2512.50	Matches:	477
Percent Similarity:	69.34%	Conservative:	172
Best Local Similarity:	50.96%	Mismatches:	268
Query Match:	49.63%	Indels:	19
DB:	9	Gaps:	7

US-10-039-073-3 (1-2883) x US-09-989-279-353 (1-941)

Qy	67	TACTGCTTAACAGCCATCTTGC	CCCAATATGCAATTTGTTCTCAGTTC	TCTCAGTGCCATCT	126
Db	15	PhelLeuLeuSerSerLeuLeuAlaLeuLeuThrVal	-----	SerThrProSer	30
Qy	127	AGTTATCACTTCACCTGAGGATCC	TGGGGCTTCCAGTAGCCACTAAT	TGGGAAGATT	186
Db	31	TrpCysGlnSerThrGlu-----	AlaSerProLysArgSerAspGlyThrProPhe		47
Qy	187	CTTTGGCAGGAGCTAAGGCTCC	CCAGTGTGGTCATTCTCTCCATTAT	GACCTCTTTGTC	246
Db	48	ProTrpAenLysIleArgLeuProGluTyr	ValIleProValHisTyrAspLeuLeuIle		67
Qy	247	CACCCCAATCTCAGCTCTCTG	GACTTGTTCATCTGAGAGATCGA	AGTCTTGGTCAGC	306
Db	68	HisAlaLeuLeuThrLeuThrPhe	TrpGlyThrThrLysValGluLeuThrAlaSer		87
Qy	307	AATGCTACCCAGTTTATCATCT	TCCACAGCAAGAGATTGAAAT	CACAAATGCCACCCCTT	366
Db	88	GlnProThrSerThrIleIleLeu	HisSerHisLeuGlnIleSerArgAlaThrLeu		107
Qy	367	CAGTCAGGAGAGATTCAAGAT	TACATGNAACCAAGAAAGACT	GAAAGTTTTCAGTTAC	426

Db 108 ArgLysGlyAlaGlyGluArgLeuSerGlu-----GluProLeuGlnValLeuGluHis 125  
Qy 427 CCTGCTCATGAACAAATTGCACTGCTGTTCCAGAGAAACTTACGCCTCACTGAAATAC 486  
Db 126 ProProGlnGluGlnIleAlaLeuLeuAlaProGluProLeuLeuValGlyLeuProTyr 145  
Qy 487 TATGTGGTATGGACTTCCAAAGCCAAAGTATGGTGATGGCTTTGAAGGGTTTATAAAGC 546  
Db 146 ThrValValIleHisIleTyrAlaGlyAsnLeuSerGluThrPheHisGlyPheTyrLysSer 165  
Qy 547 ACATACAGAACTCTGTGGTGTGAACAAGATTCTTCAGTACAGATTTCAGCCCAACC 606  
Db 166 ThrTyrArgThrLysGluGlyGluArgIleLeuAlaSerThrGlnPheGluProThr 185  
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Db 186 AlaAlaArgMetAlaPheProCysPheAspGluProAlaPheLysAlaSerPheSerIle 205  
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; APPLICANT: Gurney,Austin L.  
; APPLICANT: Kljavin,Ivar J.  
; APPLICANT: Napier,Mary A.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; APPLICANT: Ashkenazi, Avi J.			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Deenoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Pong, Sherman			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Napier, Mary A.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; FILE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: P2730P1C57			
; CURRENT APPLICATION NUMBER: US/09/989,732			
; CURRENT FILING DATE: 2001-11-19			
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; PRIOR FILING DATE: 1997-06-16			
; PRIOR APPLICATION NUMBER: 60/062250			
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QY 1861 GTGAAATTTAATGGACTCAATGGTTACTACATGTTTCACTATGAGGTCATGATGG 1920  
Db 598 IleLysPheAsnValGlyMetAsnGlyTyrTyrIleValHisTyrGluAspAspGlyTrp 617  
QY 1921 GACCAACTCATTCACAGCTGAATCAGAACCACTTCTCAGACCTTAAGGACAGAGTA 1980  
Db 618 AspSerLeuThrGlyLeuLeuLysGlyThrHisThrAlaValSerSerAsnAspArgAla 637  
QY 1981 GGTCTGATTCATGATGTTTACGCTAGTGGTCAGGGAGACTGACCCCTAGACAAAGCT 2040  
Db 638 SerLeuIleAsnAsnAlaPheGlnLeuValSerIleGlyLysLeuSerIleGlyLysAla 657

QY 2041 CTTGACATGACTTACTCCCAACATGAACAAGCAGCCCGCAGCTTCTCGAAGGTCTG 2100  
Db 658 LeuAspLeuSerLeuTyrLeuLysHisGluThrGluIleMetProValPheGlnGlyLeu 677  
QY 2101 AGTTACTTGGAAATCGTTTTTACCACATGATGAGCAGAGGAATATTTTCAGATATCTCGAA 2160  
Db 678 AsnGluLeuIleProMetTyrLysLeuMetGluLysArgAspMetAsnGluValGluThr 697  
QY 2161 AACCTCAAGGTTACCTTCTCAGTATTTTAAAGCCAGTGAATGACAGGCAAGCTGAGT 2220  
Db 698 GlnPheLysAlaPheLeuIleArgLeuLeuArgAspLeuIleAspLysGlnThrTrpThr 717  
QY 2221 GACAAAGGCTCAGCTCGGACAGAGTCTCCGCTCGGCTCTCTTGAAGCTGGCTGTGAC 2280  
Db 718 AspGluGlySerValSerGluGlnMetLeuArgSerGluLeuLeuLeuLeuAlaCysVal 737  
QY 2281 CTGAACCATGCTCTTTCGATCCAGAAAGCTGTGAACTCTTCTCCAGCTGGATGGAATCC 2340  
Db 738 HisAsnTyrGlnProCysValGlnArgAlaGluGlyTyrPheArgLysTrpLysGluSer 757  
QY 2341 AGTGGAAATTAATATACCAACAGATGTTTAAAGATTTGTATTTCTGTGGTGTCTCAG 2400  
Db 758 AsnGlyAsnLeuSerLeuProValAspValThrLeuAlaValPheAlaValGlyAlaGln 777  
QY 2401 ACAACAGCAGGATGGAATACCTTTTAGAGCAATATGAAGTGTCAAGTGTCAAGTGTGAA 2460  
Db 778 SerThrGluGlyTrpAspPheLeuTyrSerLysTyrGlnPheSerLeuSerSerThrGlu 797  
QY 2461 CAAACAAATTTCTGTATGCTTTTGTCAAGCAGCAAGCATCAGGAAAGTTTACTGAAGTTA 2520  
Db 798 LysSerGlnIleGluPheAlaLeuCysArgThrGlnAsnLysGluLysLeuGlnTrpLeu 817  
QY 2521 ATTGAACATAGGATGGAAGAAAGTTATCAAGACACAGCAAGCTTGCAGCTCTCTTCAT 2580  
Db 818 LeuAspGluSerPheLysGlyAspLysIleLysThrGlnGluPheProGlnIleLeuThr 837  
QY 2581 GCATTGCCAGCAGCTCCAAAGGGGAGCAACTAGCATGGATTTTCTAGAGAAAATTTGG 2640  
Db 838 LeuIleGlyArgAsnProValGlyTyrProLeuAlaTrpGlnPheLeuArgLysAsnTrp 857  
QY 2641 ACCATCTTCTGAAAAAATTTGACTTTGGCTCATATGACATAGGATGATCATCTCTGCG 2700  
Db 858 AsnLysLeuValGlnLysPheGluLeuGlySerSerSerIleAlaHisMetValMetGly 877  
QY 2701 ACAACAGCTCACTTTTCTCCAGGATAAGTTGCAAGAGGTGAAACTATTTTGAATCT 2760  
Db 878 ThrThrAsnGlnPheSerThrArgThrArgLeuGluGluValLysGlyPhePheSerSer 897  
QY 2761 CTTGAGGCTCAAGGATCATCTCGATATTTTCAAACCTGTTCTGGAAACGATAACCAA 2820  
Db 898 LeuLysGluAsnGlySerGlnLeuArgCysValGlnGlnThrIleGluThrIleGluGlu 917  
QY 2821 AATATAAATGGCTGGAGAGAATTTCCGACTCTCGAGGACTTGGCTA 2868  
Db 918 AsnIleGlyTrpMetAspLysAsnPheAspLysIleArgValTrpLeu 933

## RESULT 3

US-08-530-792D-23  
; Sequence 23, Application US/08530792D  
; Patent No. 5972680  
; GENERAL INFORMATION:  
; APPLICANT: Knowles, W. J.; Guraleski, D.; Haigh, W.; Letsinger, J. T.;  
; APPLICANT: Clairmont, K.; and Hart, J.  
; TITLE OF INVENTION: Glucose Transporter Vesicle Amino-peptidase  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bayer Corporation  
; STREET: 400 Morgan Lane  
; CITY: West Haven  
; STATE: Connecticut  
; COUNTRY: U.S.A.  
; ZIP: 06516

Alignment Scores:			
Pred. No.:	2,576-194	Length:	1025
Score:	2027.00	Matches:	402
Percent Similarity:	61.81%	Conservative:	310
Best Local Similarity:	44.37%	Mismatches:	158
Query Match:	40.04%	Indels:	36
DB:	2	Gaps:	5
US-10-039-073-3 (1-2883) x US-08-530-792D-23 (1-1025)			
Qy	160	CGAGTAGGCACCTAAATGGGAAACGATTTCTCTGGCAGAGCTAAGGCTCCCGAGTGTGTC	219
Db	153	ProileAlathRasnGlyuYvValPheProtrPalGlnIleAcgLeuPOThrAlaIle	172
Qy	220	ATTCCTCTCCATTATGACCTCTTTCTCACCCCAATCTCACCTCTCGAGACTTTGTTGCA	279
Db	173	IleProGlnArgTyrGluLeuSerLeuH1sProAsnLeuThrSerMetThrPheArgGly	192
Qy	280	TCGAGAAGATCGAAGCTTTGCTGAGCAATGCTACCCAGTTTATCATCTTGCCACAGCAA	339
Db	193	SerValThrIleSerLeuGlnAlaLeuGlnAspThrArgAspIleIleLeuHisSerThr	212
Qy	340	GATCTTGAATCAGCAATGCCACCTCTCAGTCAGAGGAAGATTCAAGATACATACCAACCA	399
Db	213	GlyHisAsnIleSerSerValThrPheMetSerAlaValSerSerGln-----	228
Qy	400	GGAAAAAGACTGAAGCTTTTGAGTTTACCTGTGTCATGAACAAATTCGACTGCTGTTCCA	459
Db	229	GluYvGlnValGluIleLeuGluTyrProTyrHisGluGlnIleAlaValAlaPro	248
Qy	460	GAGAAACTTACCGCTCACCTGAAATACTATATGTGGCTATGAGACTTCCAAAGCAAGTTAGGT	519



QY	1120	CACCAGTGGTTTGGCAACCTGGTCACAATGGAAATGGTGAATGATATTTGGCTTAAGGAG	1179
DB	468	HieGlnTrpPheGlyAsnLeuValThrMetGlnTrpIrpAsnAspLeuTrpLeuAsnGlu	487
QY	1180	GGTTTTGCAAAATACATGAACCTATTCGCTGTTTAATGCTACATATCCAGAGCTGCAATTT	1239
DB	488	GlyPheAlaThrPheMetGluTrpPheSerValGluLysIlePheLysGluLeuAsnSer	507
QY	1240	GATGACTATTTTGAATGTGTTTGAAGTAATTACAAAGATTTCATTGAATTCATCC	1299
DB	508	TyrGluAspPheLeuAspAlaArgPheLysThrMetArgLysAspSerLeuAsnSerSer	527
QY	1300	CGCCCTATCTCCAAACCCAGCGGAACCCGACTCAATACAGGAATGTTTGTGATGAAGTT	1359
DB	528	HieProIleSerSerSerValGlnSerSerGluGlnIleGluGluMetPheAspSerLeu	547
QY	1360	TCTCTATAACAAG---GGAGCTGTATTTGAATATATGCTCAAGATTTTCTGGGTGAGGAG	1416
DB	548	SerTyrPheLysGlnGlyAlaSerLeuLeuMetLeuLysSerTyrLeuSerGluAsp	567
QY	1417	AAATCCCAAGAGGAATAATTACAGTACTTAAAGAACTTCAGCTATAGAAATGCTAAGAAT	1476
DB	568	ValPheGlnHisAlaIleLeuLysLeuHisAsnHisSerTyrAlaAlaIleGlnSer	587
QY	1477	GATGACTTCTGGAGCAGCTCTGTCAAATAGTTGTTAGAAAGTATTTACATCTGCTGGA	1536
DB	588	AspAspLeuTrpAspSerPheAsnGlu-----	596
QY	1537	GTTTGTTCATTCGGATCCCAAGATGACAAGTACATGCTCGCTTCTCGGGGAAAAATGCA	1596
DB	597	-----ValThrGlyLysThrLeu	602
QY	1597	GAGGTCAAGAGATGATGACTACATGAGCTCTCCAGAAAGGAATCCCTCGCTGCTGGTT	1656
DB	603	AspValLysLysMetMetLysThrTrpThrLeuGlnLysGlyPheProLeuValThrVal	622
QY	1657	AAACAGACGGGTGTTTCACCTCCGAGCTGCACAGGAGCGCTTCCTCCAGGGGGTTTCCAG	1716
DB	623	GlnArgLysGlyThrGluLeuLeuLeuGlnGlnArgPhePheProSerMet-----	640
QY	1717	GAAACCCCTGAATGGAGGGCCCTGCAGGAGAGGTACTGTGGCATATCCCATGACTAC	1776
DB	641	--GlnProGluIleGlnAspSerAspThrSerHisLeuTrpHisIleProIleSerTyr	659
QY	1777	TCCAGAGTTCCTTAATGTGATCCACAGACAC-----ATTCTMAAATCAAAAGACA	1827
DB	660	ValThrAspGlyArgAsnTyrSerGluTyrArgSerValSerLeuLeuAspLysLysSer	679
QY	1828	GATACTCTGGATCTACCTCAAAAGACACAGTGGTGGATAATTAATGTGGACTCAAAATGGT	1887
DB	680	AspValIleAsnLeuThrGluGlnValGlnTrpValValValAsnThrAsnMetThrGly	699
QY	1888	TACTACATCGTTTACATATGAGGGTTCATGATGGAGCAACTCATTTACAGAGCTGAATCAG	1947
DB	700	TyrTyrIleValHisTyrAlaHisAspGlyTrpAlaAlaLeuIleAsnGlnLeuLysArg	719
QY	1948	ACCACACACTTCTCAGACCTAAGGCACAGTAGGTCTGATTCATCATGATGTTTTCAGTA	2007
DB	720	AsnProTyrValLeuSerAspLysAspArgAlaAsnLeuIleAsnAsnIlePheGluLeu	739
QY	2008	GTTGTGTGAGGAGACTGACCTTAGACAAAGCTCTTGACATGACTTACTACCTCCCAACAT	2067
DB	740	AlaGlyLeuGlyValProLeuGlnMetAlaPheAspLeuIleAspTyrLeuArgAsn	759
QY	2068	GAAACAAGACGCCCCGACTTCTCGAAGGTCGTAGTTACTTGGAAATCGTTTTTACCACATG	2127
DB	760	GluThrHisThrAlaProIleThrGluAlaLeuPheGlnThrAspLeuIleTyrAsnLeu	779
QY	2128	ATGGACAGAGGAATATTTCAGATATCTCTGAAAACCTCAACGGTTACCTTCTTCAGTAT	2187
DB	780	LeuGluLysLeuGlyHisMetAspLeuSerSerArgLeuValThrArgValHisLysLeu	799

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Qy 2188 TTTAAGCCAGTATTGACAGCAAGCTGGAGTGACAAAGGCTCAGTCTGGGACAGGATG 2247
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
800 LeuGlnAenGlnIleGlnGlnThrTrpThrAspGluGlyThrProSerMetArgGlu 819
Qy 2248 CTCGGCTCGGCTCTCTTGAAGCTGGCTGTGACCTGAACCATGCTCTTCATCCAGAAA 2307
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
820 LeuArgSerAlaLeuGluGluPheAlaCysAlaHisSerLeuGluAenCysThrThrMet 839
Qy 2308 GCTGCTCAACTCTCTCCAGTGGATGAATCCAGTGGAAAAATTAAATATACCAACAGAT 2367
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
840 AlaThrLysLeuPheAspGlyTrpMetAlaSerAsnGlyThrGlnSerLeuProThrAsp 859
Qy 2368 GTTTTAAAGATTGTGTAATCTGTGGGTGCTCAGACAAACAGCAGGATGAATTTACCTTTTA 2427
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
860 ValMetThrThrValPheValGlyAlaArgThrGluLysGlyTrpLeuPheLeuPhe 879
Qy 2428 GAGCAATATGACATGCTCAATGTCAAGTCTGAAGTCTGAACAAACAAATTCGTATGCTTGTCA 2487
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
880 SerMetTyrSerSerMetGlySerGluAlaGluLysAspLysIleLeuGluAlaLeuAla 899
Qy 2488 ACAGCAAGCATCAGGAAAAAGTTACTGAAGTTAATTCGAATAGGAAGGAAAGGTT 2547
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
900 SerSerAlaAspAlaHisLysLeuTyrTrpLeuMetLysSerSerLeuAspGlyAspIle 919
Qy 2548 ATCAAGACACAGAACTTGGCAGCTCTCTTCATGCGATTGCCAGACGTCCAAAAGGGCAG 2607
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
920 IleArgThrGlnLysLeuSerLeuIleileArgThrValGlyArgGlnPheProGlyHis 939
Qy 2608 CAACTAGCATGGGATTTTGAAGAAAAATTTGGACCCATCTTCGAAAAAATTTGACTTG 2667
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
940 LeuLeuAlaTrpAspPheValLysGluAsnTrpAsnLysLeuValHisLysPheHisLeu 959
Qy 2668 GGCTCATATGACATAAGGATGATCATCTCTGGCACAAACAGCTCACTTTTCTTCCAGGAT 2727
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
960 GlySerTyrThrIleGlnSerIleValIleArgLysThrHisLeuPheSerThrLysThr 979
Qy 2728 AAGTTGCAAGAGGTGAACATATTTTGAATCTCTTGGAGCTCAAGGATCACATCTGGAT 2787
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
980 HisLeuSerGluValGlnGluPhePheGluAsnGlnSerGluAlaThrLeuGlnLeuArg 999
Qy 2788 ATTTTCAAACCTGTTCTGGAACAGATAACCAAAAATATAAAATGCGTGGAGAGAACTCTT 2847
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1000 CysValGlnGluAlaPheGluValIleGluLeuAsnIleGlnTrpMetAlaArgAsnLeu 1019
Qy 2848 CCGACTCTGAGGACTTCGCTA 2868
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1020 LysThrLeuThrLeuTrpLeu 1026
```

## RESULT 5

```
US-09-949-016-6154
; Sequence 6154, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6154
; LENGTH: 957
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-6154
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Alignment Scores: 9.45e-136 Length: 957
Pred. No.: 1444.00 Matches: 323
Score: 53.07% Conservative: 178
Percent Similarity: 34.22% Mismatches: 361
Best Local Similarity: 28.53% Indels: 82
Query Match: 4 Gaps: 19
DB: 19
US-10-039-073-3 (1-2883) x US-09-949-016-6154 (1-957)
Qy 118 GTGCCATCTAGTATATCACTTCACTGAGGATCTGGGGCTTTCCAGTA----- 165
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
60 LeuProSerSer-----ThrAlaSerProSerGlyProProAlaGlnAspGlnAsp 76
Qy 166 -----GCCACTAATCGGGAACGATTTCTTCGTCAGGAGCTAAGGCTCCCGAGTGTG 216
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
77 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 96
Qy 217 GTCATTCTCTCCATTATGACCTCTTTGTCCACCCTCACTCCTCTCTGGACTTTGTT 276
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
97 ValAsnProValHisTyrAspLeuHisValLysProLeuLeuGluGluAspThrTyrThr 116
Qy 277 GCATCTGAGAAGATCGAAGTCTTGTGTCAGCAATGCTACCAGTTTATCATCTTGACAGC 336
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
117 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 136
Qy 337 AAGATCTTTGAAATCAAGAAATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAA 396
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
137 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 149
Qy 397 CCA--GGAAAAAGAACTGAAAGTT-----TTGAGTTTACCTCTCATGAACAAAT 444
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
150 ProSerGlyAspGlnValGlnValArgCysPheGluTyrLysLysGlnGluTyrVal 169
Qy 445 GCATCTCTGGTCCAGAGAACTTACGCTCACCTG-----AAATACTATGTGGCT 495
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
170 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 189
Qy 496 ATGGACTCTCAAGCCCAAGTTAGTGATGCTTTGAAGGGTTTTATAAAGACACATACAGA 555
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
190 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr--- 208
Qy 556 ACTCTTTGGTGGTGAACAAGAAATTTCTGCAGTAACAGATTTTTCAGCCAAACCCAGGACGC 615
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
209 ThrGluAsnGlyArgValLysSerIleAlaAlaThrAspHisGluProThrAspAlaArg 228
Qy 616 ATGGCTTTCCCTGCTTTCATGAACCGTTGTTCAAGCCCAACTTTTCAATCAAGATACGA 675
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
229 LysSerPheProCysPheAspGluProAsnLysLysAlaThrTyrThrIleSerIleThr 248
Qy 676 AGAGAGACAGGACATATTCACATATCAACATGCCAAAGGTTAAGACAATTTGAACTTGAA 735
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
249 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluSerValAsp 268
Qy 736 GGAGGTCTTTTGGAGATCACTTTGAAACTACTGTAATAAGTACATACATCTTTGTAGCC 795
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
269 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 288
Qy 796 TACATAGTTTGTGATTTTCCACTCTCTGAGTGGCTTCATTCATCAGGGGTCAAGGTGTC 855
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
289 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 308
Qy 856 ATCTATGCATCCCCAGACAAACGGATCAACACATTTATGCTTTGAGGCATCCTGAG 915
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
309 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrAlaAlaAsnIleThrLysSer 328
Qy 916 CTACTTGTATTTTATGAAAGTACTTTTGATTTGATCTACTCTCACTCTCCAACTGATTTA 975
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
329 ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys 348
Qy 976 ATTGCTATTCTGACCTTTCACCTGAGCCATCGGAAATTTGGGGCTCTATTATATAGG 1035
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
349 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 368
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Qy	1036	GAGACGTCAC	TGCTTTTTTG	ACCCCAAG	ACCTCTTCT	CGCTTCCG	ATAAACTG	TGGGTACC	1095
Db	369	GlutThrAenLeu	LeuTyArgPro	LyGluSerAla	SerAenGln	GlnArg	Valala	388	
Qy	1096	AGAGTCATAG	CCCATGAAC	TGGCCAC	CAGTGGTTT	TGCGCAAC	CTGGTCA	CAATGGGA	1155
Db	389	ThrValVala	AlaHisGlu	LeuValHis	GlnTrpPhe	GlyAenIle	ValThrMet	AspTrp	408
Qy	1156	TGGAATGATA	TTTGGCTTA	AGGAGGTTT	TGCAAAAT	TACATGGA	CACTTATC	GTGTTAA	1215
Db	409	TrpGluAsp	LeuTrpLeu	AenGluGly	PheAlaSer	PheGluPhe	LeuGlyVal	aen	428
Qy	1216	GCTACATA	CCAGAGCTG	CAATT--	GATGACTAT	TTTTTTT	TGAATGTG	TGTTGA	1272
Db	429	HisAlaGlu	ThrAspTrp	GlnMetArg	AspGlnMet	LeuLeuGlu	AspValLeu	ProVal	448
Qy	1273	ATTACAAA	GAGTTCATT	GAATTCA	TCCCGCCCT	TATCTCAA	ACGCGGAA	ACCCGACT	1332
Db	449	GlnGluAsp	SerLeuMet	SerSerHis	ProIleIle	ValThrVal	ThrThrPro	Asp	468
Qy	1333	CAAAATCAG	GAATTTG	TGATGA	GTTCCTTA	TAAACAGG	GAGCTGT	TATTTGA	1392
Db	469	GluIleThr	SerValPhe	AspGlyIle	SerTySer	LySgLySer	SerIleLeu	aGtMet	488
Qy	1393	CTCAAGAT	TTTTCTG	GGTGAGG	AGAAATTC	CAGAAAGGA	ATAATTC	AGTACTTA	1452
Db	489	LeuGluAsp	TrpTrpIle	LySPro	GluAenPhe	GlnLySgLy	CysGlnMet	TyrLeuGlu	508
Qy	1453	TTGAGCTAT	AGAATGCT	TAAGAATG	ATGCTTGT	TGGAGCAG	CTGTCTCA	ATAATGT	1512
Db	509	TyrGlnPhe	LySAsnAla	LyThrSer	AspPheTrp	AlaAlaLeu	GluGluAla	-----	526
Qy	1513	GAAGA	GATTTTAC	ATCTG	TGTTG	TGAGTTGT	CATTCGG	ATCCCAAG	1572
Db	526	-----	-----	-----	-----	-----	-----	-----	526
Qy	1573	CTCGCCTT	CTGGGGAAA	TGCAGAG	CTCAAGAG	ATGATGACT	CATCGACT	CTCCAG	1632
Db	527	-----	-----	SerArg	LeuPro	ValLySgLeu	ValMetAsp	ThrTrpThrArg	541
Qy	1633	AAAGGAAT	CCCCCTG	CTGGTGT	TAAACA	AGACGGG	TGTTCACT	CCGACTCC	1692
Db	542	MetGlyTyr	ProValLeu	aenVal-----	AsnGlyVal	LyS-----	AsnIleThr	GlnLyS	558
Qy	1693	CGCTTCTC	CCAGGGGG	TTTTCC	AGGAAGAC	CCCTGAAT	TGGAGG	CCCTGC	1746
Db	559	ArgPheLeu	Leu-----	-----	AspPro	ArgAla	aenPro	SerGlnPro	573
Qy	1747	-----	AGGTAC	CTGTG	GCATATC	CCCATTC	GACCTAC-----	-----	1791
Db	574	AspLeuGly	TyrThrTrp	AsnIlePro	ValLySgTrp	ThrGluAsp	AsnIleThr	SerSer	593
Qy	1792	AATGTGAT	CCACAGAC	CATTCTT					

Qy	2083	GCATCTTCTGCAAGGTCTGAGTTACTTGGAATCGTTTTACCAACATGATGGACAAGAAT	2144
Dy	694	ArgValIleSerAlaValThrTyrllelleSerMetPhe	708
Qy	2143	ATTTCAGATATCTCTGAAACCCTCAAGCGTTACTCTCTCAGTAGTTTAAAGCCAGTGATP	2202
Dy	709	AspLysGluLeuTyrrPrometIIeGIUgluTyrrPheGlnGlyInValLysProIleAla	728
Qy	2203	GACAGGCCAACGCTGGAGTGACAAAGGGCTCAGCTCTGGCACAGGATGCTCCGCTCGGCTCTC	2262
Dy	729	AspSerLeugLyTrpAenAepAlaGIyAspHisValThrLysLeuLeuAzcgSerSerVal	748
Qy	2263	TTGAGCTGCCCTGTGACCTGAACCATGCTCTCTTGATCCAGAAAGCTGCTGAACCTCTTC	2322
Dy	749	LeuGlyPheAlaCyLysMetGIyAspArgGluAlaLeuAenAenAlaserSerLeuPhe	768
Qy	2323	TCCAGTGGATGGATCCAGTGTGAATAATTAATATACCAACACAGATGTTTTAAAAGATTGTG	2382
Dy	769	GlUGlnTrpLeu-----AenGlyThrValserLeuProValAenLeuArgLeuLeuVal	786
Qy	2383	TATTCTGTGGGTGCTCAGACAACAGCA-----GGATGGAAATTAACCTTTTAGAGCAA	2433
Dy	787	TyrArgTyrclyMetGlnAenSerGlyAenGluIleSerTrpaenyThrLeuGluGln	806
Qy	2434	TATGAAGTGTCAATGTCAGTGTGAACAAAAAATAATCTGTATGCTTTGTGTCACAGAGC	2493
Dy	807	TyrGlnLysThrSerLeuAlaGlnGluLysGluLysLeuLeuTyrglyLeuAlaserVal	826
Qy	2494	AAGCATCAGGAAAGTTACTGAAGTTAAATTGAAGTCTAGGATGCAAGGAAGGTTATCAAG	2553
Dy	827	LysAenValThrLeuLeuSerArtyrLeuAspLeuLysAspThrAenLeuIleLys	846
Qy	2554	ACACAGAACTTGGCAGCTCTCTTCATGCGATTGGCCAGACGCTCCAAGGGCGCAGCAACTA	2613
Dy	847	ThrGlnAspValpheThrValIleArgeTyrlseTyraenSertyrGlyLysAenMet	866
Qy	2614	GCATGGATTTTGTAAAGAGAAAATTGGACCCATCTTCTGAAAAAATTGACTGGGCTCA	2673
Dy	867	AlatrpAenTrpileGlnLeuAenTpAapTyrrLeuValAenArgTyrrThrLeuAenAen	886
Qy	2674	TATGACATAAGGATGATCATCTCTGGCACACAGCTCATCTTTCTTCCAAGGATAAGTTG	2733
Dy	887	ArgAenLeuGlyArgileValThr---IleAlaGluProPheAenThrGluLeuGlnLeu	905
Qy	2734	CAAGAGGTGAAACTATTTTTTGAATCTCTTGAGGCTCAAGGATCAACATCTGGATATTTT	2793
Dy	906	TrpGlnMetGlnserPhepheAlaLysTyrrProGlnAlaGlyAlaGlyGluLysProArg	925
Qy	2794	CAAACTGTTCTGAAACGATAAACCAAAAAATATAAAATGGCTGGAGAAGAATCTTCGACT	2853
Dy	926	GluGlnValLeuGluThrValLysAenAenIleGluTrpLeuLysGlnHisazcgAenThr	945
Qy	2854	CTGAGGACTTGG	2865
Dy	946	IleArgGluTrp	949

RESULT 6  
US-09-949-016-7431  
; Sequence 7431, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCES: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7431
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7431

Alignment Scores:
Pred. No.:      2.39e-135      Length:      964
Score:          1440.00      Matches:      322
Percent Similarity: 52.97%      Conservative: 178
Best Local Similarity: 34.11%      Mismatches: 362
Query Match:      28.45%      Indels:      82
DB:              4          Gaps:      19

US-10-039-073-3 (1-2883) x US-09-949-016-7431 (1-964)
QY 118 GTGCATCTAGTTATCACTTCACTGAGGATCCTCGGGCTTCCAGTA----- 165
DB 118 GTGCATCTAGTTATCACTTCACTGAGGATCCTCGGGCTTCCAGTA----- 165
QY 166 -----GCCATAATGGGAACGATTCCTTGGCAGAGCTAAGCTCCCGAGTGTG 216
DB 166 -----GCCATAATGGGAACGATTCCTTGGCAGAGCTAAGCTCCCGAGTGTG 216
QY 84 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 103
DB 84 IleCysProAlaSerGluAspGluSerGlyGlnTrpLysAsnPheArgLeuProAspPhe 103
QY 217 GTCAATCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTGT 276
DB 217 GTCAATCTCTCCATTATGACCTCTTTGTCCACCCCAATCTCACCTCTCTGGACTTGT 276
QY 104 ValAsnProValHisIleTrpAspLeuHisValLysProLeuLeuGluAspThrTyrThr 123
DB 104 ValAsnProValHisIleTrpAspLeuHisValLysProLeuLeuGluAspThrTyrThr 123
QY 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATCTACCCAGTTTATCATCTTCACAGC 336
DB 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATCTACCCAGTTTATCATCTTCACAGC 336
QY 124 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 143
DB 124 GlyThrValSerIleSerIleAsnLeuSerAlaProThrArgTyrLeuTrpLeuHisLeu 143
QY 337 AAGATCTTGAAATCAGAAATGCCACCTTCAGTCAGAGAAAGATTCAGATCATGAAA 396
DB 337 AAGATCTTGAAATCAGAAATGCCACCTTCAGTCAGAGAAAGATTCAGATCATGAAA 396
QY 144 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 156
DB 144 ArgGluThrArgIleThrArgLeu-----ProGluLeuLysArg 156
QY 397 CCA---GGAAAGAACTGAAAGTT-----TTGAGTTACCTGCTCATGACAAATTT 444
DB 397 CCA---GGAAAGAACTGAAAGTT-----TTGAGTTACCTGCTCATGACAAATTT 444
QY 157 ProSerGlyAspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal 176
DB 157 ProSerGlyAspGlnValGlnValArgArgCysPheGluTyrLysLysGlnGluTyrVal 176
QY 445 GCATCTGCTGTTCCAGAGAACTTACCGCTCACCTG-----AAATACTATGTGGCT 495
DB 445 GCATCTGCTGTTCCAGAGAACTTACCGCTCACCTG-----AAATACTATGTGGCT 495
QY 177 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 196
DB 177 ValValGluAlaGluGluLeuThrProSerSerGlyAspGlyLeuTyrLeuLeuThr 196
QY 496 ATGACTTCCNAGCCAAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGCACATCAGA 555
DB 496 ATGACTTCCNAGCCAAAGTTAGTGATGGCTTTGAAGGGTTTATAAAGCACATCAGA 555
QY 197 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr--- 215
DB 197 MetGluPheAlaGlyTrpLeuAsnGlySerLeuValGlyPheTyrArgThrTyr--- 215
QY 556 ACTCTGCTGTTGAAACAGAAATCTTGCAGTACAGATTTTGAGCCAAACCCAGGACGC 615
DB 556 ACTCTGCTGTTGAAACAGAAATCTTGCAGTACAGATTTTGAGCCAAACCCAGGACGC 615
QY 216 ThrGluAsnGlyArgValLysSerIleValAlaThrAspHisGluProThrAspAlaArg 235
DB 216 ThrGluAsnGlyArgValLysSerIleValAlaThrAspHisGluProThrAspAlaArg 235
QY 616 ATGGCTTCTCCCTGCTTGTGTAACCGTGTTCAAAGCCCAACTTTTCAATCAAGATACGA 675
DB 616 ATGGCTTCTCCCTGCTTGTGTAACCGTGTTCAAAGCCCAACTTTTCAATCAAGATACGA 675
QY 236 LysSerPheProCysPheAspGluProAsnLysIleValThrTyrThrIleSerIleThr 255
DB 236 LysSerPheProCysPheAspGluProAsnLysIleValThrTyrThrIleSerIleThr 255
QY 676 AGAGAGAGCGGCATATTGCATATCAACATGCCAAAGGTTTAAGACAAATGAACTGAA 735
DB 676 AGAGAGAGCGGCATATTGCATATCAACATGCCAAAGGTTTAAGACAAATGAACTGAA 735
QY 256 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluGluSerValAsp 275
DB 256 HisProLysGluTyrGlyAlaLeuSerAsnMetProValAlaLysGluGluSerValAsp 275
QY 736 GGAGGTCTTTGGAGATCACTTTGAACTACTGTAAATAGTACATACCTTGTAGCC 795
DB 736 GGAGGTCTTTGGAGATCACTTTGAACTACTGTAAATAGTACATACCTTGTAGCC 795
QY 276 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 295
DB 276 AspLysTrpThrArgThrThrPheGluLysSerValProMetSerThrTyrLeuValCys 295
QY 796 TACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGGTGC 855
DB 796 TACATAGTTGTGATTTCCACTCTCTGAGTGGCTTCACTTCATCAGGGGTCAAGGGTGC 855
QY 296 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 315
DB 296 PheAlaValHisGlnPheAspSerValLysArgIleSerAsnSerGlyLysProLeuThr 315
QY 856 ATCTATGATCCCGCAGACAACGGAATCAACACATTTATGCTTTGCGAGGCATCAGTGAAG 915
DB 856 ATCTATGATCCCGCAGACAACGGAATCAACACATTTATGCTTTGCGAGGCATCAGTGAAG 915
QY 316 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrLeuAlaAsnIleThrLysSer 335
DB 316 IleTyrValGlnProGluGlnLysHisThrAlaGluTyrLeuAlaAsnIleThrLysSer 335
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916 CTACTTGTATTTTATCAAAAGTACTTTTGATATCTACTATCCACTCTCCAAACTGGATTTA 975
336 ValPheAspTyrPheGluGluTyrPheAlaMetAsnTyrSerLeuProLysLeuAspLys 355
976 ATTGCTATTCTGACTTTGCACCTGGAGCCATCGAAAATTTGGGGCTCATTTACATATAG 1035
356 IleAlaIleProAspPheGlyThrGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArg 375
1036 GAGAGCTCACTGCTTTTTCACCCCAAGACCTCTTCTGCTTCCGATAAACTGGGGTCACC 1095
376 GluThrAsnLeuLeuTyrAspProLysGluSerAlaSerSerAsnGlnGlnArgValAla 395
1096 AGAGTCATAGCCCATGAACTGGCGCACCACTGCTTTGGCAACTGCTGTCACAATGGAATG 1155
396 ThrValValAlaHisGluLeuValHisGlnTrpPheGlyAsnIleValThrMetAspTrp 415
1156 TGGAAATGATATTGCTTAAGGAGGCTTTTGCAAAATATACATGAACTTATCGCTGTTAAT 1215
416 TrpGluAspLeuTrpLeuAsnGluGlyPheAlaSerPhePheGluPheLeuGlyValAsn 435
1216 GCTACATATCCAGAGCTGCAATTT---GATGACTATTTTTCGAATGTGTGTTTGAAGTA 1272
436 HisAlaGluThrAspTrpGlnMetArgAspGlnMetLeuLeuGluAspValLeuProVal 455
1273 ATTACAAAAGATTCATTGAATTCATCCCGCTCTATCTCCAAACCGCGAAACCCCGACT 1332
456 GlnGluAspAspSerLeuMetSerSerHisProIleValThrValThrThrProAsp 475
1333 CAAATACAGGAATGTTGATGAAGTTTCTTATAACAAGGAGCTTGTATTTTGAATATG 1392
476 GluIleThrSerValPheAspGlyIleSerTyrSerLysGlySerSerIleLeuArgMet 495
1393 CTCAGGATTTTCTGGGTGAGGAGAAATTCAGAAAGGAATTAATTCAGTACTTAAAGAG 1452
496 LeuGluAspTrpIleLysProGluAsnPheGlnLysGlyCysGlnMetTyrLeuGluLys 515
1453 TTCAGTCTATAGAAATGCTAAGAAATGATGCTTGTGAGCAGTCTGTCAAAATAGTGTGTTA 1512
516 TyrGlnPheLysAsnAlaLysThrSerAspPheTrpAlaAlaLeuGluAla----- 533
1513 GAAAGTGATTTTACATCTGCTGGAGTTTGTCTCATTCGGATCCCAAGATGACAAGTAAATG 1572
533 ----- 533
1573 CTCGCCCTTCTGGGGGAAAATGCAGAGTCAAGAGATGATGACTACATGAGCTCTCCAG 1632
534 -----SerArgLeuProValLysGluValMetAspThrTrpThrArgGln 548
1633 AAAGGAATCCCTGCTGCTGTTAAACAAAGACGGGTGTTCACTCCGACTCGCAACAGGAG 1692
549 MetGlyTyrProValLeuAsnVal-----AsnGlyValLys---AsnIleThrGlnLys 565
1693 CGTTCCTCCAGGGGGTTCACGGAAGACCTGTAATGAGGGGCCCTGCAGGAG----- 1746
566 ArgPheLeuLeu-----AspProArgAlaAsnProSerGlnProProSer 580
1747 -----AGTACTCTGGCATATCCCATTTGACCTAC-----TCCAGGACTTCTTCT 1791
581 AspLeuGlyTyrThrTrpAsnIleProValLysTrpThrGluAspAsnIleThrSerSer 600
1792 AATGTCTCCACAGACACATCTTAAATCAAGACAGATACCTCTGATCTCTCTGATAAAG 1851
601 ValLeuPheAsnArgSerGluLysGluGlyIleThrLeuAsnSerSerAsnProSerGly 620
1852 ACCAGTTGGGTGAAATTTAATGTGGACTCAAAATGGTTACTACATCTTCAATGAGGGT 1911
621 AsnAlaPheLeuLysIleAsnProAspHisIleGlyPheTyrArgValAsnTyrGluVal 640
1912 CATGGATGGGACCACTATTACACAGCTGAATCAGAACCAACACACTTCTCAGACCTAAG 1971
641 AlaThrTrpAspSerIleAlaThrAlaLeuSerLeuAsnHisLysThrPheSerSerAla 660
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Db      891 TyrGlyGlySerPheSerPheSerAsnLeuIleGlnAlaValThrArgArgPheSer 910
      :::: |||||::: :::: |||||
Qy      2719 TCAAGGATAGTTCACAGAGGTGAACATATTTTGTGAATCTCTGAGGCTCAA----- 2772
      :::: |||||::: |||||
Db      911 ThrGluTyrGluLeuGlnGlnLeuGluGlnPheLysLysAspAsnGluGluThrGlyPhe 930
      :::: |||||::: |||||
Qy      2773 GATCATCATCTGGATATTTTCAACTGTCTCGGAACAGATCAACCAAAATATAAATGG 2832
      :::: |||||::: |||||
Db      931 GlySerGlyThrArgAlaLeuGluGlnAlaLeuGluLysThrLysAlaAsnIleLysTrp 950
      :::: |||||::: |||||
Qy      2833 CTGGAGAAGAACTCTCCGACTCTGAGGACTCGCTAAATGGTTAAATACT 2880
      :::: |||||::: |||||
Db      951 ValLysGluAsnLysGluValValLeuGlnTrpPheThrGluAsnSer 966
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## RESULT 8

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US-09-659-786-201
; Sequence 201, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-659-786-201

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## Alignment Scores:

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Pred. No.: 1,038-117 Length: 967
Score: 1264.50 Matches: 325
Percent Similarity: 46.62% Conservative: 158
Best Local Similarity: 31.37% Mismatches: 386
Query Match: 24.98% Indels: 167
DB: 4 Gaps: 26

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US-10-039-073-3 (1-2883) x US-09-659-786-201 (1-967)

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Qy      58 AGAGGATTTTACTGCTTAACAGCCATC-----TTGCCCAA 93
      :::: |||||::: :::: |||||
Db      3 LysGlyPheTyrIleSerLysSerLeuGlyIleLeuGlyIleLeuGlyValAla 22
      :::: |||||::: :::: |||||
Qy      94 ATATGATTTGTTCTCAGTTCACGTGCATCTAGTATCATCTCACTGAGATCTCGG 153
      :::: |||||::: |||||
Db      23 ValCysThrIleAlaLeuSerValTyrSerGlnGluLysAsnLysAsnAlaAsn 42
      :::: |||||::: |||||
Qy      154 GCTTCCAGTAGCC----- 168
      :::: |||||::: |||||
Db      43 SerSerProValAlaSerThrThrProSerAlaSerAlaThrAsnProAlaSerAla 62
      :::: |||||::: |||||
Qy      169 ---ACTAATGGGAACAGATTTCTTGGCAGGAGCTAAGCTCCCGAGTGTGCTATTCT 225
      :::: |||||::: |||||
Db      63 ThrThrLeuAspGlnSerLysAlaTrpAsnArgTyrArgLeuProAsnThrLysPro 82
      :::: |||||::: |||||
Qy      226 CTCCATTATGACCTTTTGTCCACCCCAATCTCACCTCTCTGGAC----- 270
      :::: |||||::: |||||
Db      83 AspSerTyrGlnValThrLeuArgProTyrLeuThrProAsnAspArgGlyLeuTyrVal 102
      :::: |||||::: |||||
Qy      271 TTTGTTGCATCTGAGAGATCGAAGCTTGTGTCAGCAATGTACCAATTTATCATCTTG 330
      :::: |||||::: |||||
Db      103 PheLysGlySerSerThrValArgPheThrCysLysGluAlaThrAspValIleIle 122
      :::: |||||::: |||||

```

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Qy      331 CACAGCAAGATCTTGAATCAGCAATCAGCAATCCACCTTCAGTCAGAGGAAGATTCAAGATAC 390
      :::: |||||::: |||||
Db      123 HisSerLysLysLeuAsnTyrThr----- 130
      :::: |||||::: |||||
Qy      391 ATGAACACCGAAGAAAGACTGAAGATTGTGAGTTAC-----CCTGCTCAT 435
      :::: |||||::: |||||
Db      131 LeuSerGlnGlyHisArgValValLeuArgGlyValGlyGlySerGlnProProaspIle 150
      :::: |||||::: |||||
Qy      436 GAACAAATTGACATCTGCTGTTTCCA---GAGAAACTTAGCGCTCACCTGAAA----- 483
      :::: |||||::: |||||
Db      151 AspLysThrGluLeuValGluProThrGluTyrLeuValValHisLeuLysGlySerLeu 170
      :::: |||||::: |||||
Qy      484 -----TACTATGTGGCTATGACATTTCCAAAGCCAAAGTTAGTGTAGTGCGCTTT 528
      :::: |||||::: |||||
Db      171 ValLysAspSerGlnTyrGluMetAspSerGluPheGluGlyGluLeuAlaAspAspLeu 190
      :::: |||||::: |||||
Qy      529 GAAGGGTTTTATAAAGCACATACAGAACTCTTGGTGTGTGAACACAGAATTTCTTGCAGTA 588
      :::: |||||::: |||||
Db      191 AlaGlyPheTyrArgSerGluTyrMetGlu---GlyAsnValArgLysValAlaThr 209
      :::: |||||::: |||||
Qy      589 ACAGATTTTGAGCAACCCAGGCACGATGCTTTCCCTTCTTGTGATGAACCGTTGTTTC 648
      :::: |||||::: |||||
Db      210 ThrGlnMetGlnAlaAlaAspAlaArgLysSerPheProCysPheAspGluProAlaMet 229
      :::: |||||::: |||||
Qy      649 AAAGCCAACTTTTCAATCAAGATACGAAGAGAGAGAGGCATATTTGCACTATCCAAACATG 708
      :::: |||||::: |||||
Db      230 LysAlaGluPheAsnIleThrLeuIleHisProLysAspLeuThrAlaLeuSerAsnMet 249
      :::: |||||::: |||||
Qy      709 ---CCAAAGGTTAAGACAAATGAACCTTGAAGGAGGCTCTTTTGGAGAT----- 753
      :::: |||||::: |||||
Db      250 LeuProLysGlyProSerThrProLeuPro-----GluAspProAsnTrpAsn 265
      :::: |||||::: |||||
Qy      754 -----CACTTTGAAACTACTGTAATAATGAGTACATACCTTTGTAGCTCATAGTTTGT 807
      :::: |||||::: |||||
Db      266 ValThrGluPheHisThrThrProLysMetSerThrTyrLeuLeuAlaPheIleValSer 285
      :::: |||||::: |||||
Qy      808 GATTTCCACTCTCTGAGTGGCTTCATCTCAGGGGTCAAGGTGTCCATCTATGCAATCC 867
      :::: |||||::: |||||
Db      286 GluPheAspTyrValGluLysGlnAlaSerAsnGlyValLeuIleArgIleTrpAlaArg 305
      :::: |||||::: |||||
Qy      868 CCAGACAAACGGAAATCAACACAT-----TATGCTTTGCGGGCATCACTGAAGCTACTT 921
      :::: |||||::: |||||
Db      306 ProSerAlaIleAlaAlaGlyHisGlyAspTyrAlaLeuAsnValThrGlyProIleLeu 325
      :::: |||||::: |||||
Qy      922 GATTTTATGAAAAGTACTTTGATATCTATCTATCTCACTCTCCAACTCGGATTTAATGCT 981
      :::: |||||::: |||||
Db      326 AsnPhePheAlaGlyHisTyrAspThrProTyrProLeuProLysSerAspGlnIleGly 345
      :::: |||||::: |||||
Qy      982 ATTCCTGACTTTGACCTGGAGCCATGGAATTTGGGGCCTCATTTACATATAGGAGACG 1041
      :::: |||||::: |||||
Db      346 LeuProAspPheAsnAlaGlyAlaMetGluAsnTrpGlyLeuValThrTyrArgGluAsn 365
      :::: |||||::: |||||
Qy      1042 TCACTGCTTTTGAACCCAGACCTCTTCTGCTCCGATTAACCTGGTGGTCACAGAGTC 1101
      :::: |||||::: |||||
Db      366 SerLeuLeuPheAspProLeuSerSerSerSerSerSerSerSerSerSerSerSerSer 385
      :::: |||||::: |||||
Qy      1102 ATAGCCCATGACCTGGCGCACCTGCTGTTGGCAACCTGTCACAATGGAATGTGGAAT 1161
      :::: |||||::: |||||
Db      386 IleAlaHisGluLeuAlaHisGlnTrpPheGlyAsnLeuValThrIleGluTrpTrpAsn 405
      :::: |||||::: |||||
Qy      1162 GATTTTGGCTTAAAGAGGGTTTTTGCAAAATACATGGAACCTTATCGCTGTTTAAATGCTACA 1221
      :::: |||||::: |||||
Db      406 AspLeuTrpLeuAsnGluGlyPheAlaSerTyrValGluTyrLeuGlyAlaAspTyrAla 425
      :::: |||||::: |||||
Qy      1222 TATCCAGAGCTGCATTTTGTATGATGATTTT---TTGAATGTGTGTTTGAAGTAAATTACA 1278
      :::: |||||::: |||||
Db      426 GluProThrTrpAsnLeuLysAspLeuMetValLeuAsnAspValTyrArgValMetAla 445
      :::: |||||::: |||||
Qy      1279 AAAGATTCATTGAATTCATCCCGCCCTATCTCCAAACACGCG-----GAAACCCCG 1329
      :::: |||||::: |||||
Db      446 ValAspAlaLeuAlaSerSerHisProLeuSerThrProAlaSerGluIleLeuAsnThrPro 465
      :::: |||||::: |||||

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Qy 1330 ACTCAATACAGGAAATGTTTGATGAAGTTTCTTATAACAGGAGCTGTGTAATTTGAAAT 1389
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
466 AlaGlnIleSerGluLeuPheAspAlaIleSerTyrSerIysGlyAlaSerValLeuArg 485
Qy 1390 ATGCTCAAGGATTTCTGGGTGAGGAAATTCAGAAAGGATAATTCAGTACTTAAAG 1449
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
486 MetLeuSerSerPheLeuSerGluAspValPheIysGlnGlyLeuAlaSerTyrLeuHis 505
Qy 1450 AAGTTTACGATACAAATGCTAAGAATGATGACTTGTGGAGCAGCTCG- 1497
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
506 ThrPheAlaTyrGlnAsnThrIleTyrLeuAsnLeuTrpAspHisLeuGlnGluAlaVal 525
Qy 1498 TCAATAGTTGTTAGAAAGTGATTTTACATCTCGTGGAGTTTGTTCATTCGGATCCCAAG 1557
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
526 AsnAsnArgSerIleGlnLeuProThrThr- 535
Qy 1558 ATGACAAGTAACATGCTCGCCTTCTCGGGGGAATAATGCAGAGTCAAGAGATGATGACT 1617
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
536 -----ValArgAspIleMetAsn 541
Qy 1618 ACATGGACTCTCCAGAAAGGAATCCCTGCTGCTGTTTAAACAAGACGGGTGTCACTC 1677
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
542 ArgTrpThrLeuGlnMetGlyPheProValIleThrVal- 559
Qy 1678 CGACTGCAACAGGAGCGCTTCTCCAGGGGTTTTCAGGAAGACCCCTGAA- 1728
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
560 ThrLeuSerGlnGluHisPheLeuLeu- 574
Qy 1729 TGGAGGGCCCTGCGAGAGAGGTACTCTGTGGGATATCCCATTTGACC- 1773
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
575 ThrArgProSerGluPheAsnTyrValTrpIleValProIleThrSerIleArgAspGly 594
Qy 1774 -----TACTCCACG 1782
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
595 ArgGlnGlnGlnAspTyrTrpLeuIleAspValArgAlaGlnAsnAspLeuPheSerThr 614
Qy 1783 AGTTCTTCTAATGTATCCACAGACACATTTCTAAATCAAAAGACAGATACTCTGGATCTA 1842
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
615 SerGlyAsn- 617
Qy 1843 CCTGAAAGACCAGTTGGGTGAAATTTAATGTGACTCAATGTGTTACTACATCGTTTCAAC 1902
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 -----GluTrpValLeuLeuAsnLeuAsnValThrGlyTyrTyrArgValAsn 633
Qy 1903 TATGAGGTCTCATGATGGACCAACTATTATACAGCTGAATCAGAACACACACTTCTC 1962
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
634 TyrAspGluLeuAsnTrpArgIleGlnThrGlnLeuGlnArgAspHisSerAlaIle 653
Qy 1963 AGACCTAAGGACAGAGTAGTCTGATTCATGATGTGTTTCAGCTAGTTGTGTGCGAGGAGA 2022
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
654 ProValIleAsnArgAlaGlnIleIleAsnAspAlaPheAsnLeuAlaSerAlaHisLys 673
Qy 2023 CTGACCTAGACAAGCTCTTGACATGACTTACTCTCCACATGAAACAGACGAGCCCC 2082
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
674 ValProValThrLeuAlaLeuAsnAsnThrLeuPheLeuIleGluGluArgGlnTyrMet 693
Qy 2083 GCACCTTCGAGGTCTGAGTTACTTCTGAAATCGTTTACACATGATGACAGAGGAAT 2142
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
694 ProTrpGluAlaAlaLeuSerSerLeuSerTyrPheLysLeuMetPheAspArg- 711
Qy 2143 ATTTCAGATATCTCTGAAAACCTCAAGCGTTTACCTTCTTCAGTATTTTAAAGCCAGTGATT 2202
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
712 ---SerGluValTyrGlyProMetLysAsnTyrLeuLysGlnValThrProLeuPhe 730
Qy 2203 -----GACAGGCAAGCTGGAGTGAC---AAGGCTCAGCTCGGACAGG 2244
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
731 IleHisPheArgAsnAsnThrAsnAsnTrpArgGluIleProGluAsnLeuMetAspGln 750
Qy 2245 ATGCTCCGCTCGCTCTCTCAAGCTGCGCTGACCTGACCAACCATGCTCTCTTGCATCCAG 2304
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
751 TyrSerGluValAsnAlaIleSerThrAlaCysSerAsnGlyValProGluCysGluGlu 770
Qy 2305 AAAGCTGCTGAACCTCTTCTCCAGCTGGATGGAATCCAGTGGAAAATTAATATACCAACA 2364
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Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
771 MetValSerGlyLeuPheLysGlnTrpMetGluAsnProAsnAsnAsnProIleHisPro 790
Qy 2365 GATGTTTTAAAGATTCTGTAT-----TCTGTGGTGCTCAGACAACAGCAGCATGGAAT 2418
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 AsnLeuArgSerThrValTyrCysAsnAlaIleAlaGlnGlyGlyGluGluGluTrpAsp 810
Qy 2419 TACCTTTTAGACCAATATGAACCTGTCAATGTCAAGTGTCAAGTGTCAACAAACAAATTTCTGTAT 2478
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
811 PheAlaTrpGlnPheArgAsnAlaThrLeuValAsnGluAlaAspLysLeuArgAla 830
Qy 2479 GCTTTGTCAACGAGCAAGCATCAGGAAAGTTACTGAAGTTAATTGAAGTCTAGGAAATGGAA 2538
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
831 AlaLeuAlaCysSerLysGluLeuTrpIleLeuAsnArgTyrLeuSerTyrThrLeuAsn 850
Qy 2539 CGAAAGGTTATCAAGACACAGAACTGGCAGCTCTCTTCATCGCATTCACACGCTCCA 2598
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
851 ProAspLeuIleArgLysGlnAspAlaThrSerThrIleIleSerIleThrAsnAsnVal 870
Qy 2599 AAGGGCAGCAACTAGCATGGGATTTGTAAGAGAAAAATTTGGACCCCATCTTCTGAAAAAA 2658
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
871 IleGlyGlnGlyLeuValTrpAspPheValGlnSerAsnTrpLysLysLeuPheAsnAsp 890
Qy 2659 TTTGACTTGGCTCATATGACATAAGATGATCATCTCTGGCACAACAGCTCACTTTTCT 2718
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 TyrGlyGlySerPheSerAsnLeuIleGlnAlaValThrArgArgPheSer 910
Qy 2719 TCCAAGGATAAGTTCGAAGAGGTGAACTATTTTGAATCTCTTTCAGGCTCAA----- 2772
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
911 ThrGluTyrGluLeuGlnGlnLeuGluGlnPheLysLysAspAsnGluGluThrGlyPhe 930
Qy 2773 GATACATCTCGATATTTTTCAAACTGTTCTGAAACGACATAACCAAAATATATAAATGG 2832
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
931 GlySerGlyThrArgAlaLeuGluGlnAlaLeuGluLysThrLysAlaAsnIleLysTrp 950
Qy 2833 CTGAGAGAAGATCTTCGACTCTCGAGACTTGAGGACTTGGCTAATGTTTAATCT 2880
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
951 ValLysGluAsnLysGluValValLeuGlnTrpPheThrGluAsnSer 966

RESULT 9
US-09-919-039-222
; Sequence 222, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919, 039
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 222
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 2278688CD1
US-09-919-039-222

Alignment Scores:
Pred. No.: 9,36e-114 Length: 919
Score: 1225.00 Matches: 309
Percent Similarity: 49.74% Conservative: 163
Best Local Similarity: 32.56% Mismatches: 351
Query Match: 24.20% Indels: 126
DB: 4 Gaps: 26

US-10-039-073-3 (1-2883) x US-09-919-039-222 (1-919)
Qy 163 GTAGCCACTAATGGGAAGCATTTCTTGTGGCAGAGCTAAGGCTCCCGCAGTGTGTCATT 222
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Qy 2260 CTCCTTGAAGCTGGCGCTGTGACCTGAACTGCTCTTCATCCAGAAAAGCTGCTGAATC 2319  
Db 709 ValLeuGlyLysLeuGlyLysAlaGlyHisLysAlaThrLeuGluGluAlaAargArg 728  
Qy 2320 TTTCTCCCAGTGATGGATCAGTGGAAAAATAATATACCACAACAGATGTTTTAAAGATT 2379  
Db 729 PheLysAspHisValGlu-----GlyLysGlnLeuSerAlaAspLeuArgSerPro 746  
Qy 2380 GTGTATTCTGTG-----GGTCTCAGACAACAGCAGGATGAAATTAACCTTTTA 2427  
Db 747 ValTyrLeuThrValLeuLysHisGlyAspGlyThrThrLeu-----AspIleMetLeu 764  
Qy 2428 GAGCAATATGAAGCTGTCAAGTCTGAACAAAAACAAATTTCTGTATGCTTTGTCA 2487  
Db 765 LysLeuHisLysGlnAlaAspMetGlnGluGlyLysAsnArgIleGluArgValLeuGly 784  
Qy 2488 ACGAGCAAGCATCAGAAAAAGTTACTGAAGCTTAATTAGAATAGGNAATCGAAGAAAGTT 2547  
Db 785 AlaThrLeuLeuProAspLeuIleGlnLysValLeuThrPheAlaLeuSerGluGluVal 804  
Qy 2548 ATCAAGACACAGAAGCTGGCAGCTCTCCTTCATGCATTCGACAGCGTCAAAG---GGG 2604  
Db 805 ---ArgProGlnAspThrValSerValIleGlyValAlaGlyLysSerLysHisGly 823  
Qy 2605 CAGCAACTAGCATGGATTTTGTGAAGAGAAAATTTGACCCCATCTTCGAAAAAATTTGAC 2664  
Db 824 ArgLysAlaAlaTrpLysPheIleLysAspAsnTrpGluGluLeuTyrAsnArgTyrGln 843  
Qy 2665 TTGGGCTCATATGACATGAAGATGATCATCTCTGGCACACAGCTCACTTTTCTTCCAAG 2724  
Db 844 --GlyGlyPheLeuIleSerArgLeuIleLysLeuSerValGluGlyPheAlaValAsp 862  
Qy 2725 GATAAGTTGCAAGAGTCAAACTATTTTTTCAATCTCTTGAAGCTCAAGGATCACATCTG 2784  
Db 863 LysMetAlaGlyGluValValAlaPheGluSerHisProAlaProSerAlaGluArg 882  
Qy 2785 GATATTTTTCAAACTGTTCTCGAACGATAACCAAAAAATATAAAATGCTCGAGAAGAAT 2844  
Db 883 Thrile--GlnGlnCysCysGluAsnIleLeuLeuAsnAlaAlaTrpLeuLysArgAsp 901  
Qy 2845 CTTCGAGCTGTGAGACTTGCTGCTAATG 2871  
Db 902 AlaGluSerIleHisGlnTyrLeuLeu 910

RESULT 10  
US-08-335-844A-22  
; Sequence 22, Application US/08335844A  
; Patent No. 6066503  
; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, MARGARET  
; APPLICANT: SMITH, TREVOR STANLEY  
; APPLICANT: MUNN, EDWARD ALBERT  
; APPLICANT: KNOX, DAVID PATRICK  
; APPLICANT: OLIVER, JOANNA JANE  
; APPLICANT: NEWTON, SUSAN ELIZABETH  
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Earnet & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W.  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:



```

Db 931 LeuLysAsnLeuTyrLysAsn-...AspLysArgAlaArgGluTyrGlyAlaPheGlyGly 949
Qy 2800 GTTCGGAACGATAACCAAAATATAAATGGCTGAGAGAGATCTTCCGACTCTG 2856
Db 950 AlaileGluArgSerGluHisArgValLysTrpIleGluLysHisPheArgLysLeu 968

RESULT 11
US-09-129-366-22
; Sequence 22, Application US/09129366
; Patent No. 6534638
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rochwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/129,366
; FILING DATE: 05-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,844
; FILING DATE: 09-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-241A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-129-366-22

Alignment Scores:
Pred. No.: 1,04e-107 Length: 977
Score: 1165.00 Matches: 280
Percent Similarity: 49.22% Conservative: 192
Best Local Similarity: 29.20% Mismatches: 411
Query Match: 23.01% Indels: 76
DB: 4 Gaps: 21

US-10-039-073-3 (1-2883) x US-09-129-366-22 (1-977)
Qy 115 TCAGTGCCTACTAGTATCACTTCACT-----GAGGAT 147

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Db 41 SerIleGlyLeuThrTyrTyrPheThrArgLysAlaPheAspThrThrGlyGlyAsnGly 60
Qy 148 CTTGGGGCTTCCAGTAGCCACTAATGGGAACGATTTCTTGGCAGGAGCTTAAGGCTC 207
Db 61 LysGlyAspGlnProIleValAspAsnSerProSerAla---GluGluLeuArgGlu 79
Qy 208 CCCAGTGTGGTCATCTCTCCATTATGACCTCTTTGTCCAC-----CCCAATCTC 258
Db 80 ProThrThrIleLysProLeuThrTyrAspLeuValIleLysThrTyrLeuProAsnTyr 99
Qy 259 ACCTCTCTG-----GACTTT-----GTTGCATCTGAG 285
Db 100 ValAsnTyrProProGluLysAspPheAlaIleAspGlyThrValValIleAlaMetGlu 119
Qy 286 AAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTCGACAGCAAGATCTT 345
Db 120 valValGlu-----ProThrLysSerIleValLeuAsnSerLysAsnIle 134
Qy 346 GAAATCACGAATGCCACCTTCAGTCAGAGGAAGATTCAAGATACATGAACACGAGAAA 405
Db 135 ProVal-----IleAlaAspGlnCysGluLeuPheSerAsnAsnGlnLysLeuAspIle 152
Qy 406 GAACTGAAAGTTTGGATTACCTGCTCATGAACAAATTCACCTGCTGGTTCAGAGAAA 465
Db 153 Glu---LysValValAspGlnProArgLeuGluLysValGluPheValLeuLysLys 171
Qy 466 CTTACGCTCACCTGAAATACTATGTGGCTATGCTTCCAGCCCAAGTTAGGTGATGGC 525
Db 172 LeuGluLysAsnGlnLysIleThrLeuLysIleValTyrIleGlyLeuIleAsnAspMet 191
Qy 526 TTTGAAAGGGTTTATAAAGCACATACAGAACTCTTGGTGGTGAACAAAGAATTTCTTGA 585
Db 192 LeuGlyGlyLeuTyrArgThrThrTyrThrAspLysAspGlyThrLysIleAlaAla 211
Qy 586 GTAACAGATTTTGAGCAACCCAGGACGATGGCTTCCCTTGCCTTTGTATGAACCGTTG 645
Db 212 CysThrHisMetGluProThrAspAlaArgLeuMetValProCysPheAspGluProThr 231
Qy 646 TTCAAAGCCCAACTTTTCAATCAAGATACGAAGAGAGAGAGAGGCATATTTGACACTTCA 705
Db 232 PheLysAlaAsnTrpThrValThrValIleHisProLysGlyThrSerAlaValSerAsn 251
Qy 706 ATGCCAAAGGTTAAGACAATTTGAACCTTGAAGAGGCTTTTGAAGAGATCACTTTGAA 765
Db 252 GlyIleGluLysGlyGluGlyGluValSerGlyAspTrpValThrThrArgPheAspPro 271
Qy 766 ACTGTAAATAGTAGTACATACCTTGTAGCTACATAGTTGTGTGATTTCCACTCTCTAGT 825
Db 272 ThrProArgMetProSerTyrLeuIleAlaLeuValIleSerGluPheLysTyrIleGlu 291
Qy 826 GGCTTCACTTTCATCAGGGGTCAAAGTGTCCATCTATGCATCCCGACAGCAACCGAATCAA 885
Db 292 AsnTyrThrLysSerGlyValArgPheArgIleProAlaArgProGluAlaMetLysMet 311
Qy 886 ACACATTATGCTTTGAGGATCAGTCAAGCTACTGATTTTATGAAAGTACTTTGAT 945
Db 312 ThrGluTyrAlaMetIleAlaGlyIleLysCysLeuAspTyrTyrGluAspPheGly 331
Qy 946 ATCTACTATCCTCTCCAACTGGATTAAATTGCTATTCTCTGACTTTTGACCTGGAGCC 1005
Db 332 IleLysPheProLeuProLysGlnAspMetValAlaLeuProAspPheSerSerGlyAla 351
Qy 1006 ATGGAATAATGGGGCTTCATTACATATAGGAGACGTCACCTGCTTTTGTAGCCCCAAGACC 1065
Db 352 MetGluAsnTrpGlyLeuIleThrTyrArgGluGlySerValLeuTyrAspGluAsnLeu 371
Qy 1066 TCTTCGCTTCCGATAAACTGTGGTCACCGAGAGTCAAGCCCATGAACTGCGGCACAG 1125
Db 372 TyrGlyProMetAsnLysGluArgValAlaGluValIleAlaHisGluLeuAlaHisGln 391
Qy 1126 TGGTTGGCACTGGTCAAAATGGAATGGTGGATGATATTTGGCTTAAGGAGGGTTT 1185

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Db 392 TrpPheGlyAsnLeuValThrMetLysTrpTrpAspAsnLeuTrpLeuAsnGluGlyPhe 411  
Qy 1186 GCAAAATCATGAACTTATCCCTGTTAATGCTACATATCCAGAGCTG---CAATTGAT 1242  
Db 412 AlaserPheValGluTyrlleGlyAlaAspPheIleSerAspGlyLeuTrpGluMetLys 431  
Qy 1243 GACTATTCTTCAAGTGTGTTT---GAAGTAATTTACAAAAGATTCAATTGATTCATCC 1299  
Db 432 AspPhePheLeuLeuAlaProTyThrSerGlyIleThrAlaAspAlaValaSerSer 451  
Qy 1300 CCCCCTATCTCCAAACCGGAGCCGACCTCAAAATACAGAAATGTTTGAAGTT 1359  
Db 452 HisProLeuSerPheArgIleAspLysAlaAlaAspValSerGluAlaPheAspIle 471  
Qy 1360 TCCTATACAAAGGAGCTGTATTTGAATATGCTCAAGGATTTTCTCGGTGAGGAGAA 1419  
Db 472 ThrTyArgLysGlyAlaSerValLeuGluMetLeuLeuAsnLeuValGlyAspGluAsn 491  
Qy 1420 TTCAGAAAGGATTAATTCAGTACTTAAGAGTTTCAGTATAGAAATGCTAAGATCAT 1479  
Db 492 PheLysGlnSerValSerArgTyrlleLysLysPheSerTyThrAspAsnAlaAlaGlu 511  
Qy 1480 GACTTGTGGAGAGCTGTGCAATAGTTGTTTGAAGAGTGATTTTACATCTGGTGGAGTT 1539  
Db 512 AspLeuTrpAlaAlaPhe-----AppGluThrValGlnGlyIle 524  
Qy 1540 TGTCAATCCGATCCCAAGATGCAAGTAAACATGCTCGCTTTCTCGGGGAAATGACAG 1599  
Db 525 -----ThrGlyProAsn-----GlyGlyProLeuLys 533  
Qy 1600 GTCAAGAGATGATCATACATGGAATCTCCAGAAAGGAAATCCCTCTGTTGTTTAA 1659  
Db 534 MetSerGluPheAlaProGlnTrpThrGlnMetGlyPheProValLeuThrValGlu 553  
Qy 1660 CAA---GACGGTGTCTACCTCGAGCTCAACAGAGCGCTTCTCCAGGGGGTTTCCAG 1716  
Db 554 SerValAsnAlaThrThrLeuLysValThrGlnLysArgTyArgGlnAsnLysAspAla 573  
Qy 1717 GAAGACCTGAA---TGGAGGCCCTCGCAGGAGGTACCTGTGCATATATCCCATTTGACC 1773  
Db 574 LysGluProGluLysTyArgHisProThrTyArgLysPheLysTrpAspValProLeuTrp 593  
Qy 1774 TACTCCAGAGTCTTCTAATGTGATCCACAGACACATCTTAAATCAAGACAGATACT 1833  
Db 594 TyrGlnGluAspGluGlnGlnValLysArgThrTrpLeuLysArgGluGluProLeuTy 613  
Qy 1834 CTGGATCTACCTGAAACAGACAGTGTGGTGAATTTAATGTGGACTCAATGGTTACTAC 1893  
Db 614 PheHisValSerAsnSerAspSerSerValValValAsnAlaGluArgAlaPheCys 633  
Qy 1894 ATCGTTCACTATGAGGGTCATGGATGGGACCAACTCATTACACAGCTGAATCAGAACAC 1953  
Db 634 ArgSerAsnTyArgAlaAsnGlyTrpArgAsnIleMetArgArgLeuLysGlnAsnHis 653  
Qy 1954 ACATTTCTCAGACCTTAAGACAGAGTAGTGTGATCATGTATGTGTTTTCAGCTAGTTGGT 2013  
Db 654 LysValTyGlyProArgThrArgAsnAlaLeuIleSerAspAlaPheAlaAlaAla 673  
Qy 2014 GCAGGGAGACTGACCTCAGACAAAGCTCTTCAGCATGACTTACTACTCCACATGAAACA 2073  
Db 674 ValGluGluMetAsnTyGluThrValPheGluMetLeuLysTyThrValLysGluGlu 693  
Qy 2074 AGCAGCCCGCAGCTTCTCGAAGGTCTGATGTACTTTGGAATCGTTTACCACATGATGAC 2133  
Db 694 AspTyLeuProTrpLysGluAlaIleSer-----GlyPheAsnThrIleLeuAsp 710  
Qy 2134 AGAAGGAATATTTTCAGATATCTCTGAAACCTCAAGCGTTACTTCTTCCAGTATTTAAG 2193  
Db 711 PhePheGlySerGluProGluSerGlnTrpAlaSerGluTyMetArgLysLeuMetLys 730  
Qy 2194 CCAGTGATTTGACAGGCAAGC-----TGGAGTGACAGGGCTCA 2232  
Db 731 ProIleTyAspLysSerIleLysPheIleAlaGluAsnTyLysLysAspSerLeu 750

Qy 2233 GTCTGGGACAGAGTGTCCGCTCGCTCTCTTTGAAGCTGGCTGTGACCTGAACCATGCT 2292  
Db 751 PhePheLysAsnAsnLeuGlnIleAlaValIleAspThrTyCysGlyLeuGlyGlyLys 770  
Qy 2293 CCTTGCATCCAGAAAGCTGCTGAACCTCTTCTCCAG-----TGG 2331  
Db 771 GluCysLeuGluGluMetLysLeuPheAspLysGluValMetLysCysGlnProGly 790  
Qy 2332 ATGGAATCCAGTGAAATTAATATATACCAACAGATGTTTAAAGATTGTGTATTCTGTG 2391  
Db 791 GlnGlnAlaThrAspCysValLysValThrAlaProLeuArgLysThrValTyCysTy 810  
Qy 2392 GGTCTCAGACAC-----ACAGCAGGATGGAATTTACCTTTTAGACAAATATGAATGTCA 2445  
Db 811 GlyValGlnGluGlyGlyAspGluAlaPheAspLysValMetGluLeuTyAsnAlaGlu 830  
Qy 2446 ATGTCAGTGTGCAACAAACAAATTTCTGTATCTTGTCTCAACAGCAGCAACATCAGAA 2505  
Db 831 GlnValGlnLeuGluLysAspSerLeuArgGluAlaLeuGlyCysHisLysAspValThr 850  
Qy 2506 AAGTTACTGAAGTTAATTTGAACCTAGGAATGGAA-----GGAAAGGTTTATCAAGACACAG 2559  
Db 851 AlaLeuLysGlyLeuLeuMetLeuAlaLeuAspArgAsnSerSerPheValArgLeuGln 870  
Qy 2560 AACTTGGCAGCTCTCTTCATGCGATTTGCCAGAGCTCCAAAGGGGCGAGCAATAGCATGG 2619  
Db 871 AspAlaHisAspValPheAsnIleValSerArgAsnProValGlyAsnGluLeuPhe 890  
Qy 2620 GATTTCTTAAGAGAAATTTGGACCCATCTTCTGTAATAAATTTTGACTTGGGCTCATATGAC 2679  
Db 891 AsnPheLeuThrGluArgTrpGluIleLeuLeuSerLeuSerIleArgHisArgSer 910  
Qy 2680 ATAAGGATGATCATCTCTGGCACAACAGCTCCTTTTCTTCCAAAGGATAAGTTGCAAGAG 2739  
Db 911 ValAspArgValIleLysAlaCysThrArgGlyLeuArgSerArgGluGlnValGlnGln 930  
Qy 2740 GTGAAACTATTTTGAATCTCTTTGAGCTCAAGGATCATCTGGATATTTTCAAACT 2799  
Db 931 LeuLysAsnLeuTyLysAsn---AspLysArgAlaArgGluTyArgLysPheGlyGly 949  
Qy 2800 GTTCTGCAACAGCAACCAAAATATAAATATGCTGGAGGAGAAATCTTCCGACTCTG 2856  
Db 950 AlaIleGluArgSerGluHisArgValTyTrpIleGluLysHisPheArgLysLeu 968  
RESULT 12  
US-08-335-844A-24  
; Sequence 24, Application US/08335844A  
; Patent No. 6066503  
; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, MARGARET  
; APPLICANT: SMITH, TREVOR STANLEY  
; APPLICANT: MUNN, EDWARD ALBERT  
; APPLICANT: KNOX, DAVID PATRICK  
; APPLICANT: OLIVER, JOHANNA JANE  
; APPLICANT: NEWTON, SUSAN ELIZABETH  
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-335-844A-24

Alignment Scores:
Pred. No.: 6.88e-103 Length: 972
Score: 1117.00 Matches: 279
Percent Similarity: 48.93% Conservative: 199
Best Local Similarity: 28.56% Mismatches: 391
Query Match: 22.07% Indels: 108
DB: 3 Gaps: 25

US-10-039-073-3 (1-2883) x US-08-335-844A-24 (1-972)

Qy 115 TCAGTGCATCTAGTTATCACTTCACT-----GAGGATCCTGGG 153
Db 32 SerileGlyLeuThrTyrPheThrArgLysAlaPheAspThrSerGluLysProGly 51
Qy 154 GCT-----TTCCAGTAGCCACTAATGGGAACGA 183
Db 52 LysAspAspThrGlyGlyLysAspLysAspAsnSerProSerAlaAla----- 67
Qy 184 TTTCTTGGCAGGAGCTTAAGGCTCCCGAGTGTGCTCATCTCTCCATTATGACCTTTT 243
Db 68 -----GluLeuLeuLeuProSerAsnileLysProLeuSerTyrAspLeuThr 83
Qy 244 GTC-----CACCCCAATCTCACCTCTCTGGACTTTGTT 276
Db 84 IleLysThrTyrLeuProGlyTyrValAspPheProGluLysAsnLeuThrPheAsp 103
Qy 277 GCATCTGAGAAGATCGAAGTCTTGGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGC 336
Db 104 GlyArgValGluIleSerMetValIleGluProThrLysSerIleValLeuAsnSer 123
Qy 337 AAAGATCTTGAATCAGCAATGCCACCTTCCAGTCAGAGGAAGATTCAAGATACATGAAA 396
Db 124 LysLysIleSerValIle-----ProGlnGluCysGluLeuValSer 137
Qy 397 CCAGAAAGAACGTAAAGTTTGAAGT-----TACCTGTCTCATGACAAATGCA 447
Db 138 GlyAspLysLysLeuGluIleGluSerValLysGluHisProArgLeuGluLysValGlu 157
Qy 448 CTGCTGGTTCCAGAGAATCTACGCCCTCACCTGAATACTATGTGGCTATGGACTTCCAA 507
Db 158 PheLeuIleLysSerGlnLeuGluLysAspGlnIleLeuLeuLysValGlyTyrIle 177
Qy 508 GCCAAGTTAGGTGCTTGAAGGTTTTATAAAAAGCACATACAGAACTCTTGGTGGT 567
Db 178 GlyLeuIleSerAsnSerPheGlyGlyIleTyrGlnThrTyrThrProAspGly 197
Qy 568 GAAACAGAAATCTTGCAGTAAACAGATTTTGAGCCCAACCCAGGACCGCATGGCTTCCCT 627
Db 198 ThrProLysIleAlaAlaValSerGlnAsnGluProIleAspAlaArgMetValPro 217

628 TGCTTTGATGAACCGTTGTTCAAAGCCAACTTTTCAATCAAGATACGAAAGAGAGCAGG 687
Db 218 CysMetAspGluProLysTyrLysAlaAsnThrValThrValIleHisProLysGly 237
Qy 688 CATATTGCACTATCCAACTGCGCAAGGTTAAG---ACAATTGAACCTTGAAGAGGCTCTT 744
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Db 278 SerGluPheGluTyrIleGluGlyGluThrLysThrGlyValArgPheArgIleTrpSer 297
Qy 865 TCCCCAGACAAACGGAATCAACACATTTATGCTTTGCAGGCATCATGAAGCTACTTGAT 924
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Qy 925 TTTTATGAAAAGTACTTTGATATCTACTATCTCACTCTCCAACTGGAATTTAATGCTATT 984
Db 318 PheTyrGluAspPhePheAspIleArgPheProLeuLysLysGlnAspMetIleAlaLeu 337
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Qy 1045 CTGCTTTTGAACCCCAAGACCTCTTCTGCTCCGATAAATCTGGGTGACAGAGTCATA 1104
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Qy 1165 ATTTGCTTTAAGGAGGTTTTCAAAATACATCAACTTATC---GCTGTTAATGCTTACA 1221
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Qy 1222 TATCCAGAGCTGCAATTTGATGACTATTTTTTG---AATGTGTGTTTTGAAGTAATTACA 1278
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Qy 1519 GATTTTACATCTGCTGGAGTTTGTCTATTCGATCCCAAGATGACAAAGTAAACATGCTGCC 1578
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Qy 1579 TTTCTGGGGAAATGCGAGGTCGAAGAGATGATGACTACATGGAAGTCTCCGAAAGGA 1638
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 580 LysTrpAspIleProLeuTrpTyrGlnGluGlyAspLysLysGluLysLysArgThrTrp 599  
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 600 LeuArg---ArgAspGluProLeuTyrLeuHisValSerAspAlaGlyAlaProPheVal 618  
 1870 ---AATGTGACTCAATGGTTACTACATCGTTCTACTATGAGGTCATGGATGGACCAA 1926  
 619 ValAsnAlaAspArgTyrGlyPheTyrArgGlnAsnHisAspAlaAsnGlyTrpLysLys 638  
 1927 CTCATTACACACTCAATCAGACACACACACTTCTCAGACCTTAAGCAGACAGTAGTCTG 1986  
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 2158 GAAACCTCAAGCGTTTACCTTCTCAGTATTTTAAGCCAGTGATTGACAGGCAAGC--- 2214  
 713 LysProAlaGlnThrTyrMetMetAsnIleLeuLysProMetTyrGluLysSerIle 732  
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 753 AspValIleAspMetPheCysAlaLeuGlySerGlnAspCysArgLysLysTyrLysLys 772  
 2317 CTCTTC---TCCAGTGGTGAATCCAGTGGGAAATTAATATATACCAACAGATGTTT 2373  
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 2374 AAGATT-----GTGTATCTGTGGTGTCTCAGACACAGCAGGA 2412  
 793 ArgIleAlaAlaProLeuArgSerSerValTyrCysTyrGlyValLys-----GluGly 810  
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 811 GlyAspTyrAlaSerAspLysValMetGluLeuTyrThrAlaGluThrLeuAlaLeuGlu 830  
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 US-09-129-366-24  
 ; Sequence 24, Application US/09129366  
 ; Patent No. 6534638  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRAHAM, MARGARET  
 ; APPLICANT: SMITH, TREVOR STANLEY  
 ; APPLICANT: MUNN, EDWARD ALBERT  
 ; APPLICANT: KNOX, DAVID PATRICK  
 ; APPLICANT: OLIVER, JOANNA JANE  
 ; APPLICANT: NEWTON, SUSAN ELIZABETH  
 ; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING  
 ; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF  
 ; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS  
 ; NUMBER OF SEQUENCES: 73  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
 ; STREET: Suite 701-E, 555 Thirteenth St., N.W.  
 ; CITY: Washington  
 ; STATE: D. C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/129,366  
 ; FILING DATE: 05-AUG-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/335,844  
 ; FILING DATE: 09-JAN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB PCT/GB93/00943  
 ; FILING DATE: 06-MAY-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9209936  
 ; FILING DATE: 08-MAY-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: ERNST, Barbara G.  
 ; REGISTRATION NUMBER: 30,377  
 ; REFERENCE/DOCKET NUMBER: 1181-241A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)783-6040  
 ; TELEFAX: (202)783-6031  
 ; INFORMATION FOR SEQ ID NO: 24:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 972 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-129-366-24  
 Alignment Scores:  
 Pred. No.: 6.88e-103 Length: 972  
 Score: 1117.00 Matches: 279  
 Percent Similarity: 48.93% Conservative: 199  
 Best Local Similarity: 28.56% Mismatches: 391  
 Query Match: 22.07% Indels: 108  
 DB: 4 Gaps: 25

US-10-039-073--3 (1-2883) x US-09-129-366-24 (1-972)

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Qy 154 GCT-----TTCCCGTAGCCACTAATGGGAACGA 183  
Db ||| |  
Db LysAspAspThrGlyGlyLysAspLysAspAsnSerProSerAlaAla----- 67

Qy 184 TTTTCTTGCCAGAGCTAAGGTCCCAGTGGTTCATTCTCTCCATTATGACCCTTTT 243  
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Qy 244 GTC-----CACCCCCAACTCTCACCTCTCTGGACTTTGTT 276  
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Db IleLysThrTyrrLeuProGlyTyrrValAspPheProGluLysAsnLeuThrPheAsp 103

Qy 277 GCATCTGAGAAGATCGAAGCTTGTCAGCAATGTACCAGTTTATCATCTTCGACAGC 336  
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Db GlyArgValGluIleSerMetValVallieGluProThrLysSerIleValLeuAsnSer 123

Qy 337 AAGATCTTCAAATCACAATGCCCTTCAGTCAGAGGAAGATTCAAGATACATGAAA 396  
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Db LysLysIleSerVallie-----ProGlnGluCysGluLeuValSer 137

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Db PheLeuIleLysSerGlnLeuGluLysAspGlnGlnIleLeuLeuLysValGlyTyrrIle 177

Qy 508 GCCAAGTTAGGTCTTGAAGGTTTATAAAGGCATACACACATCCTTGGTGGT 567  
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Db GlyLeuIleSerAsnSerPheGlyGlyIleTyrrGlnThrTyrrThrProAspGly 197

Qy 568 GAACAAGAAATCTTGAGTAACAGATTTTGAGCAACCCAGGCACGATGGCTTCCCT 627  
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Db ThrProLysIleAlaAlaValSerGlnAsnGluProIleAspAlaArgMetValPro 217

Qy 628 TGCTTTGATGAACCGTTGTTCAAGCCAACTTTTCAATCAAGATACGAAGAGAGCAGG 687  
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Db CysMetAspGluProLysTyrrLysAlaAsnTrpThrValThrValIleHieProLysGly 237

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Db ThrLysAlaValSerAsnGlyIleGluValAsnGlyAspGlyGluIleSerGlyAspTrp 257

Qy 745 TTGAAGATCATTGTGAAGAACTACTGTAAAATAGTACATACCTTGTAGCCTACATAGTT 804  
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Qy 805 TGTGATTTCCACTCTGAGTGGCTTCACTTCCATCAGGGGTCAAGSTGTCCTATATGCA 864  
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Db SerGluPheGluTyrrIleGluGlyGluThrLysThrGlyValArgPheArgIleTrpSer 297

Qy 865 TCCCAGACAAACCGAATCAACACATATATGCTTTGCGAGGCATCATGAAGCTACTTGAT 924  
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Db ArgProGluAlaLysLysMetThrGlnTyrrAlaLeuGlnSerGlyIleLysCysIleGlu 317

Qy 925 TTTTATGAAGAAGTACTTTGATATCTACTATCCACTCTCCAAACTGGATTTAATTCGTATT 984  
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Qy 985 CCTGACTTTCGACCTGGAGCCTAAGAAATTCGGGCCCTCATTTACATATAGGGAGAGCTCA 1044  
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RESULT 14
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; Sequence 23, Application US/08335844A
; Patent No. 6066503
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, MARGARET
; APPLICANT: SMITH, TREVOR STANLEY
; APPLICANT: MUNN, EDWARD ALBERT
; APPLICANT: KNOX, DAVID PATRICK
; APPLICANT: OLIVER, JOANNA JANE
; APPLICANT: NEWTON, SUSAN ELIZABETH
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
; TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
; TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
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; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,844A
; FILING DATE: 09-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: GB PCT/GB93/00943
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9209936
; FILING DATE: 08-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 1181-223A
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; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-335-844A-23

Alignment Scores:
Pred. No.: 3,51e-101 Length: 972
Score: 1100.00 Matches: 284
Percent Similarity: 47.02% Conservative: 190
Best Local Similarity: 28.17% Mismatches: 390
Query Match: 21.73% Indels: 144
DB: Gaps: 26

US-10-039-073-3 (1-2883) x US-08-335-844A-23 (1-972)

QY 88 CCCAAATATGCATTTGTTCTCAGTTC-----TCAGTGCCA 123
   ||| : : : : : : : : : : : : : : : : : :
Db 15 ProIleSerLeuLeuCysThrLeuPheValLeuAlaAlaValGlyLeuSerIleGly 34
   : : : : : : : : : : : : : : : : : :
QY 124 TCTAGTTATCACTTCACCT-----GAGGAT 147
   : : : : : : : : : : : : : : : : : :
Db 35 LeuThrTyrTyrPheThrArgLysAlaPheAspThrThrGlnLysGluGlnLysAspAsp 54
   ||| : : : : : : : : : : : : : : : : : :
QY 148 CTTGGGGCT-----TTCCAGTAGCCACTAATGGGGAACGATTTCTTTGG 192
   ||| : : : : : : : : : : : : : : : : : :
Db 55 SerGlyGlyLysGluLysAspAsnSerProSerAla----- 66
   ||| : : : : : : : : : : : : : : : : : :
QY 193 CAGGAGCTAAGGCTCCCGAGTGGTGCATTCCTCTCCATATGACCTCTTTGTC----- 246
   : : : : : : : : : : : : : : : : : :
Db 67 GluGluLeuLeuLeuProThrAsnIleLysProValSerTyrAspLeuAsnIleLysThr 86
   : : : : : : : : : : : : : : : : : :
QY 247 -----CACCCCAATCTCACCTCTCGGACTTTGTTGCATCTCGAG 285
   ||| : : : : : : : : : : : : : : : : : :
Db 87 TyrLeuProGlyTyrValAsnPheProGluLysAsnLeuThrPheAspAlaHisVal 106
   : : : : : : : : : : : : : : : : : :
QY 286 AAGATCGAAGTCTTTGGTCAGCAATGCTACCCAGTTTATCATCTTGCACAGCAAGATCTT 345
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Db 107 GluIleAlaMetValValGluProThrAsnSerIleValLeuAsnSerLysLysIle 126
   : : : : : : : : : : : : : : : : : :
QY 346 GAAATCATCAAGATGCCACCTTCTAGTCAGAGAGATTCAGATACATGAAACACAGGAAA 405
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QY 406 GAACGTGAAGCTTTTGAGTTACCTGCTCATGAA-----CAAATGGCACTCTGTT 456
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Db 141 LysLeuAspIleGluSerValLysMetGlnGluArgLeuAspLysLeuGluIleThrLeu 160
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Db 261 LysPheLysThrThrProProMetSerSerTyrLeuLeuAlaIleIleValCysGluPhe 280  
Qy 814 CACTCTCTGAGTGCTTCACTTCATCAGGGTCAAGGTGCTCATCTATGATCCCCAGAC 873  
Db 281 GluTyrIleGluGlyPheThrLysThrGlyValArgPheArgIleIlePheArgProGlu 300  
Qy 874 AAACGGAAATCAACACACATATGCTTTCAGCGCATCACTGAAGCTACTTGAATTTTATGAA 933  
Db 301 AlaLysArgMetThrAlaTyrAlaLeuAspAlaGlyIleArgCysLeuGluPheTyrGlu 320  
Qy 934 AAGTACTTTGATATCTACTACTCTCTCCAACTCGAATTAATTAATGCTATTCCTGACTTT 993  
Db 321 LysPhePheAspIleLysPheProLeuGluLysGlnAspMetIleAlaLeuProAspPhe 340  
Qy 994 GCACCTGAGCGCATGGAAATTTGGGCTCATATACATATAGGAGACGTCACCTGCTTTT 1053  
Db 341 ThrAlaGlyAlaMetGluAsnTrpGlyLeuIleThrTyrArgGluAspSerLeuLeuTyr 360  
Qy 1054 GACCCCAAGACCTCTTCTGCTTCGATAACTGTGGGTCCACGAGTCATAGCCCCATGAA 1113  
Db 361 AspGluLysIleTyrAlaProMetAsnLysGlnArgValAlaLeuValAlaAlaHisGlu 380  
Qy 1114 CTGGCGCACCGTGGTTGGCACTGTCACATGGAATGGTGAATGATATTTGGCTT 1173  
Db 381 LeuAlaHisGlnTrpPheGlyAsnLeuValThrLeuLysTrpTrpAspAspThrTrpLeu 400  
Qy 1174 AAGGAGGTTTTCGAAATACATCGAACTTATCGCTGTTAAT---GCTACATATCCAGAG 1230  
Db 401 AsnGluGlyPheAlaThrPheValGluTyrLeuGlyMetAspGluIleSerHisAsnAsn 420  
Qy 1231 CTGCAATTTGATGACTATTTT---TTGAATGTGTGTTTGAAGTAATTAACAAAGATTCA 1287  
Db 421 PheArgThrGlnAspPhePheLeuLeuAspGlyMetAspArgGlyMetArgAlaAspSer 440  
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Db 441 AlaAlaSerSerHisProLeuSerPheArgIleAspLysAlaAlaGluValAlaGluAla 460  
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Db 461 PheAspIleSerTyrAlaLysGlyAlaSerValLeuThrMetLeuArgAlaLeuIle 480  
Qy 1408 GGTGAGGAAATTCAGAAAGGAATAATTCACTACTTAAGAAAGTTCACTATAGAAAT 1467  
Db 481 GlyLysAspAsnTyrArgAsnAlaValGlnTyrLeuLysLysPheSerTyrSerAsn 500  
Qy 1468 GCTAAGAAATGATGACTGTGGAGCAGTCTGCAATAGTTGTTTGAAGAGTATTTACA 1527  
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Qy 1528 TCTGCTGGAGTTTCTCATTCCGATCCCAAGATGACAAGTAACATGCTCGCTTCTGGGG 1587  
Db 516 -----GlyValLysGlyProAsp-----Gly 522  
Qy 1588 GAAATCAGAGGTCAAGAGATGATGACTACATGGAATCTCCAGAAAGGAATCCCGCTG 1647  
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Qy 1648 CTGCTGTTTAAACAA---GACGGTGTTCACCTCGACTGCACACGAGGCGCTTCTCCAG 1704  
Db 543 ValLysValGluGluPheAsnAlaThrAlaLeuLysValThrGlnSerArgTyrLysThr 562  
Qy 1705 GGGGTTTTCCAGGAAGACCTGAA---TGGAGGCGCTCGAGGAGAGGTACCTGTGGCAT 1761  
Db 563 AsnLysAspAlaLeuGluProGluLysTyrArgAsnProLysTyrGlyPheLysTrpAsp 582  
Qy 1762 ATCCATTTGACCTACTCCACGAGTTCTTCTAATGTGATCCACACACACATTTCTAAATCA 1821  
Db 583 ValProLeuTrpTyrGlnGluGlyAsnSerLysGluValLysArgThrTrpLeuLysArg 602  
Qy 1822 AAGCACATACT---CTGGATCTACCTGAAAGACAGTGGGTGGAATTTAATGTGGAC 1878  
Db 603 AspGluProLeuTyrLeuAsnValAsnAsnArgAspThrSerLeuValValAsnAlaAsp 622

Qy 1879 TCAATGGTTTACTACATCGTTCACTATGAGGGTTCATGGATGGACCAACTCATTTACACAG 1938  
Db 623 ArgHisGlyPheTyrArgGlnAsnTyrAspAlaAsnGlyTyrLysLysIleIleLysGln 642  
Qy 1939 CTGAATCAAGAACACACACTTCTCAGACCTAAGACAGAGTAGGTCTGATTCATGATGTG 1998  
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Qy 1999 TTTACAGTAGTTGGTCAGGAGACGTGACCTAGACAAAGCTCTTGACACTGACTTACTAC 2058  
Db 663 PheAlaAlaAlaThrIleAspAlaIleAspTyrGluThrValPheGluLeuLeuGluTyr 682  
Qy 2059 CTCACCAATCAA----- 2070  
Db 683 AlaLysAsnGluGluGluPheLeuProTrpLysGluAlaLeuSerGlyMetPheAlaVal 702  
Qy 2071 -----ACAAGCAGCCCGCCTTCTCAGAGCTCTGAAAGCTGAGTTTAC 2106  
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Qy 2167 AAGCGTTACTCTTCTTCAAGCCAGTATTAAAGCCAGTATTGACAGGCAAGCTGGAGTGAAG 2226  
Db 737 LysAsnTyrLeuAspAspThrLeuPheThrLysIleAsnThrGln----- 751  
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Db 752 -----LysAspIleIleAspAlaTyrCysSerLeuGly 762  
Qy 2287 CATGCTCTTCGATCCAGAAAGCTGCTGAACCTTTC---TCCCAGTGGATGGAATCCAGT 2343  
Db 763 SerLysAspCysIleLysGlnTyrLysAspIlePheTyrAspGluValMetProLysCys 782  
Qy 2344 GGAATTAATAATATACCAACAGATGTTTAAAGATT-----GTG 2382  
Db 783 LysAlaGlyGluAlaAlaThrLysCysValLysValSerAlaProLeuArgAlaAsnVal 802  
Qy 2383 TATTCGTGGGTGCTCAGACAAACAGCAGATGGAAT----- 2418  
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Qy 2419 TACCTTTTAGACCAATATCACTGTCAATGCTCAAGTCTGAAGTCTGAACAAACAAATTTCTGTAT 2478  
Db 822 TyrLeuAlaGluAspValGlnLeu-----GluLysGlyIleLeuPheLys 836  
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Qy 2533 ATGGAAGGAAAGTTATCAAGACACAGAACTTGGCAGCTCTCTTCATCGGATGCCAGA 2592  
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Db 917 IleArgSerGlnGlnIleAspGlnLeuLys---AsnLeuGlnLysAsnAlaGln 935  
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956 ILeuLySHisPheHisArgLeu 963

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